(19) World Intellectual Property Organization International Bureau



(43) International Publication Date 26 July 2001 (26.07.2001)

PCT

(10) International Publication Number WO 01/53312 A1

- (51) International Patent Classification⁷: C07H 21/04, C12N 15/11, 15/63, 15/70, 15/82, 15/85, C07K 14/00
- (21) International Application Number: PCT/US00/34263
- (22) International Filing Date:

26 December 2000 (26.12.2000)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

09/488,725	21 January 2000 (21.01.2000)	US
09/552,317	25 April 2000 (25.04.2000)	US
09/598,042	9 July 2000 (09.07.2000)	US
09/620,312	19 July 2000 (19.07.2000)	US
09/653,450	3 August 2000 (03.08.2000)	US
09/662,191	14 September 2000 (14.09.2000)	US
09/693,036	19 October 2000 (19.10.2000)	US
09/727,344	29 November 2000 (29.11.2000)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US	09/488,725 (CIP)
Filed on	21 January 2000 (21.01.2000)
US	09/552,317 (CIP)
Filed on	25 April 2000 (25.04.2000)
US	09/598,042 (CIP)
Filed on	9 July 2000 (09.07.2000)
US	09/620,312 (CIP)
Filed on	19 July 2000 (19.07.2000)
US	09/653,450 (CIP)
Filed on	3 August 2000 (03.08.2000)
US	09/662,191 (CIP)
Filed on	14 September 2000 (14.09.2000)
US	09/693,036 (CIP)
Filed on	19 October 2000 (19.10.2000)
US	09/727,344 (CIP)
Filed on	29 November 2000 (29.11.2000)

(71) Applicant (for all designated States except US): HYSEQ, INC. [US/US]; 670 Almanor Avenue, Sunnyvale, CA 94086 (US).

- (72) Inventors; and
- (75) Inventors/Applicants (for US only): TANG, Y., Tom [US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). LIU, Chenghua [CN/US]; 1125 Ranchero Way #14,

San Jose, CA 95117 (US). ASUNDI, Vinod [US/US]; 709 Foster City Boulevard, Foster City, CA 94404 (US). CHEN, Rui-hong [US/US]; 1031 Flying Fish Street, Foster City, CA 94404 (US). MA, Yunqing [CN/US]; 280 W. California Avenue #206, Sunnyvale, CA 94086 (US). QIAN, Xiaohong, B. [CN/US]; 3662 Tumble Way, San Jose, CA 95132 (US). REN, Feiyan [US/US]; 7703 Oak Meadow Court, Cupertino, CA 95014 (US). WANG, Dunrui [CN/US]; 932 La Palma, Milpitas, CA 95035 (US). WANG, Jian-Rui [CN/US]; 744 Stendhal Lane, Cupertino, CA 95014 (US). WANG, Zhiwei [CN/US]; 836 Alturas Avenue, B36, Sunnyvale, CA 94085 (US). WEHRMAN, Tom [US/US]; 3210 CCSR Mol Pharm, 269 W. Campus Drive, Stanford, CA 94305 (US). XU, Chongjun [CN/US]; 4918 Manitoba Drive, San Jose, CA 95130 (US). XUE, Aidong, J. [CN/US]; 1621 S. Mary Avenue, Sunnyvale, CA 94087 (US). YANG, Yonghong [CN/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). ZHANG, Jie [CN/US]; 4930 Poplar Terrace, Campbell, CA 95008 (US). ZHAO, Qing, A. [CN/US]; 1556 Kooser Road, San Jose, CA 95118 (US). ZHOU, Ping [CN/US]; 1461 Japaul Lane, San Jose, CA 95132 (US). GOODRICH, Ryle [US/US]; 4896 Sandy Lane, San Jose, CA 95124 (US). DRMANAC, Radoje, T. [YU/US]; 850 East Greenwich Place, Palo Alto, CA 94303 (US).

- (74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky, and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

- with international search report
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

[Continued on next page]

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.





For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

5

10

15

20

25

30

35

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, fer example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1786 and 3573-5358. The polypeptides sequences are designated SEQ ID NO: 2n (wherein n = 1 to 20). The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

5

10

15

20

25

30

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1786 and 3573-5358 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-1786 and 3573-5358. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1786 and 3573-5358 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1786 and 3573-5358.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

5

10

15

20

25

30

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1-1786 and 3573-5358; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO:1-1786 and 3573-5358. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1786 and 3573-5358; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention.

Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

10

15

20

25

30

35

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., in situ hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention.

Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

10

15

20

25

30

35

5

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady

and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

5

10

15

20

25

30

35

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30

nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-20.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1786 and 3573-5358. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4²⁰ possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match $(1 \div 4^{25})$ times the increased probability for mismatch at each nucleotide position (3×25) . The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

5

10

15

20

25

30

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

9

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

5

10

15

20

25

30

35

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e.g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

5

10

15

20

25

30

35

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in ³ the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

. 11

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

5

10

15

20

25

30

35

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

5

10

15

20

25

30

35

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The

term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Ø

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

5

10

15

20

25

30

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1787-3572 and 5359-7144; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1787-3572 and 5359-7144. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1786 and 3573-5358; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO:1787-3572 and 5359-7144. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

5

10

15

20

25

30

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in

15

the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

5

10

15

20

25

30

35

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1786 and 3573-5358, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1786 and 3573-5358 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1786 and 3573-5358, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g.,

hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., DNA 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

5

10

15

20

25

30

35

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1786 and 3573-5358, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following

18

PCT/US00/34263 WO 01/53312

vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

5

10

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are 15 pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, ξ, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. 20 Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid 25 phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired 30 characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the 35 vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for

٠,

transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

5

10

15

20

25

30

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO:1787-3572 and 5359-7144 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1786 and 3573-5358 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

5

10

15

20

Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO:1-1786 and 3573-5358, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, 25 inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, 30 queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the 35

inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

5

10

15

20

25

30

35

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) Nature 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (i.e., SEQ ID NO:1-1786 and 3573-5358). For example, a derivative of a Tetrahymena L-19 IVS RNA can be

constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, e.g., Cech et al. U.S. Pat. No. 4,987,071; and Cech et al. U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel et al., (1993) Science 261:1411-1418.

5

10

15

20

25

30

35

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991)

Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above; Perry-O'Keefe et al. (1996) PNAS 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA

portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem*

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

Lett 5: 1119-11124.

5

10

15

20

25

30

35

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express

24

the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in coamplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., Basic Methods in Molecular Biology (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

10

15

20

25

30

35

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as E. coli and B. subtilis. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK,

HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the

protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

5

10

15

20

25

30

35

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

.. Ť.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:1787-3572 and 5359-7144 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358 or (b) polynucleotides encoding any one of the amino acid sequences

PCT/US00/34263 WO 01/53312

set forth as SEQ ID NO:1787-3572 and 5359-7144 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1787-3572 and 5359-7144 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:1787-3572 and 5359-7144. 10

5

15

20

25

30

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

5

10

15

20

25

30

35

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1787-3572 and 5359-7144.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

. ... ,

30

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBatTM kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

5

10

15

20

25

30

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearlTM or Cibacrom blue 3GA SepharoseTM; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propylether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

15

20

25

30

35

10

5

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al., ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

10

15

20

25

30

35

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e,g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

5

10

15

20

25

30

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered in vivo to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

5

10

15

20

25

30

35

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

5

10

15

20

25

30

35

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

5

10

15

20

25

30

35

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

5

10

15

20

25

30

35

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

5

10

15

20

25

30

35

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

5

10

15

20

25

30

35

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells in vivo or ex vivo is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

1,5

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

41

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

5

10

15

20

25

30

35

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

5

10

15

20

25

30

35

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

15

10

5

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

20

25

30

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

5

10

15

20

25

30

35

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular

45

endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

5

10

15

20

25

30

35

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus,

5

10

15

20

25

30

35

rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastborn et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic

composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

5

10

15

20

25

30

35

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

48______

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

5

10

15

20

25

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β₂ microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a Tell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and

Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

5

10

15

20

25

30

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

5

10

15

20

25

30

35

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

. .

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

15

20

10

5

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

25

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

30

35

4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention

52

may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide,

53

35

5

10

15

20

25

30

Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cisDDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin,
Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213),
Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide,
Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog),
Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna,
Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl,
Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate,
Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin,
Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

15

20

25

30

35

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen

.

recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

5

10

15

20

25

30

35

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such

transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

5

10

15

20

25

30

35

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding

molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

5

10

15

20

25

30

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (i.e., increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

57

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

30

35

5

10

15

20

25

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or

58

disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

5

10

15

20

25

30

35

- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or

differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

(i) increased survival time of neurons in culture;

5

10

15

20

25

30

35

- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
 - (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or

elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified

nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

25

30

35

20

5

10

15

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of

administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about $0.01\mu g/kg$ to 100 mg/kg of body weight, with the preferred dose being about $0.1\mu g/kg$ to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

`4" ·

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

5

10

15

20

25

30

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic

factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

5

10

15

20

25

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

30

35

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be

65

5

10

15

20

25

30

35

manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers

5

10

415

20

25

30

35

enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with

an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well

known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

5

10

15

20

25

30

35

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable

lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

5

10

15

20

25

30

35

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1 µg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions

may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

5

10

15

20

25

30

35

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, 2, 4 hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications.

Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which

71

modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

5

10

15

20

25

30

35

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC₅₀ as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to 50% of the

population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from in vitro data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 μ g/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 μ g/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

5

10

15

20

25

30

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the

invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

5

10

15

20

25

30

35

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab} , and $F_{(ab)/2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1 , IgG_2 , and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 1787, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte

Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

5

10

15

20

25

30

35

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, a goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the

target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5

10

15

20

25

30

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro. The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego,

35

California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, <u>J. Immunol.</u>, <u>133</u>:3001 (1984); Brodeur et al., <u>Monoclonal Antibody Production Techniques and Applications</u>, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

5

10

15

20

25

30

35

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal. The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin

polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

5

10

15

20

25

30

35

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigenbinding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal

5

10

15

20

25

30

antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al. (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 Fab Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab)/2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab)/2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

5

10

15

20 -

25

30

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the

binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

5

10

15

20

25

30

35

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to

PCT/US00/34263 WO 01/53312

stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

5

10

15

20

25

30

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')2 molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_{H} and V_{L} domains of one fragment are forced to pair with the complementary V_{L} and V_{H} domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular 35

defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

10

15

20

25

30

35

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced antitumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ²¹²Bi, ¹³¹I, ¹³¹In, ⁹⁰Y, and ¹⁸⁶Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

5

10

15

20

25

30

35

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon

a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and

software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length. 2.5.3%从图2.666度**T**\$2.5.5。 了**你会要呢**你去你你在这么一个。

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

30

35

5

10

15

20

25

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are

designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

10

15

20

25

30

35

5

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary.

Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid

87

probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

5

10

15

20

2 V 214

25

30

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

5

10

15

20

25

30

35

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
 - (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

5

10

15

20

25

30

35

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

5

10

. 15

20

25

30

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

5

10

15

20

25

30

Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata et al., 1985; Dahlen et al., 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller et al., 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude et al. (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

5

10

15

20

25

30

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

5

10

15

20

25

30

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook et al. (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviJI, described by Fitzgerald et al. (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *CviJI* normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*CviJI***), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *CviJI*** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *CviJI*** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

5

10

15

20

25

30

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm^2 and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

5

10

15

20

25

30

5.1.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.1.2 EXAMPLE 2

5

10

15

20

25

30

Assemblage of Novel Nucleic Acids

The contigs or nucleic acids of the present invention, designated as SEQ ID NO: 3573-5358 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

A polypeptide was predicted to be encoded by each of SEQ ID NO:3573-5358 as set forth below. The polypeptides was predicted using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptides based on a comparison of translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference. The predicted polypeptides are shown in Table 7.

- 1

5.2.2 EXAMPLE 3

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genebank. Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS:1-327.

Table 1 shows the various tissue sources of SEQ ID NO: 1-327.

The nearest neighbor results for SEQ ID NO: 1-327 were obtained by a FASTA version 3 search against Genpept release 117, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-327 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1-327 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the

signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.3.2 EXAMPLE 4

5

10

15

20

25

30

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 328-1413.

Table 1 shows the various tissue sources of SEQ ID NO: 328-1413.

The nearest neighbor results for SEQ ID NO: 328-1413 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 328-1413 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in

the Sequence Listing. The nearest neighbor results for SEQ ID NO: 328-1413 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

25 **5.3.2 EXAMPLE 5**

5

15

20

30

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1414-1652.

Table 1 shows the various tissue sources of SEQ ID NO: 1414-1652.

The nearest neighbor results for SEQ ID NO: 1414-1652 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1414-1652 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1414-1652 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.4.2 EXAMPLE 6

Novel Nucleic Acids

5

10

15

20

25

30

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 118, gb pri 118,

UniGene version 118, Genpept release 118). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1653-1745.

Table 1 shows the various tissue sources of SEQ ID NO: 1653-1745.

5

10

15

20

25

30

The homology for SEQ ID NO: 1653-1745 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1653-1745 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1653-1745 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.5.2 EXAMPLE 7

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 119, gb pri 119, UniGene version 119, Genpept release 119). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1746-1768.

Table 1 shows the various tissue sources of SEQ ID NO: 1746-1768.

5

10

15

20

25

30

The homology for SEQ ID NO: 1746-1768 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 119, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1746-1768 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1746-1768 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the PFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the PFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.6.2 EXAMPLE 8

Novel Nucleic Acids

5

10

15

20

25

30

35

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 120, gb pri 120, UniGene version 120, Genpept release 120). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1769-1786.

Table 1 shows the various tissue sources of SEQ ID NO: 1769-1786.

The homology for SEQ ID NO: 1769-1786 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and the amino acid version of Geneseq released on October 26, 2000, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1769-1786 from Genpept. The homologues with identifiable functions for SEQ ID NO: 1769-1786 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by

reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

Table 6 is a correlation table of all of the sequences and the SEQ ID NOS.

5

TABLE 1

TABLE 1			
Tissue Origin	RNA Source	Hyseq Library Name	. SEQ ID NOS:
adult brain	GIBCO	AB3001	9 19-21 50-51 65-66 72 78 80 82
1	1		85 87 107-108 113 116 123 138
	ł		140 150-152 159 169 177 192-193
	}		202-203 212-214 225-226 235-236
			251 258 268-269 272 280-281 295
,	Ì		298 301 321 326 331-332 334 356-
]	:	357 362 369 379 382-383 416 423
İ	İ		443 459-460 473 475 477 488 496
1;	ļ	1 1	500 503 519 526 547 574 582 587 608-609 613 618 633-634 645-646
1	1		652 657-658 660 669-671 678 687
			695 697 710 715 724 731 775-777
			796 804 811 857-859 862 869 899-
			900 912 919 922 924-929 933 936
ļ	ļ		962 979 988-989 996 1001 1004-
	Ì		1008 1018 1039 1047 1059 1064
			1067 1070 1078 1082 1107 1113
			1116-1117 1131 1134-1137 1140
	ļ		1149 1151 1157 1180 1206 1229
			1234 1241 1243 1258 1272-1273
1			1279 1288-1290 1294 1307-1308
]	,		1312 1320 1323 1330 1356 1360-
1		•	1361 1368 1373-1375 1379 1391
			1400 1417 1446 1468 1482 1493-
			1494 1501-1503 1506-1507 1512
-			1517 1522-1524 1530-1533 1537
			1549 1565 1578 1598 1606 1608 1623 1625 1627 1639 1643 1648-
1			1649 1653 1664 1667 1671 1696
}		,	1734 1741 1743-1744 1760-1761
			1771
adult brain	GIBCO	ABD003	3 12-14 18-19 25 30-31 34-36 43-
			145 50-51 56 58 60 65-66 68-69 80
			45 50-51 56 58 60 65-66 68-69 80 82 85 87 92 104 107-108 112-113
			82 85 87 92 104 107-108 112-113
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192-
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212-
		·	82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259
		·	82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284-
		·	82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192-193 196-197 199 203 208 210 212-214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284-288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476-
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192-193 196-197 199 203 208 210 212-214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284-288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476-478 483 491 494 496 500 503 507-
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192-193 196-197 199 203 208 210 212-214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284-288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476-478 483 491 494 496 500 503 507-508 516 519-520 525-527 534 536-
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192-193 196-197 199 203 208 210 212-214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284-288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476-478 483 491 494 496 500 503 507-508 516 519-520 525-527 534 536-540 542-543 545 555 556 569-
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476- 478 483 491 494 496 500 503 507- 508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569- 570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476- 478 483 491 494 496 500 503 507- 508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569- 570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476- 478 483 491 494 496 500 503 507- 508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569- 570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476- 478 483 491 494 496 500 503 507- 508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569- 570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476- 478 483 491 494 496 500 503 507- 508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569- 570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476- 478 483 491 494 496 500 503 507- 508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569- 570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476- 478 483 491 494 496 500 503 507- 508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569- 570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858-
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476- 478 483 491 494 496 500 503 507- 508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569- 570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858- 861 864 869 874 878 883 897 901-
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476- 478 483 491 494 496 500 503 507- 508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569- 570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858- 861 864 869 874 878 883 897 901- 902 904-905 908 911-914 916 921-
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476- 478 483 491 494 496 500 503 507- 508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569- 570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858- 861 864 869 874 878 883 897 901- 902 904-905 908 911-914 916 921- 902 904-905 908 911-914 916 921- 902 924-927 929 932-934 936-939
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476- 478 483 491 494 496 500 503 507- 508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569- 570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858- 861 864 869 874 878 883 897 901- 902 904-905 908 911-914 916 921-
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476- 478 483 491 494 496 500 503 507- 508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569- 570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858- 861 864 869 874 878 883 897 901- 902 904-905 908 911-914 916 921- 922 924-927 929 932-934 936-939 941-942 945 955-958 963 966-969
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476- 478 483 491 494 496 500 503 507- 508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569- 570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858- 861 864 869 874 878 883 897 901- 902 904-905 908 911-914 916 921- 922 924-927 929 932-934 936-939 941-942 945 955-958 963 966-969 977 979-980 985-986 990 992-993
			82 85 87 92 104 107-108 112-113 115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157 159 163 165 167 169 172 180 192- 193 196-197 199 203 208 210 212- 214 223 233 235-237 247 257 259 261 268-269 272 276 280-281 284- 288 291-292 295 297 300-301 304 307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381 393 401 408 414 419 424 426-428 430 433-436 438-439 443 445 449 453-454 459-461 468 471-473 476- 478 483 491 494 496 500 503 507- 508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569- 570 574-576 586-588 593 595 597 601 606-609 616-620 622-623 625 628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858- 861 864 869 874 878 883 897 901- 902 904-905 908 911-914 916 921- 922 924-927 929 932-934 936-939 941-942 945 955-958 963 966-969 977 979-980 985-986 990 992-993 997-1001 1005-1007 1012 1017-

		_		
Γ	Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
l			Library Name	1097 1103 1107 1109 1112 1116-
Г				1117 1119 1121 1124 1127 1130
	ļ			1134 1144-1145 1149 1151 1157-
ı				1158 1167 1170 1178 1184 1188
١				1190 1193-1194 1200 1202 1215-
1	ļ			1217 1220 1226-1227 1229 1231
1				1241 1243 1247 1252 1258 1263
1				1267 1269 1279 1281 1284 1286-
1				1289 1293-1294 1306-1307 1312
١				1316-1320 1326 1333 1338 1341
1		j		1344 1348 1351 1355-1357 1368
1	ļ			1374 1377 1380 1386 1389-1390
		1		1394 1400 1409 1414 1422-1423
				1425-1427 1437 1443 1446 1454
1		Ì		1456 1458-1459 1468 1470-1472
1				1478 1482-1483 1487-1488 1493
1				1497 1499 1506 1508-1511 1517
1				1522-1524 1530-1533 1545-1546
				1548-1550 1552 1557-1559-1563
		}		1565 1567 1569 1571 1586 1588
1				1591 1593 1595 1598-1601 1608
				1611 1620-1621 1624-1626 1628
				1630-1632 1636 1640-1641 1644-
				1645 1647 1649 1653-1655 1657
1				1664 1667 1669 1673 1678-1681
1		ļ		1686 1690 1694-1696 1701 1709
-		{		1711 1719 1722-1723 1726-1727
1				1731-1733 1738 1740 1743-1744
1				1747 1749 1753 1757-1758 1760-
1				1761 1765 1771 1785
۲	adult brain	Clontech	ABR001	9 29 68-69 113 115 146 152 206
١		1		223 245 277 307 320 324 330-331
- [ł	344 348 352 362 379 384 393 404
-			Į.	408 414 441-442 454 469 481 490
-				506 517 586 597 631 641 659 691
١				715 799 803 833 865 871 875 880
1			{	882 908 920 937 1000 1005-1006
- 1			[,	1027 1036 1041 1043 1075 1107
			1	1112 1121 1127 1136-1137 1144- 1147 1231 1238-1239 1280 1293
: 1			1	1320 1345 1355 1361 1383-1384
				1400 1417 1448 1456 1476 1507
	. :			1570 1572 1609-1610 1614 1620
- 1		į		1626 1645 1653 1754 1759 1770
		1		
- [75555	1786 5-8 15-16 168 212-213 271 278
1	adult brain	Clontech	ABR006	280-281 291-292 300-301 310 314
١		}	1	321 326 336-338 341 352 357 359-
- (360 362 369 374 379 384 393 396-
١				397 414 419-420 426-428 430 441-
				442 453 506 616-617 661 689 785
Ì			1	798 845 1018 1109 1113 1124 1148
		i		1167 1187 1207 1227 1262 1265
		1	1	1285 1312 1317-1319 1324-1327
- 1				1344 1369 1381 1400 1416 1421
		l		1427 1430-1431 1436 1471 1501
		1		1557-1559 1586 1588 1651 1653
		1		1664-1665 1671 1673 1690 1697-
		1		1698 1700 1711 1717 1719-1720
		ļ		1728 1736 1740 1743-1744 1757
		1		1760-1761
	adult brain	Clontech	ABR008	5-10 13-19 22-23 25 29 33 37-39
	gdult prain	CIONCECH	ADMOOD	43-45 50-51 54-55 57-58 60-66
				68-70 72 75 77-80 83 85 89-92 94
				99-105 108-110 112-113 116-117
	Į.		1	123 128 133 135-137 139 143 145-
	ĺ			146 148 152 154-155 157 166 168-
			İ	172 174-175 181-184 188-190 193-
	}	1	1	194 196 198-200 202 204-205 207-
	t .	1	,	

ſ	Tissue Origin	RNA Source	Uses	070 70 100
1	rissue origin	ANA SOUICE	Hyseq Library Name	SEQ ID NOS:
1				208 210 214-215 218 221-226 229
				231-232 234-241 245-247 251-253
1	•			255 257-259 268-269 271 276-281
				285-286 288 290-292 300-302 304
-	;			307 309-311 313 315 317-318 320- 322 325-326 328 330-331 333-338
1				341 344-347 349 352 354 356-357
l	i			362 369-373 376 379-380 382 384
١				387 390-391 393-394 397 399-403
J				405-411 414-415 417-420 426-428
				437-438 440-444 453-455 462 464 467 469-471 476 478 482-484 488-
1				491 497 503 506-513 516-517 520
1				524-526 528-530 532-534 537-540
Į				542 544 547-551 553 561 565-567
-1				572-574 577 581 585 587-588 590-
ļ				591 597 599 601-602 606-610 612 615-617 619-620 622-623 628-629
-				631 633-634 636-641 643 645-647
ĺ	{			651-653 655-664 669-671 673 679
		ļ		682 687 689 691-700 702 706 710
	ł	1		715-717 720-721 725-734 736-739
				742-743 746 750-752 756 758-759
1	j			762-764 766 768 773-778 780-782 784-785 787-789 794 796 799 802-
1	ļ	,		803 805 811 814-815 818 825-826
		1	-	834-837 839-840 842-843 856-859
ļ	-			861-862 865 867-872 874-875 881
1				883-884 887 889-892 894-895 897- 898 901 904 908 910 912 914 917
1		ł		919 921-924 926-927 930-932 935-
		. 1		941 943 945 949 953-954 958 961-
1		j		963 967 969 971 975 977 981-983
İ				986 988-990 992 997 999-1002
		ļ		1004-1006 1008 1012 1018-1023 1027 1029-1031 1035-1037 1047-
ı			-	1048 1053 1057 1059 1063 1068
	1			1070 1072-1075 1077 1081-1083
		[1085-1093 1095-1096 1108-1112
. -				1114-1125 1127 1131-1133 1135-
1	• .	·		1138 1142-1145 1148-1158 1160- 1163 1167 1169 1172 1175 1177
				1180 1183-1188 1191-1195 1199-
1.	,	ľ		1200 1204 1206 1211 1213-1216
1	Ī			1222-1223 1226-1227 1229-1231
	l			1234-1235 1241-1242 1244-1263
	1			1266 1269-1271 1276-1277 1279- 1281 1284-1286 1292 1294-1295
	j			1299 1305-1309 1312 1314 1316-
	_			1319 1322 1324-1327 1330 1332
	·			1334-1335 1339 1344-1346 1351
				1354-1355 1357-1358 1365-1367
	1	1		1369-1370 1373-1374 1376-1379 1381-1384 1386-1388 1392 1394
				1396-1397 1400 1403-1407 1410
	1]	ļ	1414 1419-1420 1423 1432-1433
		ļ	J	1435 1437-1438 1440-1442 1446
	ļ	İ	•	1448 1453-1455 1457 1461 1463-
1		ţ		1464 1466 1468 1471 1477 1480 1482-1483 1496 1502-1504 1507-
		ł	1	1509 1513 1519-1520 1524-1526
		1		1536 1547 1549-1552 1567 1573-
		1	1	1574 1578 1586-1589 1597-1598
		ļ	j	1601-1602 1605 1607-1609 1611-
			}	1617 1619-1621 1623 1625-1626
			1	1635-1641 1643-1645 1649 1651 1653 1656-1658 1664 1669 1671-
		ł	ľ	1674 1676-1684 1686 1689-1690
L				1694-1696 1704-1705 1708-1709
_				

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
		DIDIALY NAME	1720-1724 1726-1728 1730-1733
			1737-1740 1742-1745 1753 1756-
			1757 1759-1761 1765 1767 1771-
			1772 1776-1777 1779-1780 1786
adult brain	Clontech	ABR011	24 75 103 186 210 310-311 364-
date brown			365 508 623 710 937 1002-1003
	1		1059 1204 1609 1731-1732
adult brain	BioChain	ABR012	46 182-184 204-205 300 739 767
			1371 1549 1620 1684
adult brain	Invitrogen	ABR013	185 204-205 364-365 393 497 595
			687 692-694 830 845 1068 1320
]			1413 1640
adult brain	Invitrogen	ABR014	187 301 357 364-365 375 454 463
}			731 859 939 983 1073 1262 1270
) .			1320 1403 1640 1651 1657 1696
			1722 1738
adult brain	Invitrogen	ABR015	419 434-435 441-442 763 789 983
1			1320
adult brain	Invitrogen	ABR016	312 364-365 379 1320 1334-1335
			1674 1722 1785
adult brain	Invitrogen	ABT004	14-16 22-23 25 37-39 43 58 60
			70-72 78 86 94 107 113 116 136-
			137 143 146 152 161 173 182-184 194 196 198 210 218 229 259 267
	,		295 298 309-310 320-321 324 336-
			338 346-347 349-350 356-357 362
			371 379-380 382-383 391 393 396
	•		399 401 408 428 438 459 461 476
			482 490 502 507-509 516 526 531
		1	557 562 597 602 607-609 624 652
	1		655 667 669 671-672 687-689 695-
			696 710 712 715 721 732 739 743
			750 753 766 778 780-781 789 803
1	İ		814 826 830 837 841 857 869 874
	į.	1	894-895 925 937 949 954-956 960-
			961 963 968-969 988-989 1000
			1005-1006 1016-1019 1021 1036-
			1037 1052 1086 1090 1109 1113
			1115 1120-1121 1123-1124 1136-
	1.		1137 1140 1144-1147 1151 1167
	f .		1170 1174 1188 1193-1194 1205
	1		1225 1229 1231 1254 1258 1262
	\ '		1280 1285 1309 1312 1334-1335
			1341 1343-1344 1356-1357 1370
	1		1378-1379 1383-1384 1403-1404
1			1423 1429 1434 1442 1448 1451-
	· ·		1452 1454 1470-1472 1482 1499
		1	1525 1528-1529 1532 1536 1547
			1554 1557-1559 1561-1562 1567
			1585 1588 1590 1595 1601-1604 1608 1610-1613 1615 1619 1624
		}	1608 1610-1613 1615 1619 1624
			1666 1670 1675 1696 1704 1715
			1723 1727 1738 1760-1761 1768
,		1	1779 1785-1786
	Obs h - m - m	200003	5-8 11 17 25 68-69 80 82 87 103
cultured	Strategene	ADP001	105 110 116 136-138 168 171 188-
preadipocytes			189 196-198 261 267 276 288 293
			301 318 331 336-338 379-380 391
			400 428 430-431 510-512 520 524
			527 549 557 561 602 618 620 622
1	Į		631 637 647 670 681-682 710 731
			748 782 793-794 817 834-836 843
			845 858-859 879 882 893-895 934
1	{		960 982 986 995-996 1000 1002
	1		1005-1007 1025 1027-1028 1032
			1039 1045 1071 1078 1097 1099-
			1102 1136-1137 1140 1219-1220
	1	1	

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
110000 0119111	NA Source	Library Name	SEQ ID NOS:
			1260 1271 1297-1298 1314 1320
	[1322 1329 1339 1345 1365-1366
1		l	1370-1371 1398 1408 1423 1431
	}	İ	1437 1466 1468 1533 1539 1594 1602 1608 1614 1631 1649-1650
			1660 1662 1673 1687-1688 1696
			1711 1719-1720 1742 1746 1749
1			1760-1761 1765 1767 1771 1785
adrenal gland	Clontech	ADR002	4-10 15-16 25 29-31 43-45 47 50-
			51 55 60 62-63 65-66 75 80 102
	·		116 118 122 126 130 137 150 169-
			170 181 192 198 201-203 215 227- 228 247 251 255 267-269 271 280-
}		ł	281 285 295 298 311 336-338 342
]		j	349 351-352 354 372-373 383-385
		Į	391 400 410 415-416 424 426-427
1		İ	431 434-437 439 445 454 461 473
1			477 483 491 493 497-498 503 516
J		ļ	519 527 535 546 549 552 572-573
			581 588 595 600 602 608-610 620 628-630 637 645-646 670 679 703
			713 715 719 732 734 744-746 758
1		}	773-778 789 816 829 837 845 848
			869 875 883 898 904 912 922-923
}			930-931 942 948 952 965 967 969
			976-977 981 990 992-993 1001
		1	1004 1049 1055 1059 1071-1072 1076 1112-1113 1115 1121 1127
Į		İ	1134-1135 1151 1158 1163 1175
			1181 1188 1209 1218 1224-1225
			1227 1231 1243 1270-1271 1274
ĺ			1280 1285 1290 1293 1307 1324-
			1325 1327 1330 1342-1343 1345
ļ			1348 1365-1366 1369 1378-1379 1387 1398 1400 1405 1417 1425-
			1426 1436 1440-1441 1444 1454
			1463-1464 1488 1491 1507 1512
			1538 1546 1567 1573-1575 1588
1			1598 1609 1614 1618 1622 1624
	K.p.		1627 1634 1636 1649 1651 1658
·			1671 1674 1678-1679 1691-1692
		. •	1703 1717 1727 1731-1732 1737 1765
adult heart	GIBCO	AHRO01	4-8 10-11 15-16 18-21 34-39 44-
			46 50-52 57-58 60 62-63 71 75 82
			85 87 89 94 97 100 103-104 108-
-			110 112 114 116 118-119 122-123
			127 130-132 134 136-138 141-144
			147-151 153 163-164 168-171 179 186 192 195 197 199 204-205 212-
			215 220 225-226 229-230 232 234-
[236 251 257-260 262 265 272 274
			277 280-282 285-286 289-292 296
]			298-301 304 307 309 314 321 324-
	1		325 330 333 336-338 345 349 351-
	1	[352 354 358 361 368 370 380 383- 384 387-388 391 393 397 401 406
1		i	408-409 411-412 414-416 430-431
]	ļ	ļ 1	433-439 445-446 449 452 454-455
			457 459 462 469 472-473 476-480
	(483-484 487-490 492-493 496-498
	{	ì	503 506 508 510-513 516 519-522
]	ļ		526 534 536-540 542 546 549 553
			560-562 574-577 581-582 584 586- 587 589 593 595 597 604-609 611-
			612 615-620 622-623 626 632 637
			645-652 656-660 665-666 670-672
]		Ì	674-675 683-684 687 692-694 697
L			701 709 712 715-716 719-720 725-

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	
			726 728 730-732 735 738-739 743-
			744 746 751 753 759 761 765 770-
			771 775-780 785 788-790 796 802
ĺ	1		804 810 812 817 821 826 828 830
			837 843 845-847 849-853 857-861
Ì	i		863-864 869 871 875 877-879 881
1			883 887 890-892 894-895 897-898
			901 903 906-907 911-913 915 919
			921-925 927-928 933-935 945 958
ì	1		961-963 967 969-972 975 977-978
		·	980-986 990 992 999-1002 1005-
ì	1		1007 1010 1016 1019-1020 1022-
			1023 1025 1028-1037 1039-1040
1	1		1043 1047 1050 1054-1055 1057
1			1059 1063-1064 1067-1068 1070
			1
	ļ		1072 1075-1076 1083 1085-1087
f	Ì	ĺ	1089 1093-1094 1104 1106 1108-
<u> </u>	Į.		1109 1113 1116-1117 1119 1121
		1	1124 1126 1128 1131-1134 1144-
	}	}	1145 1148-1149 1151 1158 1167
		[1169-1170 1175 1177 1192 1196
	1	1	1199-1200 1202 1206-1208 1211
1		1	1216 1218 1222 1227-1229 1232-
	1	}	1235 1238-1241 1243-1244 1247-
	('	[1248 1250 1253-1254 1256-1258
			1261 1268 1270-1271 1277 1280-
i	1	[1282 1287 1292 1298-1299 1306
1			1308 1317-1321 1324-1325 1330
1			
1		1	1332 1334-1337 1339 1344-1345
4	1	İ	1349-1350 1354-1356 1359-1360
1		i	1365-1366 1369 1371 1374-1375
1 .		1	1378-1380 1383-1384 1389 1397
		1	1 3400 1403 1400 1417 1473 1476
		i .	1400 1403 1409 1417 1423-1426
1			1437 1439 1442 1444 1446-1447
			1437 1439 1442 1444 1446-1447
			1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519
			1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536-
			1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553
			1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588
			1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605
			1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628
			1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644-
			1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659
			1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681
			1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709
			1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727
			1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743-
			1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727
			1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102-
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215-
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215- 216 223-228 234-236 238 247 251-
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215- 216 223-228 234-236 238 247 251- 253 257-259 261-262 265-269 271-
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215- 216 223-228 234-236 238 247 251-
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215- 216 223-228 234-236 238 247 251- 253 257-259 261-262 265-269 271- 272 274 276-277 279-281 284-286 290 293 296 298-299 301-302 304
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215- 216 223-228 234-236 238 247 251- 253 257-259 261-262 265-269 271- 272 274 276-277 279-281 284-286 290 293 296 298-299 301-302 304
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215- 216 223-228 234-236 238 247 251- 253 257-259 261-262 265-269 271- 272 274 276-277 279-281 284-286 290 293 296 298-299 301-302 304 307 311-313 321 325-326 329-331
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215- 216 223-228 234-236 238 247 251- 253 257-259 261-262 265-269 271- 272 274 276-277 279-281 284-286 290 293 296 298-299 301-302 304 307 311-313 321 325-326 329-331 333 341 344 348-350 352 356 358-
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215- 216 223-228 234-236 238 247 251- 253 257-259 261-262 265-269 271- 272 274 276-277 279-281 284-286 290 293 296 298-299 301-302 304 307 311-313 321 325-326 329-331 333 341 344 348-350 352 356 358- 359 362 364-365 368 370-372 374
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215- 216 223-228 234-236 238 247 251- 253 257-259 261-262 265-269 271- 272 274 276-277 279-281 284-286 290 293 296 298-299 301-302 304 307 311-313 321 325-326 329-331 333 341 344 348-350 352 356 358- 359 362 364-365 368 370-372 374 376-377 380-382 392 395 398 400-
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215- 216 223-228 234-236 238 247 251- 253 257-259 261-262 265-269 271- 272 274 276-277 279-281 284-286 290 293 296 298-299 301-302 304 307 311-313 321 325-326 329-331 333 341 344 348-350 352 356 358- 359 362 364-365 368 370-372 374 376-377 380-382 392 395 398 400- 401 404 407-409 414-415 423-424
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215- 216 223-228 234-236 238 247 251- 253 257-259 261-262 265-269 271- 272 274 276-277 279-281 284-286 290 293 296 298-299 301-302 304 307 311-313 321 325-326 329-331 333 341 344 348-350 352 356 358- 359 362 364-365 368 370-372 374 376-377 380-382 392 395 398 400- 401 404 407-409 414-415 423-424 430-437 443-444 446 449 451 453-
adult kidney	GIBCO	AKD001	1437 1439 1442 1444 1446-1447 1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519 1521 1524 1528 1530-1534 1536- 1537 1539 1541-1542 1547 1553 1555 1560 1565 1567-1571 1588 1591 1597-1598 1601-1602 1605 1614-1616 1619-1620 1623-1628 1630-1632 1634 1636 1641 1644- 1645 1647 1649 1652-1655 1659 1662 1667 1673-1674 1680-1681 1684 1686-1688 1704-1705 1709 1711-1712 1717 1724 1726-1727 1731-1733 1737-1738 1741 1743- 1744 1749 1754-1755 1760-1761 1765 1772 1785 4-8 10-11 17-21 29-31 35-39 42- 45 50-51 56-58 60-61 64 68-69 75 77 80 82 85 87 92-94 97 100 102- 104 107-108 112 116-117 119 123 127-133 136-137 139-141 143-144 147-154 157 161-163 165-166 169 172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215- 216 223-228 234-236 238 247 251- 253 257-259 261-262 265-269 271- 272 274 276-277 279-281 284-286 290 293 296 298-299 301-302 304 307 311-313 321 325-326 329-331 333 341 344 348-350 352 356 358- 359 362 364-365 368 370-372 374 376-377 380-382 392 395 398 400- 401 404 407-409 414-415 423-424

Absolute Absolute				
490-491 493 497-505 510-513 516- 525 225 245 256-529 534 537-540 544 547 549 554-555 650 552 564 567 571-575 575 525 568-549 592-593 598-599 601 604-606 608-613 615-619 621-626 622-636 640 637-643 665-625 655 660-664 669-672 676 678-6-79 688 692-699 689 702 711 773 777 719-720 727 731 735-735 738 743 745-746 751 753 755 762-763 765 771-773 775-778 780 786 788 789 789 778-778 780 786 788 789 789-796 800 803 805 808 810-812 814-819 822 826 829 832 834-838 824-845 846-855 857-861 866-865 867 869 871 871 877-883 886-887 889-891 893-985 859-801 902 906-908 910-914 918 929 92 922-527 929-935 937 840-842 945 946-859 939 939-939-	Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
\$20 \$22 \$24 \$26-\$29 \$34 \$37-\$40 \$44 \$47 \$49 \$54-\$56 \$50 \$52 \$46 \$56 \$57 \$71-\$76 \$78 \$82 \$86-\$89 \$592-\$593 \$58-\$59 \$61 \$60-460 \$608-\$613 \$615-619 \$621-626 \$632-\$614 \$637-643 \$645-622 \$655 \$660-\$64 \$669-\$72 \$676 \$678-679 \$688 \$692-699 \$698 702 711 713 717 719-720 727 713 713 735-735 738 743 745-746 751 753 755 762-763 765 771-773 775-778 780 786 786 788-793 795-796 800 803 805 808 810-812 814-819 \$21 \$80 \$22 \$692 \$698 \$692 \$698 \$692 \$698 \$692 \$698 \$692 \$698 \$692 \$698 \$692 \$698 \$692 \$698 \$692 \$698 \$692 \$698 \$692 \$698 \$692 \$698 \$692 \$698 \$692 \$698 \$692 \$698 \$692 \$698 \$692 \$692 \$692 \$692 \$692 \$692 \$692 \$692		<u></u>	Library Name	
S44 547 549 554 556 560 562 564 567 571-576 578 582 582 586-589 592-593 598-599 601 604-606 608-613 615-619 621-626 622-63 637-643 645-626 622-657 678-679 588 692-679 589 762 711 713 717 719-720 727 731 735-735 738 743 745-746 751 733 755 752-753 743 745-746 751 733 755 752-753 765 771-713 775-778 780 786 788 783 785-796 800 803 805 808 810-812 814-819 821 826 829 832 834-838 842-85 848-855 587-861 864-865 867 869 871 874 876-883 886-887 889-891 893-985 587-861 864-865 867 869 871 874 876-883 886-887 889-891 893-985 898-900 902 906-908 910-914 918 920 922 925-927 929-915 937 940-942 945 946-949 951 951-958 960-961 963-964 969-970 972 7976-978 992-986 988-990 992-993 992-993 999-997 999-1002 1004-1008 1001012-1013 1016-1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1077-1073 1078 1085-1086 1088-1089 1092 1094 1097 1099-1102 1107-1112 1116-1119 1121 1122-1125 1132-1135 1140 1142-1143 1146-1147 1149-1150 1153-1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196-1200 1202-1204 1206-1211 1216-1221 1222-1222 1225 1227-1230 1222-1224 1223-1224 1224-1224 1224-1244 1246-1247 1253 1257-1258 1260-1261 1267-1268 1270 1272-1274 1281 1231 1135-1150 1135-1157 1159 1163 1167 1170 1178-1179 1176-1175 1176-1176 1176 1175 1176 1176 1176 1175 1176 1176			Ì	
S67 571-576 578 582 586-589 592-593 598-599 601 604-606 608-613 615-619 621-626 612-634 637-643 645-626 655 660-646 669-672 676 678-679 688 692-695 698 702 711 713 717 719-720 727 713 735-735 738 743 745-746 751 753 755 762-763 748 749 749-720 727 713 735-735 748 749 749-720 727 713 735-735 748 749 749-720 727 713 735-736 748 749 749-720 727 713 735-736 748 749 749-720 727 713 735-736 748 749 749-720 727 713 735-736 748 749 749-720 727 713 735-737 800 803 805 808 810-812 814-819 821 826 829 832 834-818 842-845 848-855 857-861 846-845 847 849-81 893-896 898-900 902 906-908 910-914 818 920 932 935-937 932-931 931-940 892-945 946-949 951 951-958 860-961 963-946 949-949 951 951-958 860-961 963-946 949-949 951 951-958 860-961 963-946 949-949 951 951-958 860-961 963-964 949-949 951 951-958 860-961 963-964 949-949 951 951-958 860-961 963-964 949-949 951 951-958 860-961 963-964 948-949 951 951-958 860-961 963-964 948-949 951 951-958 860-961 963-964 948-949 951 951-958 860-961 963-964 948-949 951 951-958 979-99-1002 1006-1008 1000 1012-1013 1016- 1017 1019-1012 1012 1012-1013 1016- 1017 1019-1012 1012 1012-1013 1016- 1017 1019-1012 1012-1013 1016- 1017 1019-1012 1016-1019-1012 1021-1020 1022 1044 1047 1050 1054-1045 1044-1068 1070-1073 1078 1085-1086 1088- 1089 1009 1004 1097 1099-102 1007 1008-1008 1004 1097 1099-102 1007 1009-1012 1012-1013 1016- 1017 1019-1012 1116-1119 1121 1121-1125 1132-1135 1140 1142- 1142 1146-1147 1149-1150 1153- 1146-1147 1149-1150 1153- 1146-1147 1149-1150 1153- 1146-1147 1149-1150 1153- 1146-1147 1149-1150 1153- 1146-1147 1149-1150 1153- 1146-1147 1149-1150 1153- 1146-1147 1149-1150 1153- 1146-1147 1149-1150 1143-1150- 1120-1179 1181 1183 1193 1196- 1200 1200 1200 12113 1131- 1232-1234 1236-1238 1237-1230 1232-1234 1236-1238 1237-1230 1232-1234 1236-1238 1237-1230 1232-1234 1236-1238 1237-1230 1232-1234 1236-1238 1237-1230 1232-1234 1236-1238 1237-1230 1232-1234 1236-1238 1237-1230 1239 1306 1308 1231-1313 1317- 1329 1306 1308 1231-1313 1317- 1329 1306 1308 1231-1313 1317- 1329 1306 1308 123			ļ	520 522 524 526-529 534 537-540
593 598-599 601 604-606 608-613 615-619 621-626 632-634 637-643 645-625 655 660-664 669-672 675 678-679 688 692-695 689 702 711 713 717 719-720 727 731 735-735 738 743 745-746-751 735 755 756 738 765 771-773 775-778 780 786 788 793 795-796 800 803 805 808 810-812 814-819 821 826 829 832 834-838 842-845 846-855 857-861 864-855 867 869 871 874 876-883 886-887 889-891, 893-896 898-900 902 906-908 910-914 918 920 922 925-927 929-915 937 940-942 945 948-949 951 951-958 960-961 963- 964 969-970 972 797-67-87 892-966 988-990 992-933 995-997 999-1002 1004-1008 1001 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1055 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088- 1098 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1201 1202-1204 1206-1211 1216- 1201 1202-1204 1206-1211 1216- 1201 1202-1204 1206-1211 1216- 1201 1202-1204 1206-1211 1216- 1201 1202-1204 1206-1211 1216- 1201 1202-1204 1206-1211 1216- 1201 1202-1204 1206-1211 1216- 1201 1202-1204 1206-1211 1216- 1201 1207-1208 1270 1272-1274 1281 1283 1287-1289 1393-1395 1393 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1426-1247 1251 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1387-1399 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1313-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1376- 1359 1367 1369 1373 1375 1376- 1359 1367 1368 1368 1361-1375 1375- 1359 1367 1366 1368 1361-1375 1375- 1359 1367 1366 1368 1361-1375 1376- 1379 1379 1378- 1379 1374 1374 17449 1376 1476- 1478 1478 1478 1478 1478 1478 1478 1478			ì	544 547 549 554-556 560 562 564
593 588-599 601 604-606 608-613 615-619 621-626 632-635 637-643 645-626 635-632 655 660-664 669-672 676 678-679 688 692-695 689 702 711 713 717 719-720 727 731 735-736 738 743 745-746 751 733 755 752-763 765 771-773 775-778 780 786 788 783 787-795 800 803 805 808 810-812 814-819 821 826 829 832 834-838 842-858 848-855 857-861 864-865 867 869 871 874 876-883 886-887 889-891 893-895 898-900 902 906-908 910-914 918 920 922 925-927 929-915 937 940-942 945 946-949 951 951-958 960-961 963-964 969-970 972 7976-978 982-986 988-990 992-993 992-993 995-997 999-1002 1004-1008 10012-1013 1016-1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088-1099 1092 1094 1097 1099-1102 1107-1109-1102 1102-112 1116-113 1146-1147 1149-1150 1153-1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196-1200 1202-1204 1206-1211 1216-1221 1222-1122 1225 1227-1230 1223-1234 1238-1244 1246-1247 1249-1244 1246-1247 1249-1244 1246-1247 1249-1244 1246-1247 1249-1244 1248-1241 1243-1224 1243-1224 1243-1224 1243-1224 1243-1224 1243-1244 1246-1247 1253 1257-1258 1260-1261 1267-1268 1270 1272-1274 1261 1263 1267-1268 1270 1272-1274 1261 1263 1267-1268 1270 1272-1274 1261 1263 1267-1268 1270 1272-1274 1261 1263 1267-1268 1270 1272-1274 1261 1263 1265 1265 1265 1265 1265 1265 1265 1265			l	567 571-576 578 582 586-589 592-
615-619 621-626 632-634 637-634 645-652 655 660-646 669-672 676 678-679 688 692-699 698 702 711 713 717 719-720 727 731 735-736 738 743 745-746 751 753 755 762- 763 765 771-773 775-787 800 803 805 808 810-812 814-819 921 826 829 932 834-838 842-845 846-855 857-861 864-865 867 669 971 874 876-883 866-887 889-891 893-895 898-900 902 906-908 910-914 918 920 922 925-927 929-935 937 940-942 945 948-949 951 951-956 960-961 969- 962 906-909 992-939 993-939 993-997 999-1002 1004-1008 1010 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1049 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088- 1098 1099 1099 1094 1037 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1201 1212-1222 1225 1227-1220 1222-1234 1238-1241 1243-1244 1246-1247 1253 1279-1274 1281 1283 1287-1299 1393-1295 1299 1306 1308 1311-1313 317- 1320 1323 1329-1330 1334-1355 1339 1341 1349-1350 1353-1357 1359 1367 1369 1379 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433-1446 1344-1450 1453-1454 1437 1445-1446 1448-1450 1453-1454 1445-1447 1445-1468 1487-1458 1453-1454 1459 1461 1465-1468 1474-1475 1475 1476 1476-1509 1509 1512 1518 1521-1522 1525 1527-1528 1527-1528 1527-1528 1527-1528 1527-1528 1527-1528 1527-1528 1527-1528 1527-1528 1527-1528 1527-1528 1527-1528 1527-1528 1527-1529 152				_
645-652 655 660-664 659-672 676 678-679 688 659-659 699 702 711 713 717 719-720 727 731 735-736 738 743 745-746 751 753 755 762- 763 765 771-773 775-778 780 786 788 793 795-796 800 803 805 808 810-812 814-819 921 826 829 832 814-838 842-845 846-855 857-861 864-865 867 869 971 874 876-883 886-887 889-9691 93-896 899-900 902 386-890 8910-914 918 920 922 225-927 929-935 337 940-942 945 948-949 951 951-958 800-961 363- 964 869-970 972 976-978 982-986 988-990 992-993 993-997 999-1002 1004-1008 1010 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088- 1089 1099 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1393-1395 1399 1341 1349-1350 1153-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1431 1431-1343 1317- 1320 1321 1329-1330 1334-1355 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1431 1431 1431-1345 1439 1349 1350 1553-1357 159 1567 1568 1568 1568 1571 1575 1578-1579 1593 1596-1567 1569 1509 1512 1518 1521-1522 1525 1527-1528 1522-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1551 1565-1566 1566 1561 1571 1575 1578-1579 1593 1596-1587 1589 1591-1592 1593 1596-1587 1589 1591-1592 1593 1596-1697 1589 1591-1592 1593 1596-1697 1589 1591-1592 1593 1596-1697 1589 1591-1592 1593 1596-1697 1589 1591-1592 1593 1596-1697 1589 1591-1592 1593 1596-1697 1589 1591-1592 1593 1596-1697 1589 1591-1592 1593 1596-1697 1589 1591-1592 1593 1596-1697 1589 1591-1592 1593 1596-1697 1589 1591-1592 1591 1591 1791 1791-1791 1791-1791 1791-1791 1791-1791 1791-1791 1791-1791 1791-1791 1791-1791 1791-1791 1791-1791 1791-1791 1791-1791 1791-1791 1791-1791 1791-1791 179		[į	1
678-679 688 692-699 698 702 711 713 717 719-720 727 731 735-736 738 743 745-746 751 753 755 762- 763 765 771-773 775-778 780 780 788 793 795-796 800 803 805 808 810-812 814-819 321 826 829 832 834-838 842-845 848-855 857-861 864-865 867 869 871 874 876-883 866-887 889-891 893-896 898-900 902 906-908 910-914 918 920 922 925-927 929-935 937 940-942 945 948-949 951 953-958 960-961 963- 964 969-970 72 976-978 982-986 988-990 992-993 995-997 999-1002 1004-1008 1001 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088- 1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125-1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 3106 1308 1311-1313 3131- 1320 1335 1341 1349-1350 1153-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1437 1439 1430-1432 1428-1431 1431 1437-1437-1438 1442- 1431 1446-1447 1449-1459 1155-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1360 1607 1606 1607 1617 1618 1575 1578-1579 1593 1596-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1616-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1644-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1696 170 1709-1711 1711- 1714 1716-1713 1723-1724 1724- 1724 1737 1737 1737 1738 1741 1743- 1744 1748-1743 1731 1773-1724 1724- 1747 1737 1737 1737 1738 1741 1743- 1744 1746-1749 1753 1750-1761 1679 1683-1684 1686 1691-1692 1696-1607 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1607 1677 1709-1711 1711- 1714 1716-1713 1723-1724 1726- 1727 1737 1737 1738 1741 1743- 1744 1746-1743 1751 1760-1761 1676-1766 1776 1780 1785		}	1	
713 717 719-720 727 731 735-736 762-763 78 743 745-746 781 753 755 762-763 765 771-773 775-778 780 786 787 793 795-796 80 803 805 808 810-812 814-819 321 826 829 832 814-818 842-85 867 869 871 874 876-83 886-887 869 871 874 876-83 886-887 889 873 878 746-83 886-887 889 873 874 876-83 886-887 889 891 893-965 898-900 902 906-908 910-914 918 920 922 925-927 922-935 937 940-942 945 948-949 951 953-988 900-961 963-964 983-990 992 996-908 910-914 918 920 922 925-927 922-935 937 992-939 993-900-902 906-908 910-914 918 920 922 925-927 929-93 993-97 993-1002 1004-1008 1010 1012-1013 1016-1017 1019-1020 1022-1031 1016-1017 1019-1020 1022-1031 1016-1017 1019-1020 1022-1031 1016-1017 1019-1020 1022-1031 1016-1017 1019-1020 1012-1013 1016-1017 1019-1020 1012-1013 1016-1017 1019-1020 1012-1013 1016-1017 1019-1020 1012-1013 1016-1017 1019-1020 1012-1013 1016-1017 1019-1020 1012-1013 1016-1017 1019-1020 1012-1013 1016-1019 1019-1020 1017-1019-1020 1018-1019-1020 1018-1019-1020 1018-1019-1020 1018-1019-1020 1018-1019-1020 1018-1019-1020 1018-1019-1020 1018-1019-1020 1018-1019-1020 1018-1019-1020 1018-1019-1020 1018-1019-1020 1018-1020				
738 743 745 746 751 733 755 762- 763 765 771-773 777-78 780 780 780 788 793 795-796 800 803 805 808 810-812 814-819 321 826 829 832 834-838 842-845 846-855 857-861 864-865 867 869 731 734 876-883 886-887 889-891 893-896 898-900 902 966-908 910-914 918 920 922 925-927 929-935 937 940-942 245 948-949 955 1953-958 960-961 961- 964 969 970 972 976-978 982-996 988-990 992-993 995-97 999-1002 1004-1008 1010 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1089-1086 1088- 1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1251 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1332 1331-1335 1315-135 1339 1341 1349-1350 1353-1357 1359 1359 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497 1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1566-1566 1566 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1629 1631-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1644 1646-1649 1653-1656 1662 1646 1666-1667 1670-1671 1676- 1679 1683-1884 1686 1691-1692 1696-1698 1701 1709-1711 1713- 1714 1716-1713 1723-1724 1724- 1727 1733 1737-1738 1741 1741- 1744 1748-1743 1731 1743- 1744 1748-1743 1741 1743- 1744 1748-1743 1731 1741- 1744 1746-1749 1785 1760-1761 1679 1683-1884 1686 1691-1692 1696-1607 1677 1678 127 1770-1761 1766-1766 1776 1776 1770-1761 1776-1776 1776 1776 1776 1776 1776 1776		i		1
763 765 771-773 775-778 780 786 787 793 795-796 800 803 805 808 810-812 814-819 921 826 829 832 834-838 842-845 846-855 857-861 866-865 867 869 871 874 876-883 886-887 888-981 893-895 898-900 912 906-808 910-914 918 920 922 925-927 925-935 937 940-942 945 948-949 951 951-958 960-961 963- 964 969-970 972 976-978 982-986 988-930 992-939 995-997 999-1002 1004-1008 1010 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088- 1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1161 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1228-1241 1243-1244 1246-1247 1255 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1281 1281-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1443-1446 1444-150 1453- 1454 1459 1461 1468-150 1453- 1454 1459 1461 1468-150 1453- 1454 1459 1461 1468-150 153- 1454 1459 1461 1468-150 153- 1454 1459 1461 1468-150 153- 1454 157-1580 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1582 1593-1588 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1566 1566 1566 1566 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1766 1776 1770 1770-1761 1773-1766 17760 1			1	713 717 719-720 727 731 735-736
788 793 795-796 800 803 805 808 810-812 814-819 821 926 829 832 834-838 842-845 848-855 857-861 864-865 867 869 871 874 876-883 886-887 889-891 871 874 876-883 886-887 889-891 893-896 898-900 902 906-908 910-914 918 920 922 925-927 929-935 937 940-942 945 948-949 951 953-958 960-961 963-964 969-970 972 978-978 992-961 963-966 988-990 992-993 995-997 999-1002 1004-1008 1010 1012-1013 1016-1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1058-1086 1088-1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1121-1125 1132-1135 1140 1142-1143 1146-1147 1149-1150 1155-1154 1157 1159 1153 1167 1170 1178-1179 1181 1183 1192 1196-1201 1201-1202 1202-1204 1206-1211 1216-1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260-1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317-1320 1323 1339-1330 1334-1335 1339 1341 1345-1346 1348-1350 1348-1357 1359 1367 1369 1373 1375-1359 1367 1369 1375 1378-1379 1394 1304 13405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442-1446 1445-1446 1448-1450 1453-1454 1459 1461 1465-1468 1474-1475 1478 1484-1450 1453-1454 1475 1478 1484-1450 1453-1454 1479 1479 1479 1487 1499 1492-1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1526-1507 1509 1512 1518 1521-1522 1525 1527-1528 1526-1560 1560 1560 1560 1560 1560 1560 1560				738 743 745-746 751 753 755 762-
788 793 795-796 800 803 805 808 810-812 814-819 821 926 829 832 834-838 842-845 848-855 857-861 864-865 867 869 871 874 876-883 886-887 889-891 871 874 876-883 886-887 889-891 893-896 898-900 902 906-908 910-914 918 920 922 925-927 929-935 937 940-942 945 948-949 951 953-958 960-961 963-964 969-970 972 978-978 992-961 963-966 988-990 992-993 995-997 999-1002 1004-1008 1010 1012-1013 1016-1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1058-1086 1088-1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1121-1125 1132-1135 1140 1142-1143 1146-1147 1149-1150 1155-1154 1157 1159 1153 1167 1170 1178-1179 1181 1183 1192 1196-1201 1201-1202 1202-1204 1206-1211 1216-1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260-1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317-1320 1323 1339-1330 1334-1335 1339 1341 1345-1346 1348-1350 1348-1357 1359 1367 1369 1373 1375-1359 1367 1369 1375 1378-1379 1394 1304 13405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442-1446 1445-1446 1448-1450 1453-1454 1459 1461 1465-1468 1474-1475 1478 1484-1450 1453-1454 1475 1478 1484-1450 1453-1454 1479 1479 1479 1487 1499 1492-1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1526-1507 1509 1512 1518 1521-1522 1525 1527-1528 1526-1560 1560 1560 1560 1560 1560 1560 1560	,			763 765 771-773 775-778 780 786
810-812 814-819 821 826 829 832 834-838 842-855 867-861 864-865 867 869 871 874 876-883 886-887 889-891 893-896 898-900 902 906-908 910-914 918 920 922 925-927 925-935 937 940-942 945 948-949 951 951-951-958 960-961 961- 964 969-970 972 976-978 982-986 988-990 992-993 995-997 997-1002 1004-1008 1010 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088- 1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1211-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1355 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1422-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1453- 1459 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1629 1638-1669 1660-1669-1699 1701 1709-1711 1713- 1714 1776-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1741 1741-1749 1751 1760-1761 1741 1741-1749 1751 1760-1761 1741 1741-1749 1751 1760-1761 1741 1741-1749 1751 1760-1761 1741 1741-1749 1751 1760-1761 1741 1741-1749 1751 1760-1761 1741 1741-1749 1751 1760-1761 1741 1741-1749 1751 1760-1761 1741 1741-1749 1751 1760-1761 1741 1741-1749 1751 1760-1761 1741 1741-1749 1751 1760-1761	,	Ì	·	1
834-838 842-845 848-855 857-861 864-865 867 869 871 874 876-833 886-887 889-891 893-896 898-900 902 906-908 910-914 918 920 922 925-927 929-935 937 940-942 945 948-949 951 953-958 950-951 963- 964 969-970 972 976-978 982-986 988-990 992-933 995-997 999-1002 1004-1008 1010 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1065-1086 1088- 1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1451 1457-1568 1552 1556-1569 1591 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1558 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1598 1598 1598 1590 1503- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1616 1618-1622 1624-1628 1631- 1616 1618-1622 1624-1628 1631- 1616 1618-1622 1624-1628 1631- 1616 1618-1622 1624-1628 1631- 1616 1618-1622 1624-1628 1631- 1616 1618-1622 1624-1628 1631- 1617 1618-1626 1688 1571 1575 1578-1579 1598 1598 1590 1600 1600- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1617 1618-1626 1688-1671 1676- 1679 1639 1701 1709-1711 1713- 1714 1716-1719 1721 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1727-1738 1741 1743- 1744 1746-1747 1743 1751 1760-1761 1744 1746-1749 1753-1760 1768 122 1300 1330 133			{	
864-865 867 869 871 874 876-883 886-867 889-891 893-896 898-900 902 906-908 910-914 918 920 922 922-927 922-935 937 940-942 945 948-949 951 953-958 960-961 963- 964 969-970 972 976-978 982-986 988-990 992-993 992-993 995-979 991-1002 1004-1008 1010 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088- 1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1113 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1211-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1233-1295 1289 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1490 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1666 1697 1670-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1744 1748-1749 1751 1760-1761 1744 1748-1749 1751 1760-1761 1744 1748-1749 1751 1760-1761 1744 1748-1749 1751 1760-1761 1746-1796 1709-1711 1713- 1744 1746-1749 1751 1760-1761 1744 1748-1749 1751 1760-1761 1744 1748-1749 1751 1760-1761 1744 1748-1749 1751 1760-1761 1744 1748-1749 1751 1760-1761 1744 1748-1749 1751 1760-1761 1744 1748-1749 1751 1760-1761 1744 1748-1749 1751 1760-1761 1744 1748-1749 1751 1760-1761		 	Į	1
886-887 889-891 893-896 898-900 902 906-908 910-14 918 920 922 925-927 929-935 937 940-942 945 948-949 951 931-958 950-961 963- 964 969-970 972 976-978 982-986 988-990 992-933 995-997 9993-1002 1004-1008 1010 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088- 1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1201 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1355 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1551 1555-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1631 1664 1666 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1631 1664 1666 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1631 1631-1692 1693-1692 1696-1699 1701 1709-1711 1713- 1714 1716-7719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1676- 1679 1683-1689 1701 1709-1711 1713- 1714 1716-1719 1773-1716-1711 1714 1716-1719 1773-1716-1711 1714 1716-1719 1773-17170-1711 1713- 1714 1716-1719 1773-1718 1741 1743- 1744 1748-1749 1751 1760-1761 1676- 1679 1689 1601 1607-168 122 1330 133 133				
902 906-908 910-914 918 920 922 925-27 929-93 937 940-942 945 948-949 951 953-958 960-961 963-964 969-970 972 976-978 982-986 988-990 992-993 935-997 999-1002 1004-1008 1010 1012-1013 1016-1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1055 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088-1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142-1143 1146-1147 1149-1150 1153-1154 1157 1159 1153 1167 1170 1178-1179 1181 1183 1192 1196-1200 1202-1204 1206-1211 1216-1219 1221-1222 1225 1227-1230 1222-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260-1261 1267-1268 1279 1271-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260-1261 1267-1268 1279 1371-1335 1371-1330 1334 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378-1378-1379 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378-1378-1379 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378-1378-1379 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378-1378-1378-1378-1378-1378-1378-1378-		ļ		864-865 867 869 871 874 876-883
925-927 929-935 937 940-942 945 948-949 951 951-958 960-961 963- 964 969-970 372 976-978 982-986 988-990 992-993 992-997 999-1002 1004-1008 1010 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088- 1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1443 1447-1448 1448-1450 1453- 1449 1445 1446 1448-1450 1453- 1449 1459 1461 1465-1466 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1549 1549 1549 1598 1506-1507 1509 1512 1518 1521-1522 1526-1559 1561 1565-1566 1566 1571 1575 1578-1579 1593 1596-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1606 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1617 1631-1649 1668 16691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1746-1749 1750-1761 1676- 1679 1631-1649 1666 1667 1670-1671 1676- 1679 1631-1649 1666 1667 1670-1761 1776- 1772 1773 1773 1778 1778 1778 1778 1778 1778			l	886-887 889-891 893-896 898-900
925-927 929-935 937 940-942 945 948-949 951 951-958 960-961 963- 964 969-970 372 976-978 982-986 988-990 992-993 992-997 999-1002 1004-1008 1010 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088- 1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1443 1447-1448 1448-1450 1453- 1449 1445 1446 1448-1450 1453- 1449 1459 1461 1465-1466 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1549 1549 1549 1598 1506-1507 1509 1512 1518 1521-1522 1526-1559 1561 1565-1566 1566 1571 1575 1578-1579 1593 1596-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1606 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1617 1631-1649 1668 16691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1746-1749 1750-1761 1676- 1679 1631-1649 1666 1667 1670-1671 1676- 1679 1631-1649 1666 1667 1670-1761 1776- 1772 1773 1773 1778 1778 1778 1778 1778 1778				902 906-908 910-914 918 920 922
948-949 951 951 953-958 960-961 963- 964 969-970 372 976-978 982-986 988-990 992-993 995-997 999-1002 1004-1008 1010 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1055 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088- 1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170- 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1221-1222 1225 1227-1230 1221-1222 1225 1227-1230 1221-1224 1228-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1299 1299-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1566-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1531 1537 1540- 1541 1547-1550 1552 1556-1559 1551 1565-1556 1566 1566 1571 1575 1578-1579 1583 1586-1587 1589 1591-1552 1554 1558 1600 1603- 1604 1606 1606 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1617 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1631-1639 1649 1644 1666-1667 1670-1671 1776-1761 1744 1746-1749 1751 1773-1778 1774 1774 1774-1771 1771-				•
964 969-970 972 976-978 982-986 988-990 992-993 995-997 999-1002 1004-1008 1010 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-055 1057-1064 1068 1070-1073 1078 1085-1086 1088- 1089 1092 1094 1097 1099-1102 1107 1199-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1227-1289 1293-1295 1299 1306 1308 1311-1313 1337- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1448 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1538 1536-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1617 1633-1644 1666 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1746-1749 1751 1778 1780 1785 adult kidney Invitrogen AKT002 AKT002 AKT002 AKT001 AKT002 AKT001 AKT002 AKT002 AKT001 AKT002 AKT002 AKT001 AKT001 AKT002 AKT001 AKT002 AKT002 AKT002 AKT002 AKT001 AKT001 AKT002 AKT002 AKT002 AKT002 AKT002 AKT003 AKT003 AKT003 AKT003 AKT003 AKT004 AKT004 AKT004 AKT004 AKT007 AKT008 AKT		ł		
988-990 992-993 995-997 999-1002 1004-1008 1010 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068- 1070-1073 1078 1085-1064 1068- 1089-1099 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1266 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1315 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1442-1445 1448-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1526 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785		1	{	
1004-1008 1010 1012-1013 1016- 1017 1019-1020 1022 1025-1031 1036 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088- 1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1331-335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1434- 1445 1445 1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1668 1571 1773 1774 1716-1719 1723-1724 1726- 1777 1733 1737-1738 1741 1743- 1744 1746-1749 1753 1760-1761 1676- 1679 1683-1684 1686 1691-1692 1695-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-3738 1741 1743- 1744 1748-1749 1751 1760-1761 1676- 1679 1683-1684 1686 1691-1692 1695-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-3738 1741 1743- 1744 1748-1749 1751 1760-1761 1676- 1679 1683-1684 1686 1691-1692 1695-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-3738 1741 1743- 1744 1748-1749 1751 1760-1761 1676- 1679 1683-1684 1686 1691-1692				
1017 1019-1020 1022 1025-1031 1035 1038-1040 1042 1044 1047 1055 1053-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088-1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142-1143 1146-1147 1149-1150 1153-1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196-1196 1299 1220-1204 1206-1211 1216-1219 1221-1222 1225 1227-1220 1223-1224 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260-1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317-13320 1323 1329-1330 1314-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378-1357 1359 1367 1369 1373 1375 1378-1357 1359 1367 1369 1373 1375 1378-1357 1349-1350 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442-1443 1445-1446 1448-1450 1453-1459 1461 1465-1468 1474-1475 1478 1484-1488 1490 1492-1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540-1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603-1604 1606 1608 1611 1613 1615-1616 1618-1622 1624-1628 1631-1692 1696-1699 1701 1709-1711 1713-1714 1716-1719 1723-1724 1726-1727 1733 1737-1738 1741 1743-1744 1746-1749 1751 1760-1761 1676-1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713-1714 1716-1719 1723-1724 1726-1727 1733 1737-3738 1741 1743-1744 1746-1749 1751 1760-1761 1676-1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713-1714 1716-1719 1723-1724 1726-1727 1733 1737-3738 1741 1743-1744 1746-1749 1751 1760-1761 1676-1679 1686-69 80 104 107-108 122 130 133			{	
1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088-1089 1099 1099 1099 1099 1099 1099 1099			1	1004-1008 1010 1012-1013 1016-
1035 1038-1040 1042 1044 1047 1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088-1089 1099 1099 1099 1099 1099 1099 1099				1017 1019-1020 1022 1025-1031
1050 1054-1055 1057-1064 1068 1070-1073 1078 1085-1086 1088-1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142-1143 1146-1147 1149-1150 1153-1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196-1200 1202-1204 1206-1211 1216-1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260-1261 1267-1268 1270 1272-1274 1281 1283 1287-1269 1299 1306 1308 1311-313 1317-1330 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378-1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442-1443 1445-1446 1448-1450 1453-1445 1459 1461 1465-1468 1474-1475 1478 1484-1488 1490 1492-1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540-1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603-1604 1606 1608 1611 1613 1615-1666 1669 1701 1709-1711 1713-1714 1716-1719 1723-1724 1726-1727 1733 1737-1738 1741 1743-1744 1746-1749 1701-1711 1713-1714 1716-1719 1723-1724 1726-1727 1733 1737-1738 1741 1743-1744 1746-1749 1701-1701 1723-1724 1726-1727 1733 1737-1738 1741 1743-1744 1746-1749 1701-1701 1701			İ	1
1070-1073 1078 1085-1086 1088- 1089 1092 1094 1097 1099-1102 1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1299 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1448 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1499 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1526 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1599 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1664-1669 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 0-21 37-39 47 52 57 60 65-66		l)	i e
1089 1092 1094 1097 1099-1102 1107 1107 1107 1107 1107 1107 1110 1112 1116-1119 1121 1123-1125 1132-1135 1140 1142-		1	1	Į.
1107 1109-1112 1116-1119 1121 1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1299 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1445-1446 1448-1450 1453- 1443 1445-1446 1448-1450 1453- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1566-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785	•		1	1
1123-1125 1132-1135 1140 1142- 1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1224 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1551 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 20-21 37-39 47 52 57 60 65-66 66-66 66-69 80 104 107-108 122 130 133				
1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170 11178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1422-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1448 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1528 1532-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785		ļ		1107 1109-1112 1116-1119 1121
1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1466 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1614 1616-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1746-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66		j	j	1123-1125 1132-1135 1140 1142-
1154 1157 1159 1163 1167 1170 1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1466 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1614 1616-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1746-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66		ļ		1143 1146-1147 1149-1150 1153-
1178-1179 1181 1183 1192 1196- 1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1322 13229-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1555-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66		Ì	ľ	
1200 1202-1204 1206-1211 1216- 1219 1221-1222 1225 1237-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1612 1634-1636 1638-1639 1641 1644 1646-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133			<u> </u>	
1219 1221-1222 1225 1227-1230 1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260-1261 1267-1268 1270 1272-1274 1281 1283 1287-1299 1293-1295 1299 1306 1308 1311-1313 1317-1320 1323 1329-1330 1334-1335 1399 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378-1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1443 1445-1446 1448-1450 1453-1454 1459 1461 1465-1468 1474-1475 1478 1448-1488 1490 1492-1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540-1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603-1604 1606 1608 1611 1613 1615-1616 1618-1622 1624-1628 1631-1622 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676-1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713-1714 1716-1719 1723-1724 1726-1727 1733 1737-1738 1741 1743-1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen		İ	{	1
1232-1234 1238-1241 1243-1244 1246-1247 1253 1257-1258 1260-1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317-1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378-1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442-1443 1445-1446 1448-1450 1453-1454 1459 1461 1465-1468 1474-1475 1478 1484-1488 1490 1492-1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540-1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603-1604 1606 1608 1611 1613 1615-1616 1618-1622 1624-1628 1631-1632 1634-1636 1638-1639 1641 1664 1666-1667 1670-1671 1676-1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713-1714 1716-1719 1723-1724 1726-1727 1733 1737-1738 1741 1743-1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133			ļ	*
1246-1247 1253 1257-1258 1260- 1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1459 1461 1465-1468 1474- 1475 1478 1844-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1593 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen				1
1261 1267-1268 1270 1272-1274 1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1666 1666 1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133	•			1232-1234 1238-1241 1243-1244
1281 1283 1287-1289 1293-1295 1299 1306 1308 1311-1313 1317-1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378-1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442-1443 1445-1446 1448-1450 1453-1454 1459 1461 1465-1468 1474-1475 1478 1484-1488 1490 1492-1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540-1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603-1604 1606 1608 1611 1613 1615-1616 1618-1622 1624-1628 1631-1632 1634-1636 1608 1611 1613 1615-1616 1618-1629 1624-1626 1662 1664 1666-1667 1670-1671 1676-1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713-1714 1716-1719 1723-1724 1726-1727 1733 1737-1738 1741 1743-1744 1748-1749 1751 1760-1761 1767-1761 1767-1767 1778 1778 1778 1778 1778 1778 1778			1	1246-1247 1253 1257-1258 1260-
1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66	•			1261 1267-1268 1270 1272-1274
1299 1306 1308 1311-1313 1317- 1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66		l	1	1
1320 1323 1329-1330 1334-1335 1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66				
1339 1341 1349-1350 1353-1357 1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1623 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133			1	1
1359 1367 1369 1373 1375 1378- 1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66	:	,		1
1379 1394 1397 1400 1403 1405 1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442-				1
1407-1409 1417 1419 1423-1424 1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133		1	· ·	1359 1367 1369 1373 1375 1378-
1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66			ĺ	1379 1394 1397 1400 1403 1405
1428-1431 1433 1437-1438 1442- 1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66				1407-1409 1417 1419 1423-1424
1443 1445-1446 1448-1450 1453- 1454 1459 1461 1465-1468 1474- 1475 1478 1488-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133			1	
1454 1459 1461 1465-1468 1474- 1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133			İ	•
1475 1478 1484-1488 1490 1492- 1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133			ĺ	
1493 1495 1497-1498 1506-1507 1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				
1509 1512 1518 1521-1522 1525 1527-1528 1532-1533 1537 1540-1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603-1604 1606 1608 1611 1613 1615-1616 1618-1622 1624-1628 1631-1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676-1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713-1714 1716-1719 1723-1724 1726-1727 1733 1737-1738 1741 1743-1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				
1527-1528 1532-1533 1537 1540- 1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133		[
1541 1547-1550 1552 1556-1559 1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				1509 1512 1518 1521-1522 1525
1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133		1		1527-1528 1532-1533 1537 1540-
1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				1541 1547-1550 1552 1556-1559
1578-1579 1583 1586-1587 1589 1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				l e
1591-1592 1594 1598 1600 1603- 1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				•
1604 1606 1608 1611 1613 1615- 1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				
1616 1618-1622 1624-1628 1631- 1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				1
1632 1634-1636 1638-1639 1641 1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				
1644 1646-1649 1653-1656 1662 1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				1
1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				1632 1634-1636 1638-1639 1641
1664 1666-1667 1670-1671 1676- 1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				1644 1646-1649 1653-1656 1662
1679 1683-1684 1686 1691-1692 1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				
1696-1699 1701 1709-1711 1713- 1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				1
1714 1716-1719 1723-1724 1726- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				1
adult kidney Invitrogen AKT002 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				
1744 1748-1749 1751 1760-1761 1763-1768 1778 1780 1785 adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				
adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133				
adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133			[1744 1748-1749 1751 1760-1761
adult kidney Invitrogen AKT002 20-21 37-39 47 52 57 60 65-66 68-69 80 104 107-108 122 130 133]		
68-69 80 104 107-108 122 130 133	adult kidness	Invitrogen	AKTOO2	
l	dante vianel	TILATOREIL	ARTUUZ	
136-137 140 142-143 149 169 174				1
		L		130-137 140 142-143 149 169 174

			SEQ ID NOS:
Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
		DIDIALY MARKE	181 197 227-228 235-236 244 251
			261-265 267 280-281 286 290 299
			301 304-305 309 312-313 339 341
			344-345 349 358 370-372 376 382-
			383 387 392 401 414 416 421 430
			443 445 449 453-454 472 487-488
			504 506 513 516 519 522 528 536-
	[540 546 554 585 587 594 598 602
]		607 616-617 626-627 636 643 662-
			664 695 709 721 735 743 761 768
	[775-777 788 796 804 814 827 837-
			838 849-850 852-853 869-870 881
			890-892 898 903 905-907 914 919
			925 927 934 941 949 952 957 960
			962 968 970 1000 1008 1029-1030
	,		1044 1052 1055 1063 1067-1068
	1		
			1073 1085 1099-1102 1107 1110-
			1111 1113 1115 1119 1126 1134
			1136-1137 1146-1148 1153 1159
	}		1192 1196 1199 1232-1233 1241
			1256 1264 1272-1273 1281 1285
	ſ		1293-1294 1299 1312 1320 1324-
	1	1	1325 1330 1344 1349 1351 1355-
			1356 1369 1378-1379 1403 1414
	1	[1419 1428-1429 1436 1446 1458
	· I	{	1463-1464 1467-1468 1470 1477-
			1478 1486 1491 1509 1519 1527
	[1	1529 1534 1547 1596 1600 1619
	1	ļ	1623 1629 1631 1634 1638 1643
	1		1647 1652 1660 1664 1667 1669-
			1670 1673 1686 1709 1727 1740
	1		1776
adult lung	GIBCO	ALG001	4-8 14 37-39 44-46 50-51 56 62-
1	1	E .	
ĭ	1	1	63 75 82 88 93 103-104 113 125
]	ļ		63 75 82 88 93 103-104 113 125 133 140 143 150 152 154 157 162
			133 140 143 150 152 154 157 162
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251-
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285
·			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504
·			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716
·			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251-252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272-
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383-
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553-
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1669 1676-1677 1684 1696 1727
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662
			133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1667-1679 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786
lymph node	Clontech	ALMO01	133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786
lymph node	Clontech	IOOMJA	133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280-
lymph node	Clontech	ALN001	133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280- 281 287 301 312 329 343 382 421
lymph node	Clontech	ALNO01	133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280- 281 287 301 312 329 343 382 421 430 433 445 451 461-462 475 481-
lymph node	Clontech	100MJA	133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280- 281 287 301 312 329 343 382 421

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			621 626 649 679 719 725-726 738 793 803 831 834-836 838 844 857- 858 866 879 905 913 928 963 976 1005-1006 1012 1038 1050 1116- 1117 1151 1199 1204 1226 1243 1265 1274 1324-1325 1339 1353 1374 1377 1440-1441 1447 1504 1549 1600 1618-1619 1631 1641 1644 1653 1687-1688 1691-1692
young liver	GIBCO	ALV001	5-8 11 20-21 46 50-51 58 65-66 75 79 82 93 97 102-103 108 110 116 139 143-144 148-149 171-172 174 187-189 194-195 198 209 214- 215 230 250 258 267-269 280-281 306 309 342 351 356 359 362 372 374 392 394 398 401 407-408 410 414 431 444 455 459 476 478 483 493 510-512 516 520 522 526 536 549 571 574-577 585 592 601-602 607 621-624 628-630 632-633 637 648 660 666-667 678 697-698 700 717 719 728 730 734 738 744-745 766 770 773 779 788 800 808 812 814 841 849-851 871 874 879 887 893 898-900 902-904 906-907 911 919 922 924 934 953 957 963 965 970 984 986 997 1001 1004 1007 1012 1029-1030 1033-1034 1052 1061 1066 1070 1076 1086 1089 1093 1099-1102 1110-1112 1116-
		27.40.02	1117 1119 1121 1125 1136-1137 1144-1145 1156-1157 1159 1196 1199-1200 1209 1211 1219-1220 1241 1244 1262 1270 1275 1279 1283 1295 1317-1320 1332 1339 1344 1359 1362-1363 1379 1383-1384 1403 1415 1430-1431 1437 1450 1467 1475-1476 1483-1484 1494-1495 1498 1505 1512 1516 1518-1519 1526 1529 1547 1550-1552 1557-1559 1565 1583 1587 1597 1609 1614 1620 1631 1637 1641 1644 1654-1655 1662 1667 1669 1684 1691-1692 1702 1711 1725 1738 1741 1743-1744 1758 1760-1761 1763-1765 1769
adult liver	Invitrogen	ALV002	5-8 17 20-21 32-33 41 55 58 64 75 77 86 89 102 108 117 119 175- 176 198 200 209 231 235-236 250 272 275-276 284 306 316 321 325 333 356 359 374 376 398 401 408 414 428 430 433-435 454 476 494 503-505 517-518 528 534 544 552 561-563 567 578 581 608-609 630 632 637 644 650 661 665 672 702 707 710 721-722 750 753 778 782 794 814 820 826 834-837 847 849- 850 858 861 874 879 893 898 904 911 918 921-922 926 946 948 972 978 986 996 1020 1027 1031 1034 1053 1063 1068 1070 1073 1086 1089 1093 1097 1113 1119 1156 1159 1195 1198-1199 1208 1220 1227 1241 1261 1272-1273 1277 1285 1308 1315 1320 1324-1325 1330 1362-1363 1375 1403 1408- 1409 1415 1431-1432 1435 1467 1469 1482 1504 1524 1542 1547

PCT/US00/34263

			GDO TO MOS.
Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	1550 1567 1578 1581 1583 1594
			1597 1601-1602 1611-1612 1615
			1618-1619 1621 1625 1637 1645
			1647 1652 1654-1655 1660 1666
			1669-1671 1684 1706 1722 1737-
			1738 1742-1744 1760-1761 1763-
			1765 1772 1774
-4-14 14-0-4	Clontech	ALV003	29 676 997 1063 1119 1536 1766
adult liver	Invitrogen	AOV001	1 4-18 20-23 29 35-40 42-48 50-
adult ovary	Inviciogen	ACTUL	51 53-58 61-63 65-66 68-69 73-75
}			77-78 80 82 85 87 89 97 100-101
1			103-104 106-108 110 113 115 118
			122-124 126 128 133-134 136-140
}			142 145-147 149-157 161 166 168-
1		[170 174 177-178 180 182-186 188-
	ļ		189 192-203 207 209 211-215 219
	1		221-224 229-230 234 242-243 246-
		}	247 255 258 260-262 265-269 271-
	1	1	272 274 277-281 284-286 288 290
1	{	1	295 299 301-302 304 307 309-311
]	<u> </u>	313-314 316 321 323-326 330 332-
	[333 335-338 341 344 349 352-353
)	1	356 358 360 362 370-372 376-377
'			379-384 387 390-392 394 397-398
	1		400 403 408-410 412 414-416 423-
			424 426-427 430-435 439 443-446 448-449 451 453-455 462-463 468-
}	l	1	471 473 476-479 481-484 487 489-
	}		494 496-497 499-501 503-505 509-
		(514 516-517 519-520 522 524 526
1	Ì	1	528-534 541-544 546-547 549 552
		1	554-555 561-564 566-567 569-570
	1.	1	572-573 575-576 579 581 583 585-
]	588 590-591 593 595 597 599 601-
1		ĺ	605 607-613 615 618-622 624-627
			630 632-633 636-640 642 644-647
]		ĺ	649-652 654-655 657-665 667-675
	1	1	677-678 681 683-684 692-695 697-
			710 714-721 723 725-727 729 732
		1	734-735 743-746 750-751 753 758
	,		763 765 767 772-773 775-778 780
1			783-784 786 788 790-791 794-796
			800 803 805 809-811 813-815 818-
			819 821-824 826 828-829 831-832
		1	837-838 843-850 852-857 859-864
			867 869 871-872 874-875 878-883
}			887-888 890-895 898-910 912-914
			916 919-922 924 926-927 929-939 941 943-946 948-951 953 955-958
		1	961-964 966-967 970-979 981-982
			985-986 988-990 992 995-997 999-
	1		1001 1004-1009 1011-1013 1016
		1	1019-1020 1024-1025 1029-1031
		1	1033-1035 1037 1039 1041-1047
1			1033-1035 1037 1039 1041-1047 1050-1051 1054-1060 1062-1064
1			1050-1051 1054-1060 1062-1064
}			1033-1035 1037 1039 1041-1047 1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090
			1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090 1094-1096 1098-1103 1106-1108
			1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090 1094-1096 1098-1103 1106-1108 1112-1117 1119-1120 1123-1127
			1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090 1094-1096 1098-1103 1106-1108 1112-1117 1119-1120 1123-1127 1131-1135 1142-1143 1146-1149
			1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090 1094-1096 1098-1103 1106-1108 1112-1117 1119-1120 1123-1127 1131-1135 1142-1143 1146-1149 1153 1156 1158 1163 1165-1166
			1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090 1094-1096 1098-1103 1106-1108 1112-1117 1119-1120 1123-1127 1131-1135 1142-1143 1146-1149 1153 1156 1158 1163 1165-1166 1169-1171 1173-1175 1177-1178
			1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090 1094-1096 1098-1103 1106-1108 1112-1117 1119-1120 1123-1127 1131-1135 1142-1143 1146-1149 1153 1156 1158 1163 1165-1166 1169-1171 1173-1175 1177-1178 1180 1183-1185 1190-1191 1195
			1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090 1094-1096 1098-1103 1106-1108 1112-1117 1119-1120 1123-1127 1131-1135 1142-1143 1146-1149 1153 1156 1158 1163 1165-1166 1169-1171 1173-1175 1177-1178 1180 1183-1185 1190-1191 1195 1197-1200 1202 1205-1214 1217-
			1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090 1094-1096 1098-1103 1106-1108 1112-1117 1119-1120 1123-1127 1131-1135 1142-1143 1146-1149 1153 1156 1158 1163 1165-1166 1169-1171 1173-1175 1177-1178 1180 1183-1185 1190-1191 1195 1197-1200 1202 1205-1214 1217- 1219 1221-1226 1232-1235 1238-
			1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090 1094-1096 1098-1103 1106-1108 1112-1117 1119-1120 1123-1127 1131-1135 1142-1143 1146-1149 1153 1156 1158 1163 1165-1166 1169-1171 1173-1175 1177-1178 1180 1183-1185 1190-1191 1195 1197-1200 1202 1205-1214 1217- 1219 1221-1226 1232-1235 1238- 1241 1243-1244 1247 1249 1252-
			1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090 1094-1096 1098-1103 1106-1108 1112-1117 1119-1120 1123-1127 1131-1135 1142-1143 1146-1149 1153 1156 1158 1163 1165-1166 1169-1171 1173-1175 1177-1178 1180 1183-1185 1190-1191 1195 1197-1200 1202 1205-1214 1217- 1219 1221-1226 1232-1235 1238- 1241 1243-1244 1247 1249 1252- 1254 1256-1258 1262 1265 1267-
			1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090 1094-1096 1098-1103 1106-1108 1112-1117 1119-1120 1123-1127 1131-1135 1142-1143 1146-1149 1153 1156 1158 1163 1165-1166 1169-1171 1173-1175 1177-1178 1180 1183-1185 1190-1191 1195 1197-1200 1202 1205-1214 1217- 1219 1221-1226 1232-1235 1238- 1241 1243-1244 1247 1249 1252-

This area order	Ditt. C	· · · · · · · · · · · · · · · · · · ·	
Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1299 1306 1308 1312 1317-1321
			1323 1327 1329-1330 1332-1333
	[1338-1339 1341 1343-1351 1356
			1359 1361 1365-1366 1371-1375
			1377-1379 1383-1384 1386 1389
		1	1394 1400 1404 1416-1417 1422-
		}	1427 1429-1431 1435-1436 1439- 1443 1445-1450 1453-1454 1459
}	ļ		1463-1464 1466 1468 1470 1474-
	i		1481 1484-1485 1488 1491 1493-
		<u> </u>	1494 1496-1498 1501-1504 1506-
		į	1507 1511-1517 1519 1521-1524
		}	1526-1527 1530-1531 1534-1536
			1538-1539 1541 1546 1548-1550
			1553 1555-1559 1561-1563 1566-
			1567 1569-1570 1572 1574-1575
		İ	1578 1580-1581 1587-1588 1590-
			1591 1595 1597-1598 1600-1606
}		i	1609 1611-1621 1623-1630 1634
			1636 1638 1641 1643 1645 1647-
			1657 1659-1662 1664 1667 1669-
]			1671 1673-1674 1676-1681 1683-
		j	1690 1699 1702-1707 1710-1711
1			1713-1714 1716-1719 1723-1724 1726-1728 1731-1733 1735 1737-
1	}		1738 1740-1741 1743-1744 1748-
		}	1751 1753 1755-1756 1760-1762
			1765 1767-1768 1770-1771 1776
			1778-1779 1783-1784 1786
adult placenta	Clontech	APL001	5-8 44-45 90-91 107-108 159 178
			311 351 414 476 503 545 574 624
			636 719 755 773 860 890-891 924
1		ł	a.m .am ama ama ama ama ama
1		!	947 955-956 962 990 992 1002
			1045 1202 1320 1369 1628 1686
			1045 1202 1320 1369 1628 1686 1713-1714 1743-1744
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490-
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490-
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857-
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776
placenta	Invitrogen	APL002	1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386-
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684 700 721 728 730 732 738 742-744
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684 700 721 728 730 732 738 742-744 746 762 765 774 780 788-789 794
	·		1045 1202 1320 1369 1628 1686 1713-1714 1743-1744 14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684 700 721 728 730 732 738 742-744

### Tissue Origin				
### Section Se	Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
### Section Page Pa			Library Name	22. 22. 22. 212. 212. 221. 222. 225.
### ### ### ### ### ### ### ### ### ##	,			884 906-908 912 919 921-923 926-
1005-1007 1010 1012 1031 1036 1042-1044 1046 1049 1059 1068 1070 1076 1089-1090 1094 1103 1109 1113 1115 1124 1140 1163 11170 1174 1177 1130 1196 1219- 1220 1226-1227 1229 1236 1241 1246 1258 1269 1271 1274 1295 1300 1300 1302 1302 1330 1334-1335 1339 1349 1351 1353 1359-1360 1346 1369 1374 1386 1397 1413 1477 1434 1436-1437 1439 1468 1474 1477 1430 1485-1487 1439 1568 1474 1477 1430 1485-1487 1439 1568 1474 1477 1430 1485-1487 1439 1568 1474 1477 1430 1485-1487 1439 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1658 1662 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760- 1727 1733 1738 1740-1741 1770- 1838 1848 1848 1848 1848 1848 1848 1848		Ì		927 934 942 949 957-958 903 577-
1042-1044 1046 1049 1059 1068 1070 1076 1069-1090 1049 4103 1109 1113 1115 1124 1140 1163 11170 1174 1177 1190 1196 1219-1220 1226-1227 1229 1236 1241 1246 1258 1269 1271 1274 1295 1301 1320 1322 1330 1334-1335 1339 1349 1315 1353 1359-1360 1364 1365 1374 1386 1397 1413 1417 1434 1436-1437 1439 1468 1471 1477 1480 1485-1487 1498 1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1658 1652 1670 1727 1733 1738 1740-1741 1760 1727 1730 1738 1739 1740 1740 1727 1730 1731 1731 1731 1731 1731 1731 173				978 983 990 992-994 998-997 999
1070 1076 1089-1090 1094 1103 1109 1113 1115 1124 1140 1165 1170 1174 1177 1190 1196 1219- 1220 1226-1227 1229 1236 1241 1246 1258 1269 1271 1274 1295 1301 1320 1322 1330 1334-1335 1339 1349 1351 1353 1359-1340 1347 1343 1375 1353 1359-1340 1347 1343 1375 1353 1359-1340 1347 1343 1346-1347 1339 1468 1474 1347 1340 1345-1347 1339 1468 1474 1347 1340 1345-1347 1349 13468 1476 1347 1349 1346 1347 1349 1468 1476 1477 1370 1370 1370 1370 1370 1370 1370 13		j		
1109 1113 1115 1124 1140 1163 1170 1174 1177 1190 1196 1219- 1220 1226-1227 1229 1236 1241 1246 1228 1229 1236 1241 1246 1228 1229 1231 1247 12295 1301 1320 1322 1330 1334-1335 1339 1349 1351 1351 1359-1360 1364 1369 1374 1366 1397 1413 1467 1434 1436-1437 1439 1468 1474 1487 1480 1485-1487 1499 1512 1522 1525 1544-1549 1553 1560 1567 1567 1567 1567 1567 15678-1659 1684 1686 1700 1727 1733 1738 1740-1741 1760-1727 1733 1738 1740-1741 1760-1727 1733 1738 1740-1741 1760-1727 1733 1738 1740-1741 1760-1727 1733 1738 1740-1741 1760-1727 1733 1738 1740-1741 1760-1727 1731 1750 152 154 156 163 169 174 176-177 129 194 196-197 212-215 227-228 247 255 258 251 282 285 288-289 30 1307 311 313 136 330 334 349 370-372 392 338 410 415 426-427 430-431 433 447 446 473 477 481-482 493 499 502-503 513 525 556 575 552-555 563-564 572-573 575-576 581-582 585 1567-564 572-573 575-576 581-582 585 1567-564 572-573 575-576 581-582 585 1567 1567 1567 1567 1567 1567 1567 156				
1170 1174 1177 1190 1196 1219-1220 1226-1227 1229 1236 1241 1246 1258 1269 1271 1274 1295 1301 1320 1332 1333 1334-1335 1339 1349 1351 1353 1353-1359 1343-1335 1339 1349 1351 1353 1359-1360 1364 1368 1374 1386 1397 1413 1417 1434 1436-1437 1439 1468 1474 1477 1480 1485-1487 1498 1512 1522 1525 1544-1549 1553 1560 1561 1551 1560 1531 1563 1565 1565 1565 1565 1565 1565				
1220 1226-1227 1229 1236 1241 1246 1225 1269 1271 1274 1295 1301 1320 1322 1330 1334-1335 1336 1339 1349 1351 1253 1359-1350 1364 1369 1374 1366 1397 1413 1417 1434 1436-1437 1439 1468 1474 1477 1480 1485-1487 1498 1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1658 1652 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1750-1761 1774 1779 1781-1782 1761 1774 1779 1781-1782 1876 1761 1774 1779 1781-1782 1876 1761 1774 1779 1781-1782 1876 1761 1774 1779 1781-1782 1876 1761 1774 1779 1781-1782 1876 1761 1774 1779 1781-1782 1876 1761 1774 1779 1781-1782 1876 1761 1774 1779 1781-1782 1876 1761 1774 1779 1781-1782 1876 1761 1774 1761-1771 179 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-3712 392 398 410 415 426-447 430-439 302 303 303 303 303 303 303 303 303 303				1109 1113 1115 1124 1140 1163
1246 1258 1269 1271 1274 1295 1301 1320 132 1330 1343-1335 1339 1349 1351 1353 1359 1360 1364 1369 1374 1386 1397 1413 1417 1434 1436-1437 1439 1468 1474 1477 1480 1485-1487 1498 1512 1522 1525 1544-1549 1553 1560 1567 1591 1500 1631 1636 1651 1654-1655 1658 1652 1670 1674 1678-1679 1684 1686 1700 1772 1733 1738 1740-1741 1760-1761 1774 1779 1781-1782 1770 1771	•			1170 1174 1177 1190 1196 1219-
1301 1320 1332 1330 1334-1335 1335-1350 1364 1369 1374 1386 1397 1413 1417 1434 1436-1437 1439 1458 1474 1477 1490 1485-1487 1498 1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1658 1662 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1779 1781-1782 1761 1774 1779 1781-1782 1761 1774 1779 1781-1782 1761 1774 1779 1781-1782 139 150 152 154 156 163 169 174 176-1771 179 194 196-197 212-215 227-226 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426-447 430-431 433 437 446 545 461 469 473 477 481-482 493 499 502-503 513 522 526 547 555 563 564 572-573 575-576 581-582 588 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 720 731 738 744 673 740 744 773 740 744 773 740 744 773 740 744 773 740 744 773 740 744 773 740 744 773 740 744 773 740 744 773 740 774 774 774 774 774 774 774 774 774				1220 1226-1227 1229 1236 1241
1339 1349 1351 1353 1359-1360 1364 1369 1374 1386 1397 1413 1417 1434 1436-1437 1439 1468 1477 1430 1485-1487 1439 1468 1477 1430 1485-1487 1439 1468 1512 1522 1525 1544-1549 1553 1360 1567 15674-1655 1658 1662 1670 1674 1678-1679 1684 1686 1700 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1773 1773 1773 1774 1779 1781-1782 1851 1555-1565 1656 1652 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1779 1781-1782 1862 1878 1878 1878 1878 1878 1878 1878 187				1246 1258 1269 1271 1274 1275
1364 1369 1374 1386 1397 1413 1446				1301 1320 1322 1330 1334-1335
1417 1434 1436-1437 1439 1489 1471 1480 1485-1487 1489 1485-1487 1489 1485-1487 1489 1485-1487 1489 1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1658 1662 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1770 1761 1777 1773 1731-1732 1738 1740-1741 1760-1761 1774 1779 1731-1732 1738 1740-1741 1760-1761 1774 1779 1731-1732 1738 1738 1740-1741 1760-1761 1777 197 1731-1732 1738 1738 1738 1738 1738 1738 1738 1738				1339 1349 1351 1353 1359-1360
1474 1477 1480 1485-1487 1498 1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1656 1667 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760 1761 1774 1779 1791-174 1779 1791-174 1779 1791-174 1779 1791-1761 1774 1779 1791-1781-1782 1761-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426-427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502-503 513 525 256 547 552-553 563-564 572-573 575-575 681-585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 747 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 889 866 859 877 905 933 910 71016 1029-1030 1034-1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-102 1104 1108 1113 1141 119 1161-1162 1175 1208-1209 1222 1227 1229 1231 1235 1235-1237 1239 1231 1233 1235 1238-1239 1243 1253 1285 1287-1289 1291-1293 1307 1311 1317-1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-424 4430 1435-1437 1445 1459 1484 1466 1490 1493 1495-1497 1501 1505 1509-1513 1527 1530-1531 1539 1602 1625 1629 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1702-1077 1797 1866 1599 1599 1602 1625 1629 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1688 1690 1699 1705 1712 1777 1778 1806 1599 1599 1602 1625 1629 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1688 1690 1699 1705 1712 1777 1778 1806 1599 1599 1602 1625 1629 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1688 1690 1699 1705 1712 1777 1778 1806 1599 1599 1602 1625 1629 1630-1632 1633 1639 1642 1649 1661-1662 1666-1667 1670 1675 1688 1690 1699 1705 1712 1777 1778 1806 1599 1675 1779 1779 18060 1675 1688 1690 1699 1705 1712 1777 1778 1806 1599 1675 1779 1779 1806 1675 1675 1679 1675 1679 1675 1679 1675 1679 1675 1679 1675 1679 1675 1679 1675 1679 1675 1679 1675 1679 1675 1679 1675 1679 1679 1679 1679 1679 1679 1679 1679				1364 1369 1374 1386 1397 1413
1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1658 1662 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760 1761 1774 1779 1781-1782 1776 1774 1779 1781-1782 15-8 10 26 30-31 47 50-51 57 68-69 82 84-85 97 102 113 119 137 139 150 152 154 156 163 169 174 176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 104 15 426-427 430-431 433 437 446 448 461 469 473 477 481-482 493 499 502-503 513 522 526 457 552-535 563-564 572-573 575-576 581-582 585 598-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 987 981 990 992-993 1007 1016 1029-1030 1034-1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1079 1091 1091 1012 1104 1108 1113 1141 1149 1161-1162 1175 1208-1209 1222 1227 1229 1231 1235 1228-1229 1243 1253 1285-1287-1289 1239 1249 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1777 1779 Genomic DNA from BAC 39316 Genetics (CITB BAC Library) Genomic DNA Fessearch From BAC 39316 Genetics (CITB BAC Library) Genomic DNA Fessearch FROM BAC 39316 Genetics (CITB BAC Library) Genomic DNA From BAC 39316 Genetics (CITB BAC Library)				1417 1434 1436-1437 1439 1466
1560 1567 1591 1600 1631 1636 1636 1650 1651 1654-1655 1658 1662 1670 1674 1678-1679 1684 1686 1700 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1779 1781-1782 1781-1782		į į		1474 1477 1480 1485-1487 1498
testis GIBCO ATSOO1 Lestis GIBCO ATSOO1		1		
1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1779 1781-1782 1760-1761 1774 1779 1781-1782 1761-1779 1781-1782 1761-1779 1781-1782 1761-1779 1781-1782 1761-1779 1781-1782 1761-1779 1781-1782 1761-1779 1781-1782 1761-1779 1781-1782 1761-1779 1781-1782 1761-1779 1781-1782 1761-1779 1781-1782 1761-1779 1781-1782 1761-1779 1781-1782 1761-1779 1781-1782 1761-1779 1781-1782 1761-1779 1781-1782 1761-1782		1		
testis GIBCO ATSO01 ATSO01 Total 1774 1779 1781-1782 5-8 10 26 30-31 47 50-51 57 68-69 82 84-85 97 102 113 119 137 139 150 152 154 156 163 169 174 176-177 192 194 196-197 212-215 227-228 247 255 258 261 262 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426-427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502-503 513 525 256 247 552-553 563-564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 89 886 886 89 677 905 913 916 919 921 926 929 937 955 960 963 971 975 977 981 990 992-993 1007 1016 1029-1030 1034-1035 1038-1039 1045 1059-1060 1064 1070 1072-1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208-1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287-1293 1307 1311 1317-1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1468 1490 1499 1699 1705 1712 1717 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Genomic DNA Research From BAC 39316 Genetics (CITB BAC Library) Genomic DNA Research FROM BAC 39316 Genetics (CITB BAC				1651 1654-1655 1658 1662 1670
testis GIBCO ATSOO1 5-8 10 26 30-31 47 50-51 57 68-69 82 84-85 97 102 113 119 137 139 150 152 154 156 163 169 174 176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 266-427 430-431 433 437 446 454 461 469 473 477 491-482 493 499 502-503 513 522 526 547 552-553 563-564 572-573 575-576 581-582 563 564 572-573 575-576 581-582 563 564 572-573 575-576 581-582 563 564 572-573 575-576 581-582 563 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 666 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 865 877 905 913 916 919 921 926 929 937 955 913 916 919 921 926 929 937 955 993 1007 1016 1029-1030 1034-1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208-1209 1222 127 1229 1231 1235 1238-1239 1243 1253 1285 1287-1289 1291-1293 1307 1311 1317-1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1464 1466 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1562 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 680 600 100 100 100 100 100 100 100 100 10		Ì		1674 1678-1679 1684 1686 1700
## ATSOO1 \$-8 10 26 30-31 47 50-51 57 68-69 82 84-85 97 102 113 19 137 139 150 152 154 156 163 169 174 176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 265 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426-427 430-431 433 437 446 454 461 469 473 477 481-482 525 585 258 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 739 198 199 502 804 809 811 814 826 831 837 843 845 848 885 866 685 670 674-675 712 719-721 723 728 731 738 475 845 859 879 950 960 963 971 975 977 981 990 992-993 1007 1016 1029-1030 1034-1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1077 1089 1097 1099-1102 1104 1108 1113 1141 1149 161-1162 1175 1208-1229 1221 1235 1238-1239 1243 1253 1285 1287-1239 1243 1373 1389 1399-1400 1409 1423-1424 1430 1435-1437 1439 1399-1400 1409 1423-1424 1430 1435-1437 1439 1565 1567 1569 1571 1577 1586 1591 1509 1509-1513 1557 1566 1591 1509 1509-1513 1557 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1675 1779 1886 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1675 1779 1886 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1675 1779 1779 1779 1777 1772 1773 1773 1775 1771 1772 1773 1775 1771 1772 1773 1775 1771 1772 1773 1775 1772 1777 1779 1779 1779 1779 1779 1779]		
69 82 84-85 97 102 113 119 137 139 150 152 154 156 163 169 174 176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426- 427 430-431 433 437 446 454 461 469 473 477 491-482 493 499 502- 503 513 522 526 547 552-553 563- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 803 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1464 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1553 1555 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1649 1645 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1777 1774 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Genomic DNA Fresearch Genetics (CITB BAC Library) Genomic DNA From BAC 39316		1		1761 1774 1779 1781-1782
69 82 84-85 97 102 113 119 137 1319 150 152 154 156 163 169 174 176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 266-427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502-503 513 522 526 547 552-553 563-564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 666 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 859 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992-993 1007 1016 1029-1030 1034-1039 1045 1039-1046 1070 1072-1073 1087 1089 1097 1099-102 1104 1108 1113 1141 1149 1161-1162 1175 1208-1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1238-1239 1243 1253 1285 1287-1289 1291-1293 1307 1311 1317-1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1444 1466 1490 1493 1496-1497 1501 1505 1509-1513 1537 1546 1549 1561-1662 1666-1667 1675 1684 1690 1699 1705 1712 1771 1724 1730 1737-1738 1752 1767 1779 686 1352 1442 666-1667 1670 1675 1684 1690 1699 1705 1712 1771 1724 1730 1737-1738 1752 1767 1779 686 1352 1412 696-1667 1670 1675 1684 1690 1699 1705 1712 1771 1724 1730 1737-1738 1752 1767 1779 686 1352 1442 666-1667 1670 1675 1684 1690 1699 1705 1712 1771 1724 1730 1737-1738 1752 1767 1779 686 1352 1442 666-1667 1670 1675 1684 1690 1699 1705 1712 1771 1724 1730 1737-1738 1752 1767 1779 686 1352 1442 666-1667 1670 1675 1684 1690 1699 1705 1712 1771 1724 1730 1737-1738 1752 1767 1779 686 1352 14412 686-1667 1670 1675 1684 1690 1699 1705 1712 1771 1724 1730 1737-1738 1752 1767 1779 686 1352 14412 686-1667 1670 1675 1684 1690 1699 1705 1712 1771 1724 1730 1737-1738 1752 1767 1779	testis	GIBCO	ATS001	5-8 10 26 30-31 47 50-51 57 68-
176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426- 427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502- 503 513 522 526 547 552-553 563- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1446 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1569 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1667 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 Genomic DNA from BAC 63118 Genetics (CITB BAC CITB BAC BAC002 1411-1412]	69 82 84-85 97 102 113 119 137
227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426- 427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502- 503 513 522 526 547 552-553 563- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1557 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1651-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Genomic DNA from BAC 39316 Genetics (CITB BAC (CITB BAC	1	,	[139 150 152 154 156 163 169 174
288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426- 427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502- 503 513 525 256 547 552-553 563- 564 572-573 575-576 581-582 585- 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 955 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1557 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1595 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Genomic DNA from BAC 39316 Genetics (CITB BAC (CITB BAC		j		176-177 192 194 196-197 212-215
349 370-372 392 398 410 415 426- 427 430-431 433 437 446 1454 461 469 473 477 481-482 493 499 502- 503 513 522 526 547 552-553 563- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1229 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1580-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1699 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC Genetics CITB BAC		į.		227-228 247 255 258 261 282 285
427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502- 503 513 522 526 547 552-553 563- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399'1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 Genomic DNA from BAC 63118 Genetics (CITB BAC Genetics (CITB BAC Genetics (CITB BAC) BAC002 1411-1412	}	ł	(288-289 301 307 311 316 330 334
469 473 477 481-482 493 499 502- 503 513 522 526 547 552-553 563- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1599 1509 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 39316 Research Genetics (CITB BAC Genetics Genetics (CITB BAC	·]	349 370-372 392 398 410 415 426-
503 513 522 526 547 552-553 563- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 4486 1490 1493 1496-1497 1501 1505 1509-1513 15527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1633 1639 1642 1649 1661-1662 1666-1667 1670 16675 1668 1690 1699 1705 1712 1771 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Research Genetics (CITB BAC Library) Genomic DNA Fresearch Genetics (CITB BAC Library) Genomic DNA Fresearch Genetics (CITB BAC Library) Genomic DNA Fresearch Genetics (CITB BAC CITB BAC		[1	427 430-431 433 437 446 454 461
564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992-993 1007 1016 1029-1030 1034-1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208-1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287-1239 1291-1293 1307 1311 1317-1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1557 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1777 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research Genetics CITB BAC Library Genomic DNA Research Genetics CITB BAC CITB	}	1		469 473 477 481-482 493 499 502-
S99-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 909 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1235 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1594 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Research from BAC 63118 Research from BAC 39316 Research from BAC 39316 Research fonetics (CITB BAC Library) BAC002 1411-1412 Research from BAC 39316 Research fonetics (CITB BAC Library) BAC002 1411-1412 Research from BAC 39316 Research fonetics (CITB BAC Library) BAC002 1411-1412 Research from BAC 39316 Research fonetics (CITB BAC Library) Research fonetics (CITB BAC Li	1			503 513 522 526 547 552-553 563-
637 647 649-650 655 650 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1651-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Research from BAC 39316 Genetics (CITB BAC Library) Genomic DNA Research from BAC 39316 Genetics (CITB BAC Cittb BAC		1		564 572-573 575-576 581-582 585
674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 Genomic DNA from BAC 63118 Research from BAC 39316 Genetics (CITB BAC Library) Genomic DNA Research From BAC 39316		l	į.	599-602 605 612 615-617 620 631
738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research from BAC 63118 Genetics (CITB BAC Library) Genomic DNA Research from BAC 39316 Genetics (CITB BAC Library) BAC002 1411-1412		1]	637 647 649-650 656 660 665 670
802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1771 7724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Genomic DNA from BAC 39316 Genetics (CITB BAC CIDTB BAC CITB BAC CIDTB BAC CITB BAC	į	-	1	674-675 712 719-721 723 728 731
802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1771 7724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Genomic DNA from BAC 39316 Genetics (CITB BAC CIDTB BAC CITB BAC CIDTB BAC CITB BAC			,	738 744 746 773 780 784 788-789
843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Genomic DNA from BAC 39316 Genetics (CITB BAC CIDTB RAC CITB BAC CIDTB RAC Genetics (CITB BAC CITB BAC			İ	802 804 809 811 814 826 831 837
913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Genomic DNA Research from BAC 39316 Genetics (CITB BAC CITB BAC CITB BAC CITB BAC	ľ	1		843 845 848 859 866 869 877 905
960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1553 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63I18 Genetics (CITB BAC Library) Genomic DNA from BAC 39316 Genetics (CITB BAC CITB BAC CITB BAC	ļ		1	913 916 919 921 926 929 937 950
993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Genomic DNA from BAC 39316 Genetics (CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC	ĺ			960 963 971 975 977 981 990 992-
1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research from BAC 63118 Genetics (CITB BAC Library) Genetics (CITB BAC Genetics (CITB GAC GENETIC (CITB GAC GENETIC (CITB GAC GENETIC (CITB GAC GENETIC (CITB GAC GENETIC (CITB GAC GENETIC (CITB GAC GENETIC (1	993 1007 1016 1029-1030 1034-
1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1777 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research BAC001 686 1352 1412 Genomic DNA Genetics (CITB BAC Library) BAC002 1411-1412 Genomic DNA Genetics (CITB BAC GENETIC (CITB BAC GENETIC (CITB BAC GENETIC (CITB BAC GE				1035 1038-1039 1045 1059-1060
1097 1099-1102 1104 1108 1113	1	1		1064 1070 1072-1073 1087 1089
1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research Genetics (CITB BAC Library Genomic DNA Genetics (CITB BAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CITB GAC Genetics (CI		1	į	1097 1099-1102 1104 1108 1113
1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287-1289 1291-1293 1307 1311 1317-1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research BAC001 Genetics (CITB BAC Library) Genomic DNA Research Genetics (CITB BAC Genetics (CITB GAC Gen	l .	Ì		1141 1149 1161-1162 1175 1208-
1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research BAC001 Genetics (CITB BAC Library) Genomic DNA Research Genetics (CITB BAC CITB BAC Genetics (CITB BAC CITB BAC Genetics (CITB BAC CITB BAC		1	• [1209 1222 1227 1229 1231 1235
1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research BACOO1 686 1352 1412 Genomic DNA Genetics (CITB BAC Library) BACOO2 1411-1412 1411-1412	}	1		1238-1239 1243 1253 1285 1287-
1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research Genetics (CITB BAC Library) BACO02 1411-1412 1411-1412	1	1		1289 1291-1293 1307 1311 1317-
1373-1374 1379 1389 1399-1400		1		1320 1330 1332 1338 1345 1369
1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research BAC001 Genetics (CITB BAC Library) Genomic DNA Research Genetics (CITB BAC CITB BAC		1	I	1373-1374 1379 1389 1399-1400
1443 1459 1484 1486 1490 1493	1]	1.	1400 1423-1424 1430 1435-1437
1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779	1		1	1442 1450 1484 1486 1490 1493
1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779	· ·			1496-1497 1501 1505 1509-1513
1549 1563 1565 1567 1569 1571				1527 1530-1531 1533 1537 1546
1577 1586 1591 1599 1602 1625		,	1	1540 1552 1565 1567 1569 1571
1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Genetics (CITB BAC Library) Genomic DNA Research from BAC 39316 Genetics (CITB BAC Description of the company to the co	1	ì	,	1243 1202 1202 1201 1202 1211
1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Genetics (CITB BAC Library) Genomic DNA Research from BAC 39316 Genetics (CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CONTROL CONT		1	1	1000 1000 1001 1000 1000 1000
1675 1684 1690 1699 1705 1712				1028 1030-1032 1030 1037 1042
1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Genetics (CITB BAC Library) Genomic DNA Research from BAC 39316 Genetics (CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC Genetics (CITB BAC CITB	}	1	1	1049 1001-1002 1000-1007 1070
1767 1779		j		10/5 1004 1030 1033 1/03 1/12
Genomic DNA Research BAC001 686 1352 1412 from BAC 63I18 Genetics (CITB BAC Library) Genomic DNA Research BAC002 1411-1412 from BAC 393I6 Genetics (CITB BAC		l l		1
from BAC 63I18 Genetics (CITB BAC Library) Genomic DNA Research BAC002 1411-1412 from BAC 393I6 Genetics (CITB BAC	}			
(CITB BAC Library) Genomic DNA Research BAC002 1411-1412 from BAC 39316 Genetics (CITB BAC			BAC001	686 1352 1412
Library) Genomic DNA Research BAC002 1411-1412 from BAC 39316 Genetics (CITB BAC	from BAC 63I18	Genetics		
Genomic DNA Research BAC002 1411-1412 from BAC 39316 Genetics (CITB BAC		(CITB BAC		
Genomic DNA Research BAC002 1411-1412 from BAC 39316 Genetics (CITB BAC		Library)		
from BAC 39316 Genetics (CITB BAC	Genomic DNA		BAC002	1411-1412
(CITB BAC				
			1	}
· · · · · · · · · · · · · · · · · · ·	1	l ·		

(m)		,	
Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
Genomic DNA	Research	BAC003	1352
from BAC 39316	Genetics		(
	(CITB BAC		
adult bladder	Library) Invitrogen	DIDOG	5 0 17 10 00 00 00
addic bradder	Invitiogen	BLD001	5-8 17-18 22-23 33 37-39 56-57
			80 93 100 120-121 169 201 237 251-252 272 278 311 348 363 382
			413 415 424 430 443 483 502 542-
•			543 562 564 607 616-617 626 635
			652 667 671 710 727 755-756 762
			773 786 788 837 840 866 893 898
	,		909 918 929 966 977 983 1016
	ļ ·		1025 1055 1073 1082 1140 1167
			1185 1189 1199 1270 1369 1481 1536 1560 1573 1596 1614 1636-
			1637 1649-1650 1654-1655 1658
			1669 1671 1690 1719 1727 1731-
			1732 1739 1741 1760-1761 1779
bone marrow	Clontech	BMD001	3-8 11 13 18 29-31 33 35-36 40
			43-45 47-48 50-51 57 60 65-66 75
			80 82 85 88-89 94 100 103 107
			110 115 118-119 124-125 133-134
			136-137 139-141 146 150 152-153 155 161 163 168-170 172 178-180
			187 192-193 197-198 203-205 210-
			213 215 217 219 222 224-226 233
			235-237 242-244 255 258 260 263-
			264 266 273 276 278 283 286 290
			295 301-302 307 312-313 321 330
}			333 339 343 352 357-358 370-371
			382 384-385 387 389 394 408 410 412 416 421 424-427 429-431 436-
			437 439 441-442 445 447 454-456
ļ			461-462 471-472 475 477-479 481-
			482 485 488 493 498 500 503-506
			513 516 519 523-524 526 530 535~
1		}	540 542 544-545 549 555 565 567
			569-577 581 583-586 588 593 601
		Į	603-604 608-609 613-619 621-622 632-633 636-637 642 649-650 656-
			660 666 670 672 674-675 679 683
			701 708 716 718-720 731 735-736
	}	j	740-742 744-745 752 761 765 772-
			773 775-778 780 785-786 789-791
	İ		796 798 802 810-812 823-824 826
}	j		830 832-833 837-838 843-844 848-
	į		855 858-859 866-867 869 878-880 883 890-892 896 903 905 908 912-
	ĺ		914 922-924 927 930-931 937 939-
	l		941 952-953 955-958 963 969 973
1	j	1	976 981 985 987 990 992 995 1000
1	j	İ	1002 1005-1007 1013 1016 1025
[ĺ	1028-1031 1033 1035 1037 1039
	l	l	1042 1044 1047 1050 1053-1054
1		j	1059 1061 1063 1066 1070-1071 1079 1106 1110-1113 1115-1117
		ļ	1124 1126 1134-1135 1142 1144-
[ſ	. [1145 1163 1172 1178 1197 1199-
!		1	1200 1202 1216-1217 1224 1227-
]			1228 1240 1246 1254 1261 1266
]			1270 1278 1281 1285 1287 1290-
[1291 1293 1299-1301 1308 1314
]		}	1317-1320 1327 1331 1339 1343
		j	1346 1349 1353 1356 1361 1367 1369 1372-1374 1379-1380 1394
	l	-	1400 1403 1406 1408 1413 1417
	ľ	1	1419 1423 1425-1427 1430-1431
	1		1433 1439 1443 1446-1449 1459
			1463-1464 1482 1486 1493-1494

Firms Origin 1	RNA Source	Hyseq	SEQ ID NOS:
Tissue Origin	RNA Source	Library Name	332 333
			1506 1509 1513 1521-1522 1524
}			1526 1528 1531 1536-1537 1543
	Į.		1546 1548-1549 1552 1554-1555
	l	:	1557-1559 1571-1572 1581 1589- 1592 1597-1600 1609 1614 1621
			1626-1628 1630-1632 1634 1636
			1638-1639 1641 1646-1647 1651
	į		1653-1655 1661-1662 1676-1681
			1684 1686 1690 1702 1707 1711
1			1713-1714 1717 1720 1722-1723
			1727 1737-1738 1740 1758 1767
	ļ		1772 1781-1782 1785-1786
bone marrow	Clontech	BMD002	11 15-16 19 30-31 35-36 68-69 75
	l		83-84 93 99 103 108-109 118 137
			139 169-170 174 177 180 190 193
			212-213 219 222 225-226 232 237
	i		255 259 264 273-274 284 286 290-
	}		292 295 301 303-304 307 312-313
			316 324 326 330 334-335 348 352-
Į.	1		353 357 360 370-373 384 386-387 397 403-404 414-416 421 425-427
			429-430 433-436 440 444 451 454
			465-466 472 475 478 491 493 516
			520 523 525 531 545 548 552 566
1			569-570 581 583 590-591 597-598
İ	1		601 616-617 621 641 650 652 656
	1		659 671 674-675 679 684 710 718-
			719 728 734 737-738 742 761 765
İ	[774-778 790 811 814 818 830 834-
)	1		836 854-855 859 866 869 871 878-
1			879 884 889 892 904 922-923 932
İ			990 992 998 1001 1004 1016 1036
			1042 1048 1051 1054-1055 1058
			1088-1089 1106 1112-1114 1155 1157 1192 1200 1223 1227-1228
			1236-1237 1260-1261 1282-1283
			1285 1287 1295 1314 1317-1321
			1324-1327 1330 1333 1341 1343
			1347 1350 1353 1355-1357 1367
}	}	1	1369-1370 1373 1377 1379 1381
			1383-1384 1394 1397 1400 1406
	ļ		1413 1417 1425-1427 1438 1442
			1446 1459-1460 1470 1493 1505
			1521 1536 1546-1549 1560 1573-
			1574 1578 1598-1600 1621 1626
			1631 1634 1646 1649 1653 1656
	1	ļ	1658 1669-1670 1683-1684 1687-
		{	1688 1690-1693 1696 1699 1702 1704 1707-1709 1711 1720 1722-
	1)	1704 1707-1709 1711 1720 1722-
	1		1723 1725 1727 1729 1731-1735
			1738-1740 1743-1740 1732 1733
)	1786
bone marrow	Clontech	BMD004	73-74 503 922 1036 1711
bone marrow	Clontech	BMD007	95-96 866 1320 1475
adult colon	Invitrogen	CLNOOL	17 56-58 103 110 117 144 150 171
addic colon	I		179 185 188-189 201 204-206 210
}		1	218-221 225-226 231 237 251 277
			288 310 312 320 333 359 386 388
•			394 408 420 455 481 485 503 510-
		1	512 590-591 615 635 647-648 665
			672 684 697 710 725-726 743 780
			786 788 826-827 848-850 854-855
1	}		858 866 872 898 918 921-923 953
	ļ	ļ	976 983 993 1005-1006 1017 1020
	Ì		1025 1027 1054-1055 1063 1068-
\	1		1069 1140 1153 1170 1185 1196
1			1199 1220 1280 1314-1315 1320
1		1	1345 1351 1355 1369 1428 1439

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	SLY ID NOS:
		-	1462-1464 1512 1556 1583 1587 1594 1596 1614 1625-1626 1631 1639 1645 1650 1675-1677 1687- 1688 1701 1713-1714 1724 1740 1765
Mixture of 16 tissues - mRNAs	Various Vendors	CTL016	401 1490 1686
Mixture of 16 tissues - mRNAs*	Various Vendors	CTL021	312 782 1132-1133 1403 1712 1715
adult cervix	BioChain	CVX001	1 4-8 11 13 18-21 25-26 30-31 33 37-39 43 46-47 58 61 64-66 71 73-74 82 85 94 100 103-104 113 118 122 126 130 134 140 147 153-156 163 170 179 181 186 192 195-196 198 201-202 218-219 222 229-231 257 266 276-277 285-286 288 298 301-302 304 307 312-314 324 326 329-330 332 335 342 352 358 362 371-372 376 379 381-382 384 388 398 400 410 414 416 419-420 426-427 430-431 433-436 439 446 448 461-462 464 471-477 479 482-483 491 493 496 503 506 510-513 516-517 526 530 535 542-544 546-547 557 561 572-573 575-577 581-582 585-586 588-589 593-594 600 602 604-605 607-609 612 615-619 623 644 650 654 657-658 662-665 670 672 680 683 691-694 698 706 708-709 711 713 720-721 727 729 731-732 737 745-747 753-754 760 765 771 774-777 780 790 793 796 798 800 803 805 818 826 828 831-832 834-836 843 847-848 851-855 857-860 864-866 869 871 876 878-880 882 887 890-891 897 899-902 905-908 912-913 916 918-919 922 927 932 934-938 944 948 955-956 958 963-964 967 969-970 972 976 978-979 983 985 990 992 1000 1005-1007 1016-1017 1024 1027 1033 1036 1038 1045 1047 1053-1056 1066-1067 1071 1073 1075 1079 1082 1098 1113 1124 1129 1134 1139 1146-1149 1163 1167 1170 1173 1175 1177 1181 1197 1200 1202 1211 1214 1216 1221-1222 1225 1227 1232-1234 1240-1241 1243 1258 1264-1265 1268 1270 1279 1287-1290 1308 1310-1311 1316 1320 1323 1327 1345 1349 1353-1354 1360 1372-1374 1383-1384 1386 1394 1397 1405-

^{*} The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphablastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

•			
Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1406 1416 1425-1427 1431 1436-
			1437 1442 1446 1448 1453 1459
			1466 1472 1478 1482 1496 1501-
		•	1503 1506 1512 1522 1527-1528
•			1531 1533 1541 1547 1569 1571
			1585 1589 1597-1598 1600 1608-
			1609 1614-1616 1620 1623-1624
	į		1626-1628 1630 1638 1641 1643
	[1649 1653 1656 1662 1667 1669
1			1674-1675 1683 1685-1688 1699
ĺ]		1702 1709-1710 1715 1717 1722
ļ.		}	1724 1729 1731-1732 1735-1739
[[1741 1743-1744 1748-1749 1755
ì	1	}	1760-1762 1767 1773 1778 1785-
(Į.	İ	1
		<u></u>	1786
diaphragm	BioChain	DIA002	137 282 289 730 780 986 1409
1	J	1	1478 1599 1614
endothelial	Strategene	EDT001	3 5-10 13 15-21 24-26 29 34 37-
cells		1	39 42 44-45 50-51 53-55 57-58
Cerrs	•		60-61 65-66 68-69 73-74 77-78 80
	j	1	82-83 85 87 89 93-96 101-105 108
			110 112-114 116 118-122 124 128
		}	133-134 137-142 147-150 152-153
	1	· ·	103-104 107-144 147-100 107-103
			161-163 166-172 176-179 187 190
	1	· ·	192 194 196-201 204-207 210 212-
	ļ	l	214 220 224 229-230 233 235-236
ĺ		ļ	240-241 251-252 258 261-262 265
	}	ļ	267-269 272 276-277 279-281 284-
1	Ì		285 288 290 295-296 301-302 310-
}	1	1	311 313 316 321 325 329 331-333
			335 340 342 351-355 360 371 375
}	}	1	380-382 384 387 390 392 397 400
	İ		
1		Į.	407-408 410 412 414 416 425-427
			431 434-436 439 444-445 449 454
]		1	463-464 472-475 477-479 486 488-
Į.			490 497-498 500-504 510-513 516-
1	ł	1	519 522 524 526-528 532-534 536-
· ·			540 542-546 548 561-563 566-567
j			572-576 579 581 585-586 589 593
1	ļ	•	595 597 599 603 607-612 615-617
1		1	620 622 626 630 632-634 638-641
			644 647 656-660 662-664 670 673
		1	
	1		678 680-682 692-697 707 709-710
:	1		712-713 719 730 732 734 736 738
.	1	1	743-746 751 759 768 771 773 775-
}	1	1	778. 783 786-789 793 800 803 805-
1	Į.		807 810-811 814 816-818 821-822
1	1	1	824 826 828-829 832 834-838 842-
1	Į	1	845 848-850 854-860 862 864 869
1	1		871 874 876-879 883 885 887 890-
1	1	1	891 894-895 898-900 903 908 910-
(1	{	913 916 919-922 924 926-928 930-
	1	1	935 939 943 948-949 951-954 957
([1	750 757 743 746-747 751-757 757
į	1		959-961 964 969-970 973 975-978
1		1	983-984 988-990 992-993 996-997
	1	1	1000 1002 1004-1013 1016-1020
1		(1022-1025 1028 1031 1033-1034
			1038-1046 1050 1055-1056 1059-
			1060 1062-1064 1067-1070 1072-
			1074 1076 1078 1082 1086-1087
{			1089-1090 1093-1097 1099-1103
			1107 1109-1113 1116-1117 1124-
			110/ 1103-1113 1110-111/ 1154-
		ì	1126 1128-1131 1134-1135 1138
			1140 1144-1145 1148-1149 1153
)	1157 1160 1163 1171 1183-1184
	1		1198-1199 1202 1205-1207 1211
		İ	1216-1217 1219 1221 1225 1229
1	ļ	1	1232-1235 1238-1241 1243-1244
			1246 1250 1253 1257-1258 1261
· · · · · · · · · · · · · · · · · · ·	<u> </u>		1440 1430 1433 143, 1830 1831

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	
1			1265-1266 1268 1270-1271 1274-
}			1277 1280-1283 1285-1286 1288-
		•	1290 1293 1295 1298 1308 1312
1			1317-1320 1324-1325 1327 1329-
			1330 1334-1335 1338 1342-1343
{	[1345-1347 1350 1355-1356 1359
}			1367 1369 1374 1376 1379 1398
1	'		1400 1406 1408 1414 1417 1419
	İ		1424-1426 1428-1431 1434-1438
1		İ	•
			1440-1442 1448 1450 1462-1466
1	į.		1468 1472 1474 1478 1487-1488
}	j .	J	1491-1493 1501-1504 1506 1509
	·	,	1511 1516 1520-1521 1526 1529
	Ì		1531 1536-1537 1539-1540 1546-
<u> </u>			1547 1549 1552 1555 1557-1559
1			1561-1565 1568 1571 1575 1578-
1			1579 1581-1583 1587-1588 1590
}			1592 1597 1605-1606 1611 1613
(1615 1618-1621 1624-1628 1630-
}			1631 1634 1636 1638 1641 1643-
			1650 1652-1659 1664 1666-1667
1			
}			1669 1671 1675-1681 1683-1688
	,		1696-1698 1703 1711 1715-1716
1 .			1719 1722-1723 1726 1731-1733
	•		1736 1739-1741 1743-1744 1749
			1755 1760-1761 1765 1767-1768
			1771-1773 1776 1779 1783-1786
Genomic clones	Genomic DNA	EPM001	286 686 1297 1303-1304 1352
from the short	from		1411-1412 1754
arm of	Genetic		
chromosome 8	Research		
	BioChain	ES0002	131-132 261 289 380 503 860 892
esophagus	PIOCUGIU	£50002	
			1000 1007 1397
fetal brain	Clontech	FBR001	62-63 89 112 126 194 322 336-338
1			379 391 411 481 546 563 607 679
:			710 867 1012 1031 1055 1251 1262
[1		1320 1407 1643 1652 1686 1731-
] ,		1732 1746 1765
fetal brain	Clontech	FBR004	68-69 90-91 139 212-213 301 331
	·		362 374 403 436 611 645-646 659
			668 670 691 785 805 845 1163
1	.		1209 1216 1232-1233 1238-1239
1	l		1387 1410 1416 1430 1496 1536
1			1547 1593
fotal basis	Clantach	200000	
fetal brain	Clontech	FBR006	5-9 25 43 60 62-63 65-66 70 72
		•	80 87 92 101 103 108 114 136 139
	1		149 152-153 157 168 171-172 175
			207-208 210 212-213 221-226 237-
			238 251-253 266 272 279-281 295
			301-302 307 310 317-318 321-324
1			330 333-334 336-338 346-347 352
			357 370 373 377 379-380 382 384
	l		391-392 397 399 402 406-408 410-
]	,		411 417 421 424 426-427 430 436-
			437 440-443 454 460 464 467 473
			476 483 488-489 495 497 508 510-
			513 516 519-520 524 530 537-540
			544 547 550 561 567 572-574 582
			590-591 595 597 604 607-609 615
			623 628-629 631 634 638-640 655
Į.			657-658 660 665 669 674-675 679
			689 691-694 696-697 699 701 706
	ľ		710 716 720 728 732 734 736 742-
j l	j		744 757-760 763 775-778 780 799
			806-807 810 817-818 826 839 843
	ł		858 861 864 871-872 884 890-891
,			I
			894-895 898 904 915 921-923 935-
ì			936 938 945 950 952 955-956 958-
1	t t	i i	,
			959 961 963 967 969-971 990 992

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
	_ }.	Library Name	
			999 1001 1005-1006 1008 1013
ł			1016 1022 1024 1029-1030 1032
1	j		1035 1042 1047-1048 1052 1056
{			1065 1067 1070 1082 1089 1109
) !	1		1114-1115 1119 1131 1143-1149
<u> </u>			1151 1153-1156 1160 1163 1167
1 1	1		1172-1173 1178 1184 1186 1188
1 1			1190-1200 1211 1216 1222-1223
1			1226-1227 1229 1231 1236 1245
]			1253-1255 1258 1260 1262 1266
			1270-1273 1281 1287 1308-1309
)	1		I
1			1314 1317-1320 1326 1334-1335
į ('		1339 1341 1344 1350 1356 1369-
			1371 1373 1376 1379 1381-1382
1			1386 1392 1396-1398 1419 1423
'	1		1425-1426 1428-1429 1432 1437
1			1440-1441 1448 1466 1470 1482
			1502-1503 1507 1511 1513 1516
			1519 1536 1544 1549-1550 1557-
	(1559 1573 1589-1590 1598 1608
]		1611-1614 1619 1621 1625-1626
1.	1		1640 1651 1657-1658 1676-1679
1	į į		1
			1693 1696 1703-1704 1713-1714
1	1		1718 1720 1722 1724 1726 1728
]		1730-1733 1735-1736 1738-1739
1	\		1742 1745 1755 1759-1761 1765
1	}		1767 1771-1772 1777 1779-1780
	1		1786
fetal brain	Clontech	FBRs03	235-236 520 864 1068 1188 1587
fetal brain		FBT002	15-18 20-21 24-25 29 34 43 61-63
retal brain	Invitrogen	101002	77-78 98 101 103 107-108 128 130
Ĺ]		136 146 148 165-166 171 174 181
[1		185 196-198 204-205 208 223 230
1	1 1		
			235-236 251 253 261 268-269 280-
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757 1759-1761 1765 1771 1774 1776
		PHIDAA	235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757 1759-1761 1765 1771 1774 1776 1778 1781-1782 1786
fetal heart	Invitrogen	FHR001	235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757 1759-1761 1765 1771 1774 1776 1778 1781-1782 1786
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757 1759-1761 1765 1771 1774 1776 1778 1781-1782 1786
fetal heart	Invitrogen	FHR001 FKD001	235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757 1759-1761 1765 1771 1774 1776 1778 1781-1782 1786

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
Tisage Origin	RNA Source	Library Name	SEQ ID NOS:
			258 277 280-281 307 310 314 330
			371 387 392 395 403 422-423 431 436 443 455 469 500 519 522 542
	1		563 572-573 585 600 619 623 650
	Ì		654 657-658 660 679 719 731 780
}			798 821 833 844 854-855 857 864
1]	}	868 878 911 929 958 960 969 990
	ţ		992 1007 1046 1087 1103 1129
			1371 1376 1391 1422 1425-1426
			1440-1441 1470 1543 1598 1601
1	į		1618 1631 1651 1654-1655 1669
fetal kidney	Clontech	FKD002	1678-1679 1691-1692 1733 1785 352 384 426-427 440 583 602 1060
l recar krancy	Clonecen	110002	1131 1324-1325 1636
fetal kidney	Invitrogen	FKD007	20-21 82 163 335 679 988-989
fetal lung	Clontech	FLG001	1000 1227 1230 1320 1554 35~36 94 323 371 398 426-427 445
20002 20119		12001	473 549 560 604 616-617 626 631
			649 651 719 746 786-787 832 842
			849-850 864 894-895 1075 1178
)		1182 1200 1206 1309 1311 1345 1429 1493 1567 1576 1620 1686
fetal lung	Invitrogen	FLG003	9 15-16 29 41 47 68-69 83 88-89
1	[-	102 124 137 152-153 165 196 224
			229 231 249 254 256 267 291-292
			300 325 333 344-345 352 373 376 379 384 408 426-427 430 432 467-
			468 475 483 488 493 516 531 535
			545 547 549 564 582 602 623 644
			660 662-664 670 673 725-726 728
			761 766-767 774 805 830 852-853 864 875 921 932 937 946 949 963
			988-989 1014 1016-1017 1024 1027
			1090 1097 1170 1185 1200 1215-
			1216 1224 1258 1290 1309 1320
			1342 1347 1355 1369 1381 1413- 1414 1431 1438 1449 1491 1512
		'	1536 1547 1557-1560 1567 1590
	÷		1601 1636 1644 1653-1655 1662
			1667 1671 1675 1680-1681 1706 1739 1760-1761 1769
fetal lung	Clontech	FLG004	103 276 334 465-466 737 843 1131
			1614 1658
fetal liver-	Columbia	FLS001	3-11 13 15-21 25 30-39 41-48 50-
spleen	University		51 54 56-58 60-66 68-69 72 75 77-80 82-83 85 87 89 92-103 105-
}			110 112 116-124 126-127 130 133
ļ .			135-139 141 144 147-149 152-153
]	,		157 163-165 167-172 174 176-178
			180 186 188-190 193-194 196 198- 200 202-206 210-214 219 221-231
			233-236 240-244 246-247 250-251
			255-256 258 261-265 268-269 272
			274 276-278 280-281 284-286 288
	ļ		293 295 299-301 304 306-307 309 311 314 316 318 320-321 326 329-
			332 342 344-345 350 352-353 356-
		[358 360 362 370-374 376 378-384
	1		386-387 390 392-393 400-401 403
	1	ļ	406 408 410-412 415 417 419 422- 437 439-442 444-445 448 452-454
		j	456 459 461-470 472-479 481-483
	.	ļ	487-488 490-491 493 500-501 503-
			506 509-513 515-520 522-524 526-
	ļ	ļ	529 531 534 536-540 542 547-549 553-554 561-562 564 567-568 571-
	ł	}	576 579 581 583 585-597 599-605
	L		

123

Tissue Origin RNA Source Hyseq Library Name 607 610-613 615-621 623-6628-634 636-640 644 647-6660 665 669-670 672 674-6681-682 684 690-695 697 7710 713-714 716-719 725-7711 734 736 738 740-741 748 750-751 759-766 768 777 779 783-788 793 796 7885 808 810-812 814 818-88 824 826-832 834-837 843-88 867 869-876 878-883 887 897-898 902 904-914 916 928 930-937 939 945-950 960-961 963-965 967 969 978 980-983 986 988-990 978 980-983 980 988-990 978 980-983 980 988-990 988-990 978 980-983 980 988-990 978 980-980 988-990 978 980-980 988-990 978 980-980 988-990 978 980-980 988-990 978 980-980 988-990 978 980-980 988-990 978 980-980 988-990 9	550 655- 675 678 702 708- 728 730- 743-746 772 704- 798 800- 819 821- 847 849- 849-895 919 921- 953-958 971 974- 992-993 008 1012 1028- -1044
607 610-613 615-621 623-6 628-634 636-640 644 647-6 660 665 669-670 672 674-6 681-682 684 690-695 697 7 710 713-714 716-719 725-7 731 734 736 738 740-741 7 748 750-751 759-766 768 7 777 779 783-788 793 796 7 805 808 810-812 814 818-6 824 826-832 834-837 843-6 867 869-876 878-883 887 8 897-898 902 904-914 916 9 928 930-937 939 945-950 9 960-961 963-965 967 969 9 978 980-983 986 988-990 995-997 1000-1002 1004-1014 1016-1019 1025-1026 1031 1033 1035-1036 1039 1047 1049-1050 1053-1056	550 655- 675 678 702 708- 728 730- 743-746 772 704- 798 800- 819 821- 847 849- 849-895 919 921- 953-958 971 974- 992-993 008 1012 1028- -1044
628-634 636-640 644 647-6 660 665 669-670 672 674-6 681-682 684 690-695 697 7 710 713-714 716-719 725-7 731 734 736 738 740-741 7 748 750-751 759-766 768 7 777 779 783-788 793 796 7 805 808 810-812 814 818-8 824 826-832 834-837 843-8 867 869-876 878-883 887 8 897-898 902 904-914 916 9 928 930-937 939 945-950 9 960-961 963-965 967 969 9 978 980-983 986 988-990 995-997 1000-1002 1004-1014 1016-1019 1025-1026 1031 1033 1035-1036 1039 1047 1049-1050 1053-1056	550 655- 675 678 702 708- 728 730- 743-746 772 704- 798 800- 819 821- 847 849- 849-895 919 921- 953-958 971 974- 992-993 008 1012 1028- -1044
660 665 669-670 672 674-6 681-682 684 690-695 697 7 710 713-714 716-719 725-7 731 734 736 738 740-741 7 748 750-751 759-766 768 7 777 779 783-788 793 796 7 805 808 810-812 814 818-6 824 826-832 834-837 843-6 867 869-876 878-883 887 897-898 902 904-914 916 9 928 930-937 939 945-950 9 960-961 963-965 967 969 978 980-983 986 988-990 9 978 980-983 986 988-990 9 995-997 1000-1002 1004-10 1014 1016-1019 1025-1026 1031 1033 1035-1036 1039-1047 1049-1050 1053-1056	775 678 702 708- 728 730- 743-746 772 774- 798 800- 819 821- 847 849- 889-895 919 921- 953-958 971 974- 992-993 008 1012 1028- -1044
710 713-714 716-719 725-7 731 734 736 738 740-741 7 748 750-751 759-766 768 7 777 779 783-788 793 796 7 805 808 810-812 814 818-8 824 826-832 834-837 843-8 867 869-876 878-883 887 8 897-898 902 904-914 916 9 928 930-937 939 945-950 9 960-961 963-965 967 969 9 978 980-983 986 988-990 9 995-997 1000-1002 1004-10 1014 1016-1019 1025-1026 1031 1033 1035-1036 1039 1047 1049-1050 1053-1056	728 730- 743-746 772 774- 798 800- 819 821- 847 849- 889-895 919 921- 953-958 971 974- 992-993 008 1012 1028- -1044
731 734 736 738 740-741 7 748 750-751 759-766 768 7 777 779 783-788 793 796 7 805 808 810-812 814 818-8 824 826-832 834-837 843-8 867 869-876 878-883 887 8 897-898 902 904-914 916 9 928 930-937 939 945-950 9 960-961 963-965 967 969 9 978 980-983 986 988-990 9 995-997 1000-1002 1004-101014 1016-1019 1025-1026 1031 1033 1035-1036 1039 1047 1049-1050 1053-1056	743-746 772 774- 798 800- 819 821- 847 849- 889-895 919 921- 993-958 971 974- 992-993 008 1012 1028- -1044
748 750-751 759-766 768 76 777 779 783-788 793 796 76 805 808 810-812 814 818-8 824 826-832 834-837 843-8 867 869-876 878-883 887 8 897-898 902 904-914 916 9 928 930-937 939 945-950 9 960-961 963-965 967 969 9 978 980-983 986 988-990 9 995-997 1000-1002 1004-10 1014 1016-1019 1025-1026 1031 1033 1035-1036 1039 1047 1049-1050 1053-1056	772 774- 7798 800- 819 821- 847 849- 889-895 919 921- 953-958 971 974- 992-993 008 1012 1028- -1044
777 779 783-788 793 796 78 805 808 810-812 814 818-8 824 826-832 834-837 843-8 867 869-876 878-883 887 88 897-898 902 904-914 916 928 930-937 939 945-950 960-961 963-965 967 969 978 980-983 986 988-990 995-997 1000-1002 1004-1014 1016-1019 1025-1026 1031 1033 1035-1036 1039 1047 1049-1050 1053-1056	798 800- 819 821- 847 849- 889-895 919 921- 953-958 971 974- 992-993 008 1012 1028- -1044
805 808 810-812 814 818-8 824 826-832 834-837 843-8 867 869-876 878-883 887 8 897-898 902 904-914 916 9 928 930-937 939 945-950 9 960-961 963-965 967 969 978 980-983 986 988-990 9 978 980-983 986 988-990 995-997 1000-1002 1004-10 1014 1016-1019 1025-1026 1031 1033 1035-1036 1039 1047 1049-1050 1053-1056	819 821- 847 849- 889-895 919 921- 953-958 971 974- 992-993 008 1012 1028- -1044
824 826-832 834-837 843-8 867 869-876 878-883 887 8 897-898 902 904-914 916 9 928 930-937 939 945-950 9 960-961 963-965 967 969 9 978 980-983 986 988-990 995-997 1000-1002 1004-10 1014 1016-1019 1025-1026 1031 1033 1035-1036 1039 1047 1049-1050 1053-1056	847 849- 889-895 919 921- 953-958 971 974- 992-993 008 1012 1028- -1044
867 869-876 878-883 887 8 897-898 902 904-914 916 9 928 930-937 939 945-950 9 960-961 963-965 967 969 9 978 980-983 986 988-990 9 995-997 1000-1002 1004-10 1014 1016-1019 1025-1026 1031 1033 1035-1036 1039 1047 1049-1050 1053-1056	889-895 919 921- 953-958 971 974- 992-993 008 1012 1028- -1044
897-898 902 904-914 916 9 928 930-937 939 945-950 9 960-961 963-965 967 969 9 978 980-983 986 988-990 9 995-997 1000-1002 1004-10 1014 1016-1019 1025-1026 1031 1033 1035-1036 1039 1047 1049-1050 1053-1056	919 921- 953-958 971 974- 992-993 008 1012 1028- -1044
960-961 963-965 967 969 978 980-983 986 988-990 995-997 1000-1002 1004-1014 1016-1019 1025-1026 1031 1033 1035-1036 1039 1047 1049-1050 1053-1056	971 974- 992-993 008 1012 1028- -1044
978 980-983 986 988-990 9 995-997 1000-1002 1004-10 1014 1016-1019 1025-1026 1031 1033 1035-1036 1039- 1047 1049-1050 1053-1056	992-993 008 1012 1028- -1044
995-997 1000-1002 1004-10 1014 1016-1019 1025-1026 1031 1033 1035-1036 1039- 1047 1049-1050 1053-1056	008 1012 1028- -1044
1014 1016-1019 1025-1026 1031 1033 1035-1036 1039- 1047 1049-1050 1053-1056	1028- -1044
1031 1033 1035-1036 1039- 1047 1049-1050 1053-1056	-1044
1047 1049-1050 1053-1056	
1 104, 1043, 1030, 1032, 1030	1058- l
1059 1061-1064 1067-1070	1072-
1074 1076 1078 1082 1085	-1087
1089-1090 1097 1099-1103	1107-
1113 1115-1119 1121-1123	1125
1127-1128 1131-1134 1136	
1144-1150 1153 1159-1160 1170 1175 1177-1178 1188	1190-
1170 1175 1177-1178 1180	1208-
1132 1133-1200 1202 1303	-1222
1225 1227 1234 1237 1241	
1246-1247 1251 1254 1258	3 1261
1266 1268 1270-1273 1277	/-1282
1284-1285 1287-1290 1294	1299-
1300 1306-1308 1313-1320	1324-
1325 1327 1330 1332-1333 1341 1343 1345-1347 1349	9-1350
1341 1343 1343-1347 1343	
1369-1370 1372-1374 1376	
1381 1383-1384 1386 1389	9-1391
1400 1402-1403 1405-1410	0 1413
1415 1417-1419 1422-1429	9 1431
1435-1437 1439-1442 1445	5-1446
1448-1449 1454 1458-1459	
1470 1472 1474 1477-1478 1482 1485 1491-1493 1498	
1501-1507 1509 1511-1513	2 1516-
1519 1524-1526 1529 1533	2 1536-
1541 1546-1547 1549-1550	0 1552-
1554 1562 1564 1569 157	2 1574-
1575 1578 1581 1583 158	7-1588
1591-1592 1594-1595 159 1600-1604 1611-1612 161	/-1598 4-1615
1600-1604 1611-1612 1611	4-1625
1627-1628 1630-1632 163	4-1639
1645-1651 1653-1662 166	4 1667-
1669 1671 1673-1674 167	6-1688
1690 1696 1701-1703 170	6-1709
1711 1713-1714 1718-171	.9 1722
1724-1727 1731-1733 173	3 1740-
1741 1743-1744 1746 174 1752 1754 1760-1765 176	:0 1131- :7-1773
1752 1754 1760-1765 176	
	35-39 42
44-45 48 50-51 54-55 57	7-58 61 64
68-69 73-75 78 80 82 84	1 87 95-98
100 103 105 107-108 110	3 112-113
116-119 122-125 128 130) 137-138
145 147-153 155 157 159) 161-163 = 177 101
166 168 171-172 174-175 188-189 193-194 196-198	8 200-203 2 1// TOT
188-189 193-194 196-196	, 200 200

Tissue Origin	RNA Source	Hyseq	SBQ ID NOS:
Tissue Origin	RNA Source	Library Name	Sag 15 Nos.
[206 212-215 219-221 223 225-229
1			231-232 240-244 246-247 250-251
1			258-259 262 264 268-269 272 275 277 280-281 284 286 288 290-292
į Į			277 280-281 284 286 288 290-292
]			318 320-321 323 325 329 331 334
]			342 348-349 352-353 356 359 368
· (371 374 376-379 381-384 386-387
<u> </u>	٠		392-393 397-398 400-401 403 410-
		· ·	413 421 423 426-427 429-430 433-
,	'		436 438 440 443 445 448 451-452
			454-455 460-463 465-467 469 471- 473 475-476 478-479 481-483 487
			490-491 493-494 497 500-501 503-
		•	505 509-513 515-517 519-520 524
1			526-531 534 537-542 544 547 552-
			554 556 558 561-562 564-567 571-
]			577 583-587 590-591 593 595 597
į į			601 604-606 608-613 616-617 619-
		1	624 626-632 634 637-642 644 647
}			674-675 681-682 685 688 690 696
			698 700-703 707 709-710 713 717
			719-721 723-724 728 731-732 734
			737-738 742-745 748 752 754 759
}	}		763-766 768 770 773-777 780 782
			784 786 791 795-798 801-802 805
	[808 811-812 818 823-824 826-827
	(832 834-837 839 843 846 848-856 858-861 865 867 869 871 873-874
		}	876 878 881-882 887 889 892 894-
			898 901-902 904 906-908 913-915
			919 921-924 926-932 934-935 937
\(\) .			939-941 943 946-947 950 953 958
,			961 965-967 971 973-975 977-979
ł		ł	981 984-985 990 992-993 995-997
		}	999 1001 1004-1007 1009-1011
		}	1031 1033-1035 1039-1042 1044-
			1045 1049 1053 1055-1056 1058-
			1059 1062 1064-1065 1067-1070
:		·	1072-1074 1079 1082 1087 1089
	}		1093 1097 1099-1103 1105-1107
	1	1	1109-1114 1123 1125-1127 1132-
		1	1134 1140 1143-1145 1148-1150
	1	į	1177-1178 1181-1184 1190-1192
	1		1195-1197 1199 1204 1206 1208
	1	1	1211 1214 1216 1219 1227 1230
)	1	1234-1235 1237 1240-1241 1243
1	1		1245 1247 1256 1258 1260-1261
1			1264 1268 1270-1271 1275 1278- 1279 1284-1286 1288-1289 1299-
1	ł		1301 1306 1308 1312 1314 1317-
1	•	}	1319 1323-1325 1327-1330 1334-
			1335 1339 1343-1347 1349-1350
			1354-1355 1357 1360 1362-1363
			1365-1367 1369 1372 1376 1378-
1			1380 1386 1389-1391 1394 1400
)	,		1403 1406 1409 1416-1419 1422-
			1427 1429 1435 1437-1438 1440-
1		-	1442 1446 1448-1450 1453 1460- 1461 1468 1470 1472 1474-1475
		1	1461 1468 1470 1472 1474-1475
1			1498 1500-1504 1506 1508-1509
j			1511-1512 1516 1518-1519 1521
			1524-1528 1531 1536-1538 1543
			1547 1550 1554 1556 1564 1567-
<u></u>	<u> </u>	<u> </u>	1569 1580 1587-1588 1591-1592

			200 100
Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	1597-1598 1600-1601 1611-1612
	i		1618-1628 1630-1631 1635-1638
	1		1641 1646-1649 1652 1654-1659
			1661-1662 1664 1667-1669 1674
	ł		1676-1679 1683-1684 1686-1688
			1691-1692 1699 1702 1707 1711
			1713-1714 1717 1719 1722 1726-
			1727 1730-1733 1738 1740 1743-
			1744 1748-1752 1758 1760-1761
			1763-1764 1767 1769 1772-1773
			1776 1779 1783-1786
fetal liver-	Columbia	FLS003	103 300 318 321 352 372 379 381
	University	F13003	384 392-393 403 422 424 429 434-
spleen	Ourserprey		435 440 444 453 503 515 544 592
	1		978 1064 1324-1325 1327 1333
			1357 1369 1378 1418 1424 1622
	[1646 1649 1680-1681 1689-1690
Ì			1717 1743-1744 1769
fetal liver	Invitrogen	FLV001	15-16 26 34 58 61 64 70 75 78 89
recar river	THATCTOGEN	5 TA 0 O T	98 105 112 116 120-121 123 133
l	[151 166 176 180 194-196 198 200
1	}		204-206 210-211 220 225-226 230
1	{		235-236 239 247 259 261 267 272
]		277 280-281 303 310 313 317 320-
1			321 329 344 356 371 374 376 379-
		•	382 395 408 412 414 419 429 434-
			435 441-442 465-466 490 494 504-
ļ			506 509 522 527 534 552-553 562
	1		567 569-570 572-574 607 631 657-
			658 667 669 672 685-686 702 717
			725-726 732 748 759 761 778 784
İ			786 809 817 829 837 857 861 872-
ł			873 875 881 889 894-895 909 911
			916 954 963 967 974 977 986 988-
			989 993 995 997 1000 1005-1006
)	1008 1014-1015 1020 1042-1043
1			1070 1086-1087 1089-1090 1118-
	Į		1119 1122 1144-1145 1148 1153
l	ł	İ	1157 1159 1183 1195-1196 1227
]			1250 1257-1258 1262 1267 1280
	1		1285 1307 1312 1314 1317-1320
,	1	}	1344-1345 1349-1350 1355 1362-
-	{	l .	1363 1403 1405 1415 1419 1425-
	1	İ	1426 1429 1431 1442 1448 1463-
1	1		1464 1469-1470 1489 1528 1536
1			1539 1549-1550 1557-1562 1577
	İ	1	1583 1598 1601 1611 1615 1622
	1		1644 1649 1666 1674 1706 1721
	1	1	1738 1746 1763-1765 1774 1776
		}	1779
604-1 12	Clontech	FLV002	676 998 1719
fetal liver		FLV004	93 133 214 301 355 374 379 555
fetal liver	Clontech	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	581 601 679 837 847 859 1123
			1236 1270 1313 1324-1325 1327
{			1355 1367 1425-1426 1536 1690
			1733 1760-1761
	 		26 37-39 50-51 58 84 86 89 98
fetal muscle	Invitrogen	FMS001	113 128 131-132 139 155 172 186
	1		113 128 131-132 139 155 172 166
	1.	1	261 276 282 286 302 325 359 361
		1	376 379 383 398 412-413 419 430
		ì	3/0 3/9 303 390 412-413 419 430
1	1	{	436 448 452 462-463 473 477 503
	1		519 529 561 569-570 590-591 597
	1	1	607 623 626 635 647 660 672 715
		1	725-726 730 733 761 775-777 788
1	l	1	826 837 860 874 913 915 921 935
Í			
	ļ		970 980 986 988-990 992 1000-
		}	970 980 986 988-990 992 1000- 1001 1007 1014 1027 1035-1036 1045 1060 1064 1070 1083 1097

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1099-1102 1116-1117 1121 1164
Į.		ļ	1173 1198 1208 1228 1240 1258
\			1266 1270 1277 1298 1317-1320
	1	İ	1324-1325 1329 1336-1337 1369
J]		1383-1384 1399-1400 1403 1409
ì			1303-1304 1399-1400 1403 1409
ļ	1	ļ	1433 1505 1514 1542 1551 1554
!			1557-1559 1562 1589 1599 1620
}	l		1632 1644 1650 1652 1671 1675
			1712 1725-1726 1743-1744 1754
			1766
fetal muscle	Invitrogen	FMS002	119 221 273 402 426-427 463 547
1			599 736 869 1000 1033 1083 1266
1	(1431 1440-1441 1468 1545 1599
<u> </u>	}		1673 1678-1679 1687-1688 1710
			1712-1714 1723 1725 1731-1733
1			1743-1744 1760-1761 1767
fetal skin	Invitrogen	FSK001	1 4-11 15-16 20-23 25 29 33 40
			43 46 56-57 60-61 64-66 75 82 87
}]		97-98 105 107-108 113 118-119
			123 133 135-137 139 144 146 148
			1
1			151-153 156 163 170 176 180 188-
	ĺ		189 197-198 200 202-203 210 218
			222 231 246-247 261 263 265-270
	[277 285-286 290 293 299 301 307
)			311 321 325 328 330 333-335 339
			341 345 351-352 355-356 358-359
	l l		362 368 370 372 376 379-382 384
			388 394 404-405 408-409 411-412
	}	•	419-420 424 426-427 436 441-442
			445 448-449 454 462 465-466 472
	}		476 490 493 504 506 509 515-517
			519 526 531 537-540 547 549 560-
			561 567 572-573 581 584 589 611-
			612 615 623 630-631 635 647 649
	1		651 657-658 660 662-665 667 669
			672 676 678 681 688 701 704-705
			709-710 713 717 720-721 725-726
			728-729 732 748 750 753 759 764
i			766 770 775-777 780-781 786 788-
!			789 798 809 811 814 816-817 822
			824-826 831 842 857 859 861 863-
. (
·]	•		864 881 894-895 908 910-911 916
			918 922-923 928 932-933 935 937
		1	946 948-949 953 960-961 966-967
	1	!	970 975 977 986 990 992-993 999-
i	1	ľ	1000 1004 1007 1013 1018 1025
	1		1027 1032 1035 1041-1043 1054
ſ		1	1057-1058 1060 1062-1064 1069
	}	}	1072 1077 1090-1091 1097 1099-
		ļ	1103 1108 1113 1119 1123 1128
	ĺ	1	1131 1134 1140 1148-1149 1152-
	1		1153 1156 1163 1167 1178 1182
			1189 1192 1195-1196 1198 1201-
}	j	ļ	1
	Ì		1205 1208 1211-1212 1216 1219-
	ł		1220 1222 1225 1240 1243 1258
	i		1266-1267 1274 1277 1280 1282-
	Ì		1285 1299 1310 1317-1322 1324-
	!		1325 1329-1330 1342 1344 1346
1	ĺ		1349-1351 1354-1357 1365-1366
})	}	1369 1371 1373 1376 1378 1380
		ļ	1383-1384 1387 1399-1400 1405
Ì		ł	1410 1427 1429 1431 1433-1435
1	Ì	1	1439-1441 1448-1449 1454 1457
İ		Ì	1468 1470 1472 1475 1480-1481
1	-	1	1487 1490-1491 1493 1498 1509
		j	1512 1521 1525-1526 1529 1535-
	1]	1536 1547 1549 1557-1559 1588
ľ	1	Ì	1592 1595 1597-1598 1601 1603-
	1		1604 1608 1611 1614 1618 1624-
		——————————————————————————————————————	

			SEQ ID NOS:
Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
		DIDIALY Name	1626 1632 1634 1636 1641 1643-
			1644 1646 1654-1657 1660-1662
			1665 1668 1675 1685 1687-1689
•			1702-1703 1709-1710 1716 1719
			1724 1727 1731-1732 1737-1740
	i		1742 1747 1749 1755 1760-1761
			1765 1772 1776-1777 1779-1780
			1786
fetal skin	Invitrogen	FSK002	13 286 302 307 313 321 330 335
			339 341 354 370 372 385 400 402
			408 414 426-427 433 436 450 454 515 544 585 598 767 810 845 939
			1076 1109 1155 1317-1320 1326
			1333-1335 1343 1347 1350 1369-
			1371 1377-1378 1391 1397 1422
			1466 1647 1656 1678-1679 1687-
			1688 1693 1718 1721 1725 1731-
			1732 1739 1755
fetal spleen	BioChain	FSP001	110 137 211 353 589 927 1108
			1639 1771
umbilical cord	BioChain	FUC001	4-8 10 12 14 17 33-36 44-46 57
			64 68-69 75 82 85 101 104 113-
			114 116 119 122-124 133 137 153-
	j l		154 157 161 163 166-167 175 181-
	[184 186 192 197-198 200-202 212-
			215 230 234 246-247 251 256 263
			267 271-272 280-281 284 295 301
			314 317 321 326 333-335 345 351
	}		356 368 371-373 379-380 386 390 392 394 406 408-410 412 414 416
			420 424 427 430-436 438 444-446
[454 459 461 463 467 473 482-483
			486 488 490 495 504 509 524 526
ļ			537-540 547 555 561 574-577 588-
			591 593 606 615 620-621 632 637
ļ			645-647 650 659-660 662-664 667-
}			668 674-675 684 687 696 698 701
			703-705 709 711 714 719-720 725-
			727 732 749-750 762 765 771 775-
			777 780 789-791 793 796 802-803
ł			814-817 822 833 843 845 848 858
			861 864 875 879 888 894-895 897-
1		•	900 903 906-907 911-912 925 930-
!			933 936 940 948 953 960 966 977
	1		984 990 992 998 1000-1001 1005-
[1007 1016 1023 1025 1037 1046-
}			1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113
,			1115 1134 1144-1148 1151 1154
[1156 1163 1171 1197 1204-1205
	Ì		1208 1216 1218 1224 1234-1235
	1		1243-1244 1246 1279 1283 1286-
			1287 1298 1316 1320 1344 1346
1	[1350 1357 1359 1371 1373 1375
	1]	1381 1398 1400 1403 1408 1414
ļ.			1424 1427-1428 1431 1433 1440-
		[1442 1446 1454-1455 1479 1482
	1		1484-1485 1489 1492-1493 1504-
		ł	1505 1513 1525 1527 1536 1538
		}	1546 1565 1567 1571 1573 1575-
	1		1576 1578-1579 1591 1595 1600-
}		1	1601 1608 1612 1615 1621 1624
		Į	1626 1636-1637 1647-1648 1651
		1	1653 1656 1658 1661-1662 1672
		1	1675 1682 1684 1686-1688 1690
	1	1	1709-1710 1722 1727 1729 1735-
		7777.002	1738 1740-1741 1760-1761 1768 4 9 11-13 17-18 22-23 25 37-39
fetal brain	GIBCO	HFB001	4 9 11-13 17-18 22-23 25 37-39
1	i	}	47-41 DA-DT D4-22 20 00-01 02-00

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	
			72 75 77 80 82 85 90-91 94 100- 102 107 110 112-116 118-119 122-
			123 126 128 134 136-140 147-148
			153-155 157 161 165 169-172 175
1			181 186 188-189 197-198 204-206
			208 210 215 222-223 225-226 230
			235-238 240-241 247 253 256-258
			260-262 267-269 276 279-281 284 286 289 298 300-302 307 310 318
			321-323 325 330-331 339 341 346-
ļ ·			349 352 354 356-359 362 364-365
			371-372 377 379-380 382 384 387
			390 400 408 414-416 419 424 431
			434-435 438 441-443 449 451 453-
			455 457-463 470 472-473 475 477- 478 482-483 486-488 490-491 493
			496 499-500 502-504 506-507 509-
			512 516 519-520 522 525-526 529-
			530 537-540 543-544 546-547 566-
			567 569-570 572-582 585 588 590-
			591 593 595 599 601 604 606-609 611-612 614-620 622-624 630 632
]	.		636 643 645-647 650-652 654 659
			661 665 667-668 670-672 676 678
ĺ		!	681 687 689 692-694 697 699 710
		ĺ	714 717 721 727 729-732 734 736
			738 743-746 750-751 759 763 766 770 772 775-777 784 789 791 796
		•	799 802-805 810-811 814 819-821
			824 826 830 834-837 839-850 854-
}	i		856 858-860 862 864 869 871 876-
			877 879 883 886-887 890-891 893-
			895 898-901 905 908-910 912-916 919 922-923 925 927 930-933 935-
			938 948 952-960 963-964 967 969-
			972 975 978-979 981 983 986-987
		•	990 992 995 997 999-1002 1005-
			1009 1011-1013 1016 1018-1019
			1023 1026 1029-1031 1033-1035 1038 1041 1047 1050 1053 1057
			1059 1064 1068 1070 1072-1073
			1078-1079 1081-1082 1086 1089
; ;			1094 1097 1103 1107-1109 1113-
,			1115 1121-1122 1127 1134-1135
			1138 1140 1143 1148-1151 1153 1156-1157 1159 1167 1170 1175
	İ	·	1193-1194 1200 1202 1207-1209
			1211 1216 1219-1220 1226-1227
	j		1229 1232-1234 1240-1241 1243
	j		1246 1249-1251 1253-1254`1258 1267-1268 1271 1276 1279 1282
	[1285-1289 1293-1294 1305 1307-
	Ì	1	1308 1312 1316 1320 1327 1338-
	ļ		1339 1341-1344 1346 1349 1355-
.]]	1	1357 1359 1365-1366 1369-1370
	!	ļ	1373-1375 1379 1386 1389 1394 1398 1409 1413-1414 1416-1417
ľ	1	(1420-1421 1425-1427 1430 1433
1]	ľ	1437 1439 1442 1445-1452 1454-
ļ	j	j	1457 1459 1463-1464 1468 1470
	·		1474 1477-1479 1489 1492 1494
1			1497-1498 1501-1503 1507 1509
1	Ì		1511-1513 1517 1520-1521 1524- 1526 1531-1533 1535 1537-1538
			1547 1554 1556-1559 1564-1567
	j	}	1571 1584 1587 1589 1594 1599-
			1601 1611-1612 1614-1616 1619-
-	·		1620 1625-1628 1630-1631 1634
			1637-1638 1640-1643 1645 1648-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
		TINEALY HAME	1649 1651 1653-1655 1657-1658
į			1664-1665 1667 1669 1673 1678-
			1679 1683-1684 1686 1693 1701
			1704-1705 1709 1713-1714 1717-
			1720 1724 1727-1728 1731-1733
ĺ			1737-1738 1743-1744 1752 1754-
			1755 1757 1760-1761 1765 1772
			1779 1785
macrophage	Invitrogen	HMP001	5-8 110 204-205 503 634 678 859
			878 933 988-989 1379 1448 1504
infant brain	Columbia	IB2002	10 12-13 15-18 22-23 25 29 34
	University		37-39 43 47 50-51 54-56 58 60-63
		,	65-66 68-69 72-74 80 82-83 86 88-92 97 100 102-104 106-108 110
			112-113 115-116 118 123 128 130
			134-136 138-139 143 147-149 151-
j	Ì	ĺ	152 154-155 163 165-167 169 172-
	1	ł	175 181-184 186 193-196 198 201
	({	203-205 209-210 214-215 222 224-
		j	226 231-232 235-236 239 246-247
	}		252 257 260 268-269 272 276-277
	l	1	279-281 286 288 291-292 295 298
	j]	300-301 304 307 310 313 321-323
	{		330-331 333-334 339 346-347 349
	ļ	}	352 356-357 362 371-372 377 379-
			380 383-384 392 397 401 406 408
		1	411 413-414 416 418-419 422 428
	ļ		430-431 434-435 438 443 449 453-
			454 461 464-466 469-470 472-473
			475-476 478 482-483 487 490 492
			494 497 503 507-508 510-513 516 519-520 524-526 530-534 536-540
			547 550-551 561 563-564 566-567
•			572-576 579 581-582 584-587 590-
		ł	591 593 595-597 607-609 611-613
	İ	1	616-617 620 622-624 627 631 637
	(641 645-647 650-655 657-658 660-
	ļ	1	665 667-675 689 691 695 697 699
		ì	703 707 713-715 717 721 728-731
]	733-736 739 743 745 751 755 759
	İ	1	763 769-770 772 778 780-781 785
			788-789 793-794 799 803 808 811
	· ·]	814 825-826 830 834-836 840-843
	1		845 848-850 854-855 860 862 864-
	1	1	865 870 872 875-876 878 886 888
			890-891 894-896 898 903-904 916- 917 919 922-925 927-928 930-932
	1	(934-936 938 941 945-946 948-950
		1	953-954 959-962 966-969 977 979
			981 986-990 992 997 999-1000
		1	1004-1006 1014 1016 1018-1019
			1024-1025 1033 1036 1047 1051-
		(1052 1054-1055 1057-1059 1063-
		}	1064 1068-1070 1073 1081-1082
1			1085 1089 1108-1113 1118-1120
)		1123-1124 1130 1132-1138 1140
1			1149 1151 1153-1154 1163-1170
}	1		1172 1174-1175 1183-1184 1188
			1190 1193-1194 1196-1197 1199
1	1		1204 1208-1209 1211 1218-1222
			1226-1227 1229 1231 1234 1241
			1247 1249 1251 1256 1258 1261-
	1		1262 1269 1274 1279 1281 1283 1285 1287-1289 1294-1295 1305
			1285 1287-1289 1294-1295 1305
		Ì	***** **** **** **** ****
			1307 1313-1314 1316-1320 1329
			1307 1313-1314 1316-1320 1329 1332 1341-1342 1345 1349 1356
			1307 1313-1314 1316-1320 1329 1332 1341-1342 1345 1349 1356 1362-1363 1365-1366 1368-1370
			1307 1313-1314 1316-1320 1329 1332 1341-1342 1345 1349 1356

Tissue Origin RNA Source Siper SEQ ID NOS:	Tissue Origin	RNA Source	Vieno	OTO TO MO
1423 1429-1431 1435-1436 1435-1 1441 1443 1447-1449 1451-1455 1468 1470-1471 1475 1479 1462-1465 1468 1470-1471 1475 1479 1462-1465 1468 1470-1471 1475 1479 1462-1465 1468 1470-1471 1475 1479 1462-1465 1469 1502-1503 1505-1507 1509 1522-1523 1525 1528 1531-1533 1542 1546-1547 1549-1550 1554-1555 1554 1555 1563 1565-1567 1569 1575 1560 1563-1566 1566-1567 1569 1575 1560 1563-1566 1566-1568 1567 1624 1626-1627 1630-1633 1637 1639-1640 1642 1644 1646 1621 1624 1626-1627 1630-1633 1637 1639-1640 1642 1644 1646 1659 1624 1625-1637 1630-1633 1637 1639-1640 1642 1644 1647 1552 1654-1655 1658-1659 1664-1665 1672-1673 1676-1681 1689-1688 1693-1695 1701-1702 1708 1708 1771-7720 1723-1724 1726-1728 1773 1728-1738 1742 1748 1748 1773 1778 1787 1774 1774 1775 1774 1775 1776 1777 1777 1775 1776 1777 1777 1777 1775 1776 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1777 1	1200dc Oligin	MA Source		SEQ ID NOS:
1441 1443 1447-1449 1451-1452 1468-1465 1467 1475 1479 1482-1468 1486 1470-1471 1475 1479 1482-1483 1485 1489-1499 1502-1503 1505-1507 1509 1522-1523 1528 1528 1531-1533 1542 1546-1547 1549-1550 1554-1555 1563 1555-1567 1509 1522-1523 1528 1528 1528 1530 1554-1555 1563 1565-1567 1509 1522-1523 1528 1526-1550 1554-1555 1563 1565-1567 1569 1575 1580 1563-1586 1588 1590 1592-1593 1595 1588 1506-1601 1608-1610 1612 1612-1614-1616 1619 1621 1624 1626-1627 1630-1633 1637 1639-1640 1642 1644 1647 1652 1654-1655 1672-1673 1676-1681 1685-1688 1693-1695 1701-1702 1704 1708 1717-1720 1723-1724 1726-1728 1733 1735-1741 1743-1744 1752 1775-1775 1762 1765 1771 1774 1708 1717-1772 1723-1724 1726-1728 1733 1735-1741 1743-1744 1752 1755-1758 1762 1765 1771 1774 1708 1777-1778 1766 1771 1774 1768 1777-1778 1766 1771 1774 1765 1771 1774 1768 1777-1778 1766 1771 1774 1765 1777-1778 1766 1771 1774 1765 1771 1774 1765 1771 1774 1765 1771 1774 1765 1771 1774 1765 1771 1774 1765 1771 1774 1765 1771 1774 1765 1771 1774 1765 1771 1774 1765 1771 1774 1765 1771 1774 1765 1771 1774 1776 1776 1776 1776 1776 1776				1423 1429-1431 1435-1436 1439-
1468 1470-1471 1475 1479 1482-1483 1485 1489-1494 1496 1499-1499 1502-1503 1505-1507 1509-1507 1509-1522-1523 1528			1	
1483 1485 1493-1494 1496 1490-1501 1509 1522-1523 1525 1528 1531-1533 1542 1546-1547 1549-1550 1554-1555 1563 1565-1567 1569 1575 1580 1583-1586 1588 1589 1592-1593 1595 1598 1600-1601 1608-1601 1612 1614-1616 1619 1621 1624 1626-1627 1630-1633 1637 1639-1640 1642 1644 1647 1652 1654-1655 1658-1659 1664-1665 1672-1673 1676-1681 1685-1688 1693-1695 1701-1702 1704 1708 1777-1773 1776-1778 1776-1779 1774 1777-1778 1776-1779 1774 1777-1778 1776-1779 1774 1777-1778 1776-1779 1774 1777-1778 1776-1779 1774 1776-1779 1774 1777-1778 1776-1779 1774 1777-1778 1776-1779 1774-1779-1779 1774 1777-1778 1776-1779 1774 1777-1778 1776-1779 1776-1779 1774 1777-1778 1776-1779 1774 1777-1778 1776-1779 1774 1777-1778 1776-1779 1774 1777-1778 1776-1779 1774 1777-1778 1776-1779 1774 1777-1778 1776-1779 1774 1777-1778 1776-1779 1774 1777-1778 1776-1779 1774 1777-1778 1776-1779 1774 1777-1778 1776-1779 1776-1779 1774-1779-1779 1774-1779-1779 1774-1779-1779-1779-1779-1799-1799-1799-				
1499 1502-1503 1505-1507 1509 1522-1523 1523 1523 1523 1523 1523 1523 1523 1523 1523 1523 1523 1525 1563 1565-1567 1569 1575 1580 1580-1500-1601 1608-1610 1612 1614-1616 1619 1621 1624 1627 1629-1628 1629-1625 1629-				
1522-1523 1525 1528 1531-1531 1542 1546-1537 1549-1550 1554- 1555 1563 1565-1567 1569 1575 1508 1583-1586 1588 1580 1592- 1593 1595 1598 1600-1601 1608- 1610 1612 1614-1616 1619 1621 1624 1626-1627 1630-1633 1637 1639-1640 1642 1644 1644 1647 1652 1654-1655 1658-1659 1664-1665 1672-1673 1676-1681 1685-1688 1693-1695 1701-1702 1704 1708 1717-1727 1723-1724 1726-1728 1733-1735-1741 1742-1744 1752 1735-1728 1762 1765 1771 1774 1775-1778 1786 1762 1765 1771 1774 1775-1778 1786 1762 1765 1771 1774 1775-1778 1786 1762 1765 1771 1774 1775-1778 1786 1762 1765 1771 1774 1771-1778 1786 1762 1765 1771 1774 1771-1778 1786 1762 1765 1771 1774 1771-1778 1786 1762 1765 1771 1774 1771-1778 1786 1762 1765 1771 1774 1771-1778 1786 1762 1765 1771 1774 1772-1778 1786 1762 1765 1771 1774 1771-1778 1786 1762 1765 1771 1774 1771-1778 1786 1762 1765 1771 1774 1771-1778 1786 1762 1765 1771 1774 1771-1778 1786 1762 1765 1771 1774 1771-1778 1786 1762 1765 1771 1774 1771-1778 1786 1762 1765 1771 1774 1771-1778 1786 1762 1765 1771 1774 1771-1778 1786 1762 1765 1771 1774 1771-1778 1776 1777 1777 1777 1777 1777 1777	}	}	}	
1542 1546-1547 1549-1550 1555-1551 1550 1556 1565-1567 1569 1575 1550 1550 1550-1551 1550 1550-1550 1550-1550 1550-1550 1550-1550 1550-1560-1601 1601-1601-1601-1601-1601-1601-16				
1555 1563 1565-1567 1569 1575 1592 1593 1595 1598 1600-1601 1608-1601 1612 1614-1616 1619 1621 1624 1626-1627 1630-1633 1637 1639-1640 1642 1644 1647 1652 1654-1655 1656-1659 1664-1665 1662-1657 1676-1681 1685-1688 1693-1695 1701-1702 1704 1708 1717-1720 1723-1724 1726-1728 1733 1735-1741 1743-1744 1752 1755-1768 1762 1675 1876 1761 1771 1774 1776-17178 1786 1771-1778 1786 1771-1778 1786 1771-1778 1786 1771-1778 1786 1771-1778 1786 1771-1778 1786 1771-1778 1786 1771-1778 1786 1771-1778 1786 1771-1778 1786 1782-1741 1743-1744 1752 1755-1758 1762 1765 1771 1774 1777-1778 1786 1782-1778 1782-		1	{	
1580 1583-1586 1580 1592-1601-1601 1608- 1610 1612 1614-1616 1619 1621 1624 1626-1627 1630-1633 1637 1639-1640 1642 1644 1647 1652 1654-1655 1658-1659 1669-1665 1672-1673 1676-1681 1695-1688 1693-1695 1791-1702 1702 1702 1708 1773 1775-1781 1741 1743-1744 1752 1733 1735-1788 1782 1765 1771 1774 infant brain		ļ		
1593 1595 1598 1600-1601 1608- 1610 1612 1614-1616 1619 1621 1624 1626-1627 1630-1633 1637 1629-1640 1642 1644 1647 1652 1624-1655 1658-1659 1664-1665 1672-1673 1676-1681 1685-1688 1633-1695 1701-1702 1704 1708 1771-1720 1723-1724 1726-1728 1733 1735-1741 1743-1744 1752 1733 1735-1741 1743-1744 1752 1735-1778 1766 1771-1778 1786 1771-1778 1786 1771-1778 1786 1771-1778 1786 1771-1778 1786 1771-1778 1786 1782-1728 1736 1733-1731 107 110 112 118 123 128 133 135-137 146 148 152 124 128 123 135-137 146 148 152 125 126 169 174 194 198 20 215 223 225-226 229 235-226 247 260 276-221 266 290-292 295-300-301 310 322 324 331 334 339 346-347 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 371 376-377 382 349-350 352 357 372 357 356-368 349-378 382 389 384-895 889 904 917 349-379 379 379 379 379 379 379 379 379 379		Ì		
1610 1612 1614-1616 1619 1621 1621 1621 1626-1627 1630-1633 1637 1639-1640 1642 1644 1647 1652 1654-1655 1658-1659 1664-1655 1658-1659 1664-1655 1658-1659 1664-1655 1658-1659 1664-1655 1670-1702 1704 1708 1708 1707-1702 1703-1704 1708 1708 1707-1702 1703-1704 1708 1708 1707-1702 1703-1704 1708 1708 1707-1708 1765 1771 1774 1775 1775 1776 1775 1776 1776 1776 1777 1778 1765 1771 1774 1777-1778 1765 1771 1774 1777-1778 1765 1771 1774 1777-1778 1765 1771 1774 1777-1778 1765 1771 1774 1777-1778 1765 1771 1774 1777-1778 1765 1771 1774 1777-1778 1765 1771 1774 1777-1778 1786 1762 1777-1778 1786 1762 1777-1778 1786 1762 1777-1778 1786 1762 1777-1778 1786 1762 1777-1778 1786 1762 1777-1778 1786 1762 1777-1778 1786 1762 1777-1778 1786 1777-1778 1786 1762 1777-1778 1786 1777-1778 1786 1782 1777-1778 1786 1782 1777-1778 1786 1782 1777-1778 1786 1782 1777-1778 1786 1782 1777-1778 1786 1782 1777-1778 1786 1782 1782 1782 1782 1782 1782 1782 1782				
1624 1626-1627 1630-1633 1637 1639-1640 1642 1644 1647 1652 1654-1655 1664-1665 1665-1668 1668-1658 1668-1658 1668-1658 1668-1658 1668-1658 1668-1658 1668-1658 1668-1658 1668-1658 1668-1658 1672-1702 1704 1704 1704 1704 1704 1707 1707 1706 1704 1708 1717-1720 1723-1724 1726-1728 1733 1735-1741 1743-1744 1752 1735-1778 1768 1762 1765 1771 1774 1775 1768 1775 1778 1768 1775 1778 1768 1777 1778 1768 1777 1778 1768 1777 1778 1768 1777 1778 1768 1777 1778 1768 1777 1778 1768 1777 1778 1768 1777 1778 1768 1777 1778 1768 1777 1778 1768 1777 1778 1768 1777 1777 1778 1768 1777 1777 1778 1768 1777 1777 1778 1768 1777 1777 1778 1768 1777 1778 1768 1777 1777 1778 1768 1777 1777 1778 1768 1777 1777 1778 1768 1777 1777 1778 1768 1777 1777 1778 1768 1777 1				
1639-1640 1642 1644 1647 1652 1654-1655 1658-1659 1664-1655 1672-1673 1676-1681 1685-1688 1693-1585 1701-1702 1704 1704 1708 1707-1702 1704 1704 1708 1717-1702 1703-1704 1704 1708 1717-1702 1703-1704 1704 1708 1717-1702 1703-1704 1704 1708 1717-1702 1703-1704 1704 1708 1707-1718 1765 1771 1743-1744 1752 1755-1773 1758 1762 1765 1771 1774 1777-1778 1786 1762 1765 1771 1774 1777-1778 1786 1762 1765 1771 1774 1777-1778 1786 1762 1765 1771 1774 1777-1778 1786 1762 1765 1771 1774 1777-1778 1786 1780 1800-101 107 110 112 118 123 123 123 133 133-17 146 148 182 123 128 133 133-17 146 148 182 123 128 133 133-17 146 148 182 123 128 133 133-17 146 148 182 123 128 133 133-17 146 148 182 123 128 128 139 133-137 146 148 182 123 128 123 128 133 133-17 146 148 182 123 124 124 124 124 124 124 124 124 124 124	•			
1654-1655 1658-1659 1664-1665 1672-1688 1693-1693 1672-1673 1676-1681 1685-1688 1693-1695 1701-1702 1704 1708 1717-1720 1723-1724 1726-1728 1733 1735-1741 1743-1744 1752 1735-1778 1765 1777 1778 1786 1755-1778 1762 1765 1777 1778 1786 1755-1778 1765 1777 1778 1786 1755-1778 1778 1778 1778 1778 1778 1778 1778				
1672-1673 1676-1681 1685-1688 1693-1695 1701-1702 1704 1708 1708 1675-1695 1701-1702 1704 1708 1707-1702 1704 1708 1717-1720 1723-1724 1726-1728 1733-1741 1743-1744 1752 1735-1758 1762 1765 1771 1774 1775-1778 1786 1777-1778 1786 1777-1778 1786 1777-1778 1786 1778-1786 1778-178 1786 1778-1				1654-1655 1658-1659 1664-1665
1717-1720 1723-1724 1726-1728 1733 1735-1741 1743-1744 1752 1755-1758 1762 1765 1771 1774 1755-1758 1762 1765 1771 1774 1755-1758 1762 1765 1771 1774 1757-1776 1786 1777-1776 1786 1777-1776 1786 178-80 88 100-101 107 110 112 118 123 128 133 135-137 146 148 152 123 125-226 292 235-236 247 260 225-226 292 235-236 247 260 225-226 292 235-236 247 260 226-229 295 300-301 310 322 324 331 333 346-347 349-350 352 357 371 376-377 382 384 403 408-409 414-415 453-455 472 476 478-479 490 503 7516 520 530 534 536-540 551 563 572-576 585 587 590-591 593 595-596 601 606 612 616-617 620 622-624 650 652-653 661 665 670-671 674-675 678 689 715 727 727-728 730 734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 898 904 917 917 991 992-1920 32935-936 466 960 606 612 616-617 610-6100 6100 1001-61006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1220 1123 1127 1144-1145 1120 1123 1127 1124-1145 1120 1123 1127 1126 1288 1288 1288 1288 1289 1395 1346 1357 1355 1366 1378-1379 1388 1400 1403 1431 1436 1440-1441 1446-1447 1457 1459 1451 1459 1503 1507 1509 1536 1546 1557-1559 1567 1572 1587 1593 1644 1647 1657-1658 1673 1679-1691 1663 1664 1701-7702 1708-1709 1713-1714 1719 1757 1760-1761 1663 1664 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1664 1701-7702 1708-1709 1713-1714 1719 1757 1760-1761 1664 1701-7702 1708-1709 1713-1714 1719 1757 1760-1761 1664 1701-7702 1708-1709 1713-1714 1719 1757 1760-1761 1664 1701-7702 1708-1709 1713-1714 1719 1757 1760-1761 1664 1701-7702 1708-1709 1713-1714 1719 1757 1760-1761 1664 1701-7702 1708-1709 1713-1714 1719 1757 1760-1761 1664 1701-7702 1708-1709 1713-1714 1719 1757 1760-1761 1664 1701-7702 1708-1709 1713-1714 1719 1757 1760-1761 1664 1701-7702 1708-1709 1713-1714 1719 1757 1760-1761 1664 1701-7702 1708-1709 1713-1714 1719 1757 1760-1761 1664 1701-7702 1708-1709 1713-1714 1719 1757 1760-1761 1664 1701-7702 1708-1709 1709 1709 1709 1709 1709 1709 1709	1		l	1672-1673 1676-1681 1685-1688
1733 1735-1741 1742-1744 1752 1755-1758 1765 1765 1771 1771 1772 1775-1758 1766 1771 1774 1777-1778 1786 1771-1778 1786 1881-101-101-101-101-101-101-101-101-101				1693-1695 1701-1702 1704 1708
1755-1768 1762 1765 1771 1774 1777-1778 1766 infant brain	1			
infant brain Columbia University IB2003 I77-18 20-23 29 34 43 60 68-69 78-80 88 100-101 107 110 112 118 123 128 133 135-137 146 148 152 159 166 169 174 194 192 203 215 223 225-226 229 235-236 247 260 276-281 286 290-292 295 300-301 310 322 324 331 334 339 346-347 349-350 352 357 371 376-377 382 384 403 408-409 414-413 453-455 472 476 478-479 490 503 507 516 520 530 534 536-540 551 563 572- 576 585 587 590-591 593 595-596 601 606 612 616-617 606 622-624 650 652-653 661 665 670-671 674- 675 678 689 715 717 727-728 730 734 759 775-777 780-787-780-780 806-807 811 824 845-846 864 869 875 882 889 894-895 890 4917 919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1228-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1988 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1661 1663 1-664 1701-1702 1702-1702 1708-1709 1713-1714 1719 175 1760-1761 1765 1771 1779 infant brain Columbia IBM002 101 12 119 175 279-281 321 334]		
Infant brain	1	[•
University 78-80 88 100-101 107 110 112 118 123 128 133 135-137 146 148 152 159 166 169 174 194 198 203 215 223 225-226 229 235-236 247 260 276-281 286 290-292 295-300-301 310 322 324 331 334 339 346-347 349-350 352 357 371 376-377 382 384 403 408-409 414-413 453-455 472 476 478-479 490 503 507 516 520 530 534 536-540 551 563 572- 576 585 587 590-591 593 595-596 601 606 612 616-617 620 622-624 650 652-653 661 665 670-671 674- 675 678 689 715 717 727-728 730 734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 890 4917 919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1643-1664 17071-1702 1708-1708 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain Columbia University infant brain Columbia 1EM002 10 12 119 175 279-281 321 334	infant best	Columbia	700000	
123 128 133 135-137 146 148 152 159 166 169 174 194 198 203 215 223 225-226 229 235-236 247 260 276-281 286 290-292 295-300-301 310 322 324 331 334 339 346-347 349-350 352 357 371 376-377 382 384 403 408-409 414-415 453-455 472 476 478-479 490 503 507 516 520 530 534 5587 590-591 593 595-596 601 606 612 616-617 620 622-624 650 652-653 661 665 670-671 674-675 678 689 715 717 727-728 730 734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 898 904 917 919 921-923 932 935-36 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144-1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1306 1314 1327 1333 1344 1347 1350 1356-1357 1365-1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557-1559 1567 1572 1587 1575 1575 1589 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1668-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain Columbia IBM002 101 113 139 152 260 279 290-292 374 377 551 563 608-609 635 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1439 1507 1615 1640 1694-1695 1763-1764 1767 1779 infant brain Columbia IBM001 10 12 119 175 279-281 321 334	intant brain		TR5003	
159 166 169 174 194 198 203 215	1	OUTAGERICA	,	
223 225-226 229 235-236 247 260 276-281 286 290-292 295 300-301 310 322 324 331 334 339 346-347 349-350 352 357 371 376-377 382 384 403 408-409 441-415 453-455 472 476 478-479 490 503 507 516 520 530 534 536-540 551 563 572-576 585 587 590-591 593 595-596 601 606 612 616-617 620 622-624 650 652-653 661 665 670-671 674-675 678 689 715 717 727-728 730 734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 889 804 917 9919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144-1145 1149 1151-1125 1126 1126 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365-1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557-1559 1567 1572 1587 1579 1589 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1609 1765 1771 1778 1076 1770 1773 1774 1719 1757 1760-1761 1765 1771 1778 1079 173-1714 1719 1757 1760-1761 1765 1771 1778 1079 173-1714 1719 1757 1760-1761 1765 1771 1778 1079 173-1714 1719 1757 1760-1761 1765 1771 1778 1079 173-1714 1719 1757 1760-1761 1765 1771 1778 1079 173-1714 1719 1757 1760-1761 1765 1771 1778 1079 173-1714 1719 1757 1760-1761 1765 1771 1778 1079 173-1714 1719 1757 1760-1761 1765 1771 1778 1079 173-1714 1719 1757 1760-1761 1765 1771 1778 1079 173-1714 1719 1757 1760-1761 1765 1771 1778 1079 173-1714 1719 1757 1760-1761 1765 1779 1779 1079 173-1714 1719 1757 1760-1761 1765 1779 1779 1079 1779 1779 1779 1079 1779 1779 1779 1079 1779 1779 1779 1779 1079 1779 1779 1779 1779 1779 1779 1779	1	1		
276-281 286 290-292 295 300-301				
310 322 324 331 334 339 346-347 349-350 352 357 371 376-377 382 384 403 408-409 414-415 453-455 472 476 478-479 490 503 507 516 520 530 534 536-540 551 563 572- 576 585 587 590-591 593 595-596 601 606 612 616-617 620 622-624 650 652-653 661 665 670-671 674- 675 678 689 715 717 727-728 730 734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 899 804 917 919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1706 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain Columbia IBM002 101 113 139 152 260 279 290-292 University infant brain Columbia IBM002 101 113 139 152 260 279 290-292 1327 1397 1431 1498 1507 1615 1640 1594-1695 1763-1764 1767 1779	}			276-281 286 290-292 295 300-301
349-350 352 357 371 376-377 382 384 403 408-409 414-415 453-455 472 476 478-479 490 503 507 516 520 530 534 536-540 551 563 572- 576 585 587 590-51 593 595-596 601 606 612 616-617 620 622-624 650 652-653 661 665 670-671 674- 675 678 689 715 77 727-728 730 734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-89 898 904 917 919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1166 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1345 1346-1345 1365-1357 1365-1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1661 1683-1684 1701-1702 1708-17061 1765 1771 1778 infant brain Columbia University IBM002 101 113 139 152 260 279 290-292 374 377 551 563 608-609 653 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779 infant brain Columbia University 188001 10 12 119 175 275-281 321 334				310 322 324 331 334 339 346-347
384 403 408-409 414-415 453-455 472 476 478-479 490 503 507 516 520 530 534 536-540 551 563 572- 576 585 587 590-591 593 595-596 601 606 612 616-617 620 622-624 650 652-653 661 665 670-671 674- 675 678 689 715 717 727-728 730 734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 898 904 917 9919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1706 1713-1714 7119 177 1706-1761 1765 1771 1778 infant brain Columbia University IBM002 101 113 139 152 260 279 290-292 University infant brain Columbia Columbia 185001 10 12 119 175 279-281 321 334				
S20 530 534 536-540 551 563 572- 576 585 587 590-591 593 595-596 601 606 612 616-617 620 622-624 650 652-653 661 665 670-671 674- 675 678 6869 715 717 727-728 730 7734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 898 904 917 919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1228-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain				
576 585 587 590-591 593 595-596 601 606 612 616-617 620 622-624 650 652-653 661 665 670-671 674-675 678 689 715 717 727-728 730 734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 899 904 917 919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144-1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365-1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557-1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1643 1664 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain				472 476 478-479 490 503 507 516
601 606 612 616-617 620 622-624 650 652-653 661 665 670-671 674- 675 678 689 715 717 727-728 730 734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 899 904 917 919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1663-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain		}		520 530 534 536-540 551 563 572-
650 652-653 661 665 670-671 674- 675 678 689 715 717 727-728 730 734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 898 904 917 919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain		ĺ		
675 678 689 715 717 727-728 730	İ			
734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 898 904 917 919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1664 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain Columbia University IBM002 IBM002 IOI 113 139 152 260 279 290-292 374 377 551 563 608-609 653 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779 infant brain Columbia University IBS001 IO 12 119 175 279-281 321 334				
806-807 811 824 845-846 864 869 875 882 889 894-895 898 904 917 919 921-923 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain				
875 882 889 894-895 898 904 917 919 921-923 932 935-936 946 950 954 962 977 979 999 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain Columbia University IBM002 101 113 139 152 260 279 290-292 374 377 551 563 608-609 653 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779 infant brain Columbia Columbia IBS001 10 12 119 175 279-281 321 334				
919 921-923 932 935-936 946 950 954 962 977 979 979 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 16683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain		ĺ		806-807 811 824 845~846 864 869
954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1661 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain Columbia University IBM002 IBM002 IBM002 IO1 113 139 152 260 279 290-292 Winversity IBM002 IO3 1507 1509 1536 1546 1557- 1640 1694-1695 1763-1764 1767 1779 infant brain Columbia University IBM002 ID4 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779 infant brain Columbia IBM011 IBM012 ID5 119 175 279-281 321 334)		
1005-1006 1009 1011 1017 1024		· [
1033 1037 1043 1055 1057 1109				
1114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 1761 1778 1779 1770 1770 1771 1771 1771 1772 1771 1773 1771 1773 1771 1773 1771 1773 1771 1773 1771 1774 1771 1775 1770	•			
1145 1149 1151-1153 1160 1167				
1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 1765 1771 1778 101 113 139 152 260 279 290-292 374 377 551 563 608-609 653 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779 101 101 12 119 175 279-281 321 334 1		·		
1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365-1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557-1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 1 1765 1771 1778 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				
1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain	1	.		1202 1206 1209 1220-1221 1226
1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain				· · · · · · · · · · · · · · · · · · ·
1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain		1		
1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778				
1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 Infant brain	1		İ	
1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 Infant brain				· •
1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 1760 1761 1765 1771 1778 1760 1761 1765 1771 1778 1760 1761 1765 1771 1778 1760 1761 1765 1771 1778 1760 1761 1765 1771 1778 1760 1761 1765 1771 1778 1760 1761 1765 1771 1778 1760 1761 1760 1761 1760 1761 1760 1761 1760 1761 1760 1761 1760 1761 1760 1761 1760 1761 1760 1761 1760 1761 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760 1760				· ·
1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 infant brain Columbia IBM002 101 113 139 152 260 279 290-292 374 377 551 563 608-609 653 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779 infant brain Columbia IBS001 10 12 119 175 279-281 321 334	1			f
1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 1765 1771 1778 101 113 139 152 260 279 290-292 374 377 551 563 608-609 653 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779 101 101 101 101 101 101 101 101 101 1				•
1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 1765 1771 1778 101 113 139 152 260 279 290-292 374 377 551 563 608-609 653 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779 11fant brain Columbia IBS001 10 12 119 175 279-281 321 334 1168 1709 170 1709 1175 279-281 321 334 1176 1709 1176 1779	[İ	!
1713-1714 1719 1757 1760-1761 1765 1771 1778 1765 1771 1778 101 113 139 152 260 279 290-292 374 377 551 563 608-609 653 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779 116ant brain Columbia IBS001 10 12 119 175 279-281 321 334 1265 1765 1760 1760 126 176 1779 126 176 1760 1760 126 176 1760 1760 126 176 1760 1760 126 176 1760 1760 126 1760 126 1760 1]	1		
Infant brain Columbia IBM002 101 113 139 152 260 279 290-292 374 377 551 563 608-609 653 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779 infant brain Columbia IBS001 10 12 119 175 279-281 321 334		1		
infant brain Columbia University		ł	ŀ	
University 374 377 551 563 608-609 653 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779 infant brain Columbia IBS001 10 12 119 175 279-281 321 334	infant brain	Columbia	IBM002	
814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779 infant brain Columbia IBS001 10 12 119 175 279-281 321 334				
infant brain Columbia IBS001 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779 10 12 119 175 279-281 321 334		- I		
infant brain Columbia IBS001 10 12 119 175 279-281 321 334		ĺ		f
infant brain Columbia IBS001 10 12 119 175 279-281 321 334		{		
infant brain Columbia IBS001 10 12 119 175 279-281 321 334		1		
20 20 275 275 202 522 553				
University 371 446 551 563 623 652 667 669	intant brain		IBS001	
		university		371 446 551 563 623 652 667 669

Tissue Origin RNA Source Library Name Comparison RNA Source Hyseq Comparison	5 1229 7-1319 0-1441 2 1546 0 1618 2 94 105 -208 212- 321 326 446 462 527 535 567 586 662-664 775-777 849 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
671-672 819 949 966 111: 1151 1188 1193-1194 1194 1258 1265 1271 1287 131' 1324-1325 1342 1423 1444 1448 1471 1482 1525 153: 1562 1569 1588 1591 1614 1647 1649 1658 1ung,	5 1229 7-1319 0-1441 2 1546 0 1618 2 94 105 -208 212- 321 326 446 462 527 535 567 586 662-664 775-777 849 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
1258 1265 1271 1287 131 1324-1325 1342 1423 1446 1448 1471 1482 1525 1533 1562 1569 1588 1591 1616 1647 1649 1658 lung, fibroblast 153 157 197-198 203 207 213 223 262 266 283 302 333 356 370 427 430 436 472 493 498 503 516 519 537-540 542-544 562 565 599-600 607 615 630 647 692-694 712 719 745 748 794-796 810 837 843-847 856 869 876 903 934 953 964 975-976 984 1000 10 1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	7-1319 0-1441 2 1546 0 1618 2 94 105 -208 212- 321 326 446 462 527 535 567 586 662-664 775-777 849 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
1324-1325 1342 1423 1444 1448 1471 1482 1525 1533 1562 1569 1588 1591 1610 1647 1649 1658 lung, fibroblast 153 157 197-198 203 207 213 223 262 266 283 302 333 356 370 427 430 436 472 493 498 503 516 519 537-540 542-544 562 565 599-600 607 615 630 647 692-694 712 719 745 748 794-796 810 837 843-847 856 869 876 903 934 953 964 975-976 984 1000 10 1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	0-1441 2 1546 0 1618 2 94 105 -208 212- 321 326 446 462 527 535 567 586 662-664 775-777 849 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
1448 1471 1482 1525 1533 1562 1569 1588 1591 1610 1647 1649 1658 lung, fibroblast Strategene LFB001 5-9 17 20-21 25 68-69 83 153 157 197-198 203 207- 213 223 262 266 283 302 333 356 370 427 430 436 472 493 498 503 516 519 537-540 542-544 562 565 599-600 607 615 630 647 692-694 712 719 745 748 794-796 810 837 843-847 856 869 876 903 934 953 964 975-976 984 1000 10 1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	2 1546 0 1618 2 94 105 -208 212- 321 326 446 462 527 535 567 586 662-664 775-777 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
1562 1569 1588 1591 1616 1647 1649 1658 1019, Strategene LFB001 5-9 17 20-21 25 68-69 80	0 1618 2 94 105 -208 212- 321 326 446 462 527 535 567 586 662-664 775-777 849 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
lung, Strategene LFB001 5-9 17 20-21 25 68-69 8: 153 157 197-198 203 207-213 223 262 266 283 302 333 356 370 427 430 436 472 493 498 503 516 519 537-540 542-544 562 565 599-600 607 615 630 647 692-694 712 719 745 748 794-796 810 837 843-847 856 869 876 903 934 953 964 975-976 984 1000 10 1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	2 94 105 -208 212- 321 326 446 462 527 535 567 586 662-664 775-777 849 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
lung, fibroblast Strategene fibroblast LFB001 5-9 17 20-21 25 68-69 8: 153 157 197-198 203 207- 213 223 262 266 283 302 333 356 370 427 430 436 472 493 498 503 516 519 537-540 542-544 562 565 599-600 607 615 630 647 692-694 712 719 745 748 794-796 810 837 843-847 856 869 876 903 934 953 964 975-976 984 1000 10 1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	-208 212- 321 326 446 462 527 535 567 586 662-664 775-777 849 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
fibroblast 153 157 197-198 203 207- 213 223 262 266 283 302 333 356 370 427 430 436 472 493 498 503 516 519 537-540 542-544 562 565 599-600 607 615 630 647 692-694 712 719 745 748 794-796 810 837 843-847 856 869 876 903 934 953 964 975-976 984 1000 10 1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	-208 212- 321 326 446 462 527 535 567 586 662-664 775-777 849 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
213 223 262 266 283 302 333 356 370 427 430 436 472 493 498 503 516 519 537-540 542-544 562 565 599-600 607 615 630 647 692-694 712 719 745 748 794-796 810 837 843-847 856 869 876 903 934 953 964 975-976 984 1000 10 1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	321 326 446 462 527 535 567 586 662-664 775-777 849 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
333 356 370 427 430 436 472 493 498 503 516 519 537-540 542-544 562 565 599-600 607 615 630 647 692-694 712 719 745 748 794-796 810 837 843-847 856 869 876 903 934 953 964 975-976 984 1000 10 1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	446 462 527 535 567 586 662-664 775-777 849 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
472 493 498 503 516 519 537-540 542-544 562 565 599-600 607 615 630 647 692-694 712 719 745 748 794-796 810 837 843-847 856 869 876 903 934 953 964 975-976 984 1000 10 1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	527 535 567 586 662-664 775-777 849 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
599-600 607 615 630 647 692-694 712 719 745 748 794-796 810 837 843-847 856 869 876 903 934 953 964 975-976 984 1000 10 1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	662-664 775-777 849 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
692-694 712 719 745 748 794-796 810 837 843-847 856 869 876 903 934 953 964 975-976 984 1000 10 1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	775-777 849 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
794-796 810 837 843-847 856 869 876 903 934 953 964 975-976 984 1000 10 1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	849 854- 955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
856 869 876 903 934 953 964 975-976 984 1000 10 1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	955-956 05-1007 3 1064 3 1134 3 1232- 5 1311
964 975-976 984 1000 10 1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	05-1007 3 1064 3 1134 3 1232- 5 1311
1024-1025 1033 1039 105 1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	3 1064 3 1134 3 1232- 5 1311
1070 1072 1082 1112-111 1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	3 1134 3 1232- 5 1311
1136-1138 1140 1195 122 1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	3 1232- 5 1311
1233 1246 1279 1285 129 1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	5 1311
1320 1334-1335 1343 142 1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	
1446 1478 1482 1493 150 1552 1555 1567 1575 158 1620 1625 1632 1638 164	7-1428
1620 1625 1632 1638 164	
	2 1598
1690 1696 1702 1711 173	3 1741
1760-1761 1778 1785 Tung tumor Invitrogen LGT002 5-10 18 20-21 29 33-36	40 43 53
lung tumor Invitrogen LGT002 5-10 18 20-21 29 33-36 54-55 61 65-66 68-70 73	
88-89 93-94 100 103 106	
113 115-116 118-119 123	
130-132 135-137 139-141	
147-148 151-153 155-156	159 161
164 169 171 179-180 185	
194 196-199 203-208 210	
216-217 219 222 233 240	
246 251-252 255-256 261 272 276-277 279-281 284	
290 295 298 301-302 309	
321 329 332 341-342 344	
352 358-360 363 368 370	
380-381 384 389-390 398	400 409
414 423 426-427 430 432	
444 450-451 454 462 468	
480-483 487-488 490-491	
498 500 503-506 509-512	
519 521-523 526 530 534 547 554 557 564 566-567	
585-586 588-589 595-596	
611-612 615 619 621 623	
632-633 644 647 649 651	
660 662-665 667 669 672	
696 700 706 710 713 716	718-719
722-723 728 734-739 743	
763 765-766 773-778 784	
789 791 800 802-803 809	
824 826 828-829 832 838	
845 849-850 852-855 857 866 874 878-880 882 887	
897-898 902 904 906-907	
918-920 922 924-925 927	
934-935 937 947 950 953	
961 963 966-967 969 973	977-979
981 984 986-987 990 992	2-993 995
997 999-1001 1005-1007	1009
1012-1013 1018 1020 102	22-1024
1026 1029-1030 1033 103	

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
	lati boardo	Library Name	, sing in Nos.
			1045 1047-1050 1052 1054-1055
			1059 1063-1064 1067-1071 1073-
	·		1074 1078 1085 1087 1089 1095-
			1097 1104 1106-1107 1109 1112 1116-1117 1119 1126 1134-1135
	ļ		1139 1141-1142 1144-1145 1148
	Ì		1152-1153 1156-1158 1167 1170
Ì		ł	1172 1178 1195-1196 1198-1200
			1202 1204 1208 1214 1216 1219
			1222 1227 1234 1241 1247 1252
			1257-1258 1265 1267-1270 1276
	'		1278 1280-1281 1283 1285 1288-
			1289 1295 1300 1305 1308 1312
			1317-1321 1329 1338-1339 1341
			1344-1346 1349-1351 1353-1355
			1357 1365-1366 1369 1378-1379 1383-1385 1394 1397 1400 1402-
			1403 1408 1417 1419 1423-1426
			1431 1433-1436 1438 1444 1446-
}			1448 1454-1455 1460 1466 1468
			1470 1474 1480-1481 1483 1486-
			1488 1490-1491 1494-1496 1506
			1508-1509 1511-1512 1515-1516
			1519 1523-1524 1528-1529 1536-
			1540 1546 1549-1550 1555 1560-
			1561 1565 1567 1569 1575 1588
			1591 1593-1594 1596-1598 1600-
			1602 1608 1614-1616 1618 1620
			1624-1625 1627-1632 1636 1639
}			1644-1645 1647-1649 1652-1653
		·	1656-1662 1664 1666-1667 1670- 1671 1673-1675 1678-1679 1683
			1685-1688 1690-1692 1696-1699
)			1705 1709 1716-1717 1722 1727
			1730 1735 1739 1741 1743-1744
1 1			1
			1748-1749 1753 1760-1762 1765
			1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776
			1
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188-
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325-
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426-
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454-
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426-
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537-
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906-
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269-
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317 1319-1320 1339 1345-1346 1348
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317 1319-1320 1339 1345-1346 1348 1350-1351 1357 1367 1369 1379
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317 1319-1320 1339 1345-1346 1348 1350-1351 1357 1367 1369 1379 1381 1383-1384 1386-1387 1389
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317 1319-1320 1339 1345-1346 1348 1350-1351 1357 1367 1369 1379 1381 1383-1384 1386-1387 1389 1394 1397 1405 1423 1425-1428
lymphocytes	ATCC	LPC001	1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317 1319-1320 1339 1345-1346 1348 1350-1351 1357 1367 1369 1379 1381 1383-1384 1386-1387 1389 1394 1397 1405 1423 1425-1428 1431 1437 1446 1448 1461 1466

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
iissue Ofigin	IGM BOULCE	Library Name	
			1638 1647-1649 1651 1658-1659
			1664 1676-1677 1680-1681 1687- 1688 1699 1711 1715-1716 1726
			1728 1737 1740 1746 1748 1752
			1756 1758 1777 1779
leukocyte	GIBCO	LUC001	3-4 10-11 13 15-18 20-21 24-25
icanocyce			30-31 35-36 40 43-45 48 50-51
			54-58 60-63 68-69 75 79-80 82-83
			85 88-91 93-96 98 100 103-104 107-108 112 116 119 123 125-128
			134-140 142 147-149 151 153 155
		Į	157 162-163 167 169-172 174 177-
	1		179 186 190 192-199 203-207 210
	}	l	212-215 217-219 222-223 229 235-
	1		236 247 251 255-258 260 262 272 274-277 280-281 285-286 297-301
į			307-310 313-314 316-317 321 325-
}			330 333-334 340-342 348-349 352
1		1	354-358 370-371 380-385 387-388
		1	400 405 408-410 412 414-416 421-
			425 430-431 434-435 437 439 441-
	1		442 445-451 453-454 456 459 461- 464 468-472 474-479 481 483-485
			487-491 496 499-501 503-504 509-
)			513 516-519 522 526-527 529-531
			534 536-540 542 547-549 553-559
	1		566-567 571 574-577 579 582 584- 586 589 593 595-597 601-602 604
		}	606-607 611-613 615-621 623 627-
			629 633 636-637 642 644-650 655
	ļ	1	659-660 662-665 667 669 674-675
			678 682-684 692-696 698 700 706
			708 710 716-720 725-726 729-736 738-739 743-746 749 751 753 756
			759 765-766 768 770-778 780 784-
			786 788-790 793 796 798 800 802-
			803 810-811 814 817 819 826 828-
	1		830 832 834-836 838 843 845-860
	}		863-864 866-871 877-879 881-892 894-896 898 902 904-914 916 919-
			925 927 930-932 935-936 941-942
	1 .		945 948-949 953 955-956 958 960-
	}	,	962 964 967 970-971 973 975 977
		Į.	985-990 992-993 995-996 999-1002
Ì	l	1	1004-1009 1011 1014 1017-1019 1022-1023 1025 1027 1029-1031
]	1	1033-1036 1038 1041 1043 1047
		1	1050 1053-1054 1058-1059 1061-
	1	1	1062 1064 1068 1070 1072 1078
	}	1	1085-1086 1089-1091 1093 1097
	•		1106-1107 1110-1113 1115-1117 1122-1123 1125 1129 1132-1133
		(1135-1137 1140-1145 1152 1158
		ł	1163 1168 1170-1174 1176-1178
}			1180 1182-1183 1186 1195 1198-
			1200 1202 1205-1206 1211 1216
1			1219-1221 1223-1227 1230-1236 1238-1242 1247 1252 1254 1256
1			1258 1261-1262 1264-1265 1269-
}			1270 1272-1275 1277 1280-1284
			1287-1293 1299-1300 1306 1308
			1312-1313 1317-1320 1322 1324-
	1		1330 1333-1335 1339 1341 1343-
		}	1347 1349 1353-1357 1359-1361 1365-1367 1369-1370 1373-1374
		1	1377 1379-1381 1386-1387 1394
	1	}	1400 1403 1409 1419 1423 1425-
		-	1428 1430-1431 1433-1434 1437-
}	1		1438 1440-1442 1446-1448 1450
L			

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
	ICVA BOUTCE	Library Name	
			1453 1458-1459 1463-1464 1468
			1470-1471 1474 1477-1478 1482- 1488 1490-1493 1496-1501 1504
	ļ		1506 1509 1512-1513 1516 1519
	•		1521-1522 1524-1525 1527-1528
		i	1531 1534 1538 1541 1545-1547
			1549-1550 1553 1555-1556 1560 1565 1567 1575 1580 1589 1591
			1594 1596 1598 1600-1602 1606-
			1608 1611 1614 1620-1621 1624
			1626-1629 1631-1632 1636 1638-
			1639 1641 1644-1645 1648-1650
			1653-1655 1658-1660 1662 1669- 1670 1675-1679 1684-1688 1690-
	ĺ		1692 1696 1700 1702 1707-1709
	į		1711 1716-1717 1720 1723 1725-
			1727 1733 1737-1738 1741 1743-
	ł		1744 1748-1749 1752 1755 1760-
	ļ		1762 1765 1769 1771-1772 1781- 1784 1786
leukocyte	Clontech	LUC003	4 35-36 44-45 61 68-69 75 82 102
			119 139 154 179 197 244 280-281
	1		324 372 404 430-431 455 461 476-
{	{		477 481 503 537-540 554 575-576 581 589 608-609 621-622 624 630
	} .		632 647 662-664 669 679 698 764
			773 775-777 802 848 851 856-857
	}		879 905-907 915 949 952 990 992
			1002 1113 1119 1170 1183 1216
			1236-1237 1241 1275 1346 1353
			1357 1359 1377 1506 1515 1534 1553 1591 1600 1613~1614 1621
			1628 1670 1676-1677 1691-1692
}		}	1699 1733 1738 1772
melanoma from	Clontech	MELO04	25 35-36 43 80 104 126 128 150
cell line ATCC #CRL 1424	l		163 166 188-189 197 210 215 220 271 277 280-281 310 317 336-338
#CRL 1424		}	345 351 372 380-381 383 387 412
ĺ			415-416 430 445 448 454 456 467
ļ			481 490 499 503 526 528 546 548
			567 575-576 588 601 613 615 647
į .	(660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878
		}	883 887 905 914 932 934 958 976
	ļ		985 990 992 999-1000 1025 1031
1	(1038 1050 1055 1068 1074 1088
1	}		1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200
[1		1214-1215 1217 1226-1227 1235
		}	1238-1239 1244 1253 1278 1280
	Į.		1293 1311 1320 1330 1334-1335
{	{		1345 1355 1367 1386-1387 1394
	}	}	1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541
	{		1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631
		}	1638 1647 1653 1660 1667 1669-
	}		1670 1680-1681 1696 1704 1715
(1		1724-1725 1731-1732 1750 1760-
		Magazi	1761
mammary gland	Invitrogen	MMG001	5-8 10 12 14-18 20-21 24-25 29 33-39 42-43 52 55-58 60-64 68-69
	}	}	71 73-74 79-80 82 89 98 100 103
	1		106 108 112 123 128 133-137 144-
1	1	[146 148 150-152 154 158-159 165-
i		1	1
] }		166 170-172 174 176 178 181-185
	·		188-190 194-198 201-206 210 217-

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	
			290 297 299 301 304 309-312 318
			320-321 323-325 327-329 331-332 334 339 341 344-345 348 350 356
			i
			359-360 362-363 368 371 376 379-
			383 388 390 393-395 397-398 405
	i		408 412 414-415 423 430 434-437
			441-444 448 451-455 462-464 474
			476 479 482 485-486 488 490 494-
			495 498 503 506 509-512 516-517
	{		519-520 522 527 529 534 537-541
			.547 549 554 557 562 572-574 587
			589-591 597 602 607 618 623 628-
			629 632 634-640 644 647-648 650-
			652 655 657-658 660 665 667 669-
			672 674-676 679 682 688 695-696
}	1		706-707 710 713 717 720 722-730
			732-734 736 738 743 747-748 750
	1		755 759 761 766 770 780 784 786-
			789 794 803 806-807 809 814 817-
1	[•	822 827-829 837 842 854-858 863-
i			864 866 869-870 872 878 881 889
1	1		893-900 904 906-907 911 916 919
1			921-923 926 935-937 946 948-949
			953-954 957 960-961 963 965-966
			970 977-978 984-989 993-997
1	1 1		1000-1001 1005-1006 1008 1013-
			1014 1016-1017 1023 1025 1027
	ł i		1032-1033 1036 1039 1043 1045
	1		1055 1057-1058 1063 1068-1075
	1		1077-1078 1085 1087 1089-1091
	į į		1095-1102 1107-1108 1112-1119
	1		1121-1123 1131-1133 1136-1137
			1139-1142 1144-1145 1148-1149
	İ		1153 1159 1167 1170 1172-1173
İ			1183-1185 1190-1192 1196-1199
}	1.		1207-1208 1212 1216-1218 1222-
			1223 1225 1231 1234 1240-1241
			1247 1253-1254 1258-1259 1261-
1			1262 1270-1280 1283 1285-1286
1			1298 1307 1314 1316-1320 1323-
			1325 1330 1334-1335 1342-1345
	[1349-1352 1354-1355 1359 1369-
	1		1370 1377 1379 1381 1383-1384
	1		1389 1405 1414 1419 1421-1423
	j		1425-1426 1428-1429 1431 1434-
i			1437 1439 1448-1449 1454 1457
	}		1460-1464 1466 1471 1480-1483
	1		1487 1489-1491 1493 1505 1507
].	ļ	1512 1519 1526-1528 1532 1534
		1	1536 1539 1542 1547 1549-1550
		1	1554 1561-1562 1564 1567 1572
	İ	1	1576-1579 1581-1582 1587-1588
		ļ	1592 1594 1596-1597 1601-1602
		[1607-1608 1610 1612-1616 1618
			1621-1622 1625-1626 1631 1635-
			1636 1641 1643-1644 1647 1650
1		į	1652 1654-1655 1657-1658 1660
	1	1	1662 1664-1666 1669-1671 1673-
		}	1674 1676-1677 1680-1685 1689-
			1692 1701 1706 1713-1715 1719-
		1	1720 1723-1728 1730-1732 1738
			1740 1742-1744 1746-1747 1749
1]	1740 1742-1744 1746-1747 1749
	1		1/51 1/53 1/60-1/64 1/65-1/66
			1771 1774 1776-1777 1779 1783-
L	<u> </u>		1784 1786
induced neuron	Strategene	NTD001	29 35-36 80 116 123 156 163 181 214 230 280-281 284-285 307 321
	i	1	
cells	ł .	ì	224 230 200 201 201 200 200
cells			330 340 358 371 375 377 380 382 422 424 492 497 532-533 542 546

Tissue Origin RNA Source Hyseq SEQ ID NOS: Library Name 549 566 586 595 612 645-64 734 775-778 780 792 799 82 856 858 875 936 953 985 99 1041-1043 1055 1072 1104 1 1194 1206 1223 1246 1253 1 1288-1289 1291 1294 1311 1 1349 1359 1412 1423 1485 1 1623 1645 1684 1705 1715 1	1 826 0 992 .
549 566 586 595 612 645-64 734 775-778 780 792 799 82 856 858 875 936 953 985 99 1041-1043 1055 1072 1104 1 1194 1206 1223 1246 1253 1 1288-1289 1291 1294 1311 1 1349 1359 1412 1423 1485 1 1623 1645 1684 1705 1715 1	1 826 0 992 .
856 858 875 936 953 985 99 1041-1043 1055 1072 1104 1 1194 1206 1223 1246 1253 1 1288-1289 1291 1294 1311 1 1349 1359 1412 1423 1485 1 1623 1645 1684 1705 1715 1	0 992
1041-1043 1055 1072 1104 1 1194 1206 1223 1246 1253 1 1288-1289 1291 1294 1311 1 1349 1359 1412 1423 1485 1 1623 1645 1684 1705 1715 1	
1194 1206 1223 1246 1253 1 1288-1289 1291 1294 1311 1 1349 1359 1412 1423 1485 1 1623 1645 1684 1705 1715 1	
1288-1289 1291 1294 1311 1 1349 1359 1412 1423 1485 1 1623 1645 1684 1705 1715 1	
1349 1359 1412 1423 1485 1 1623 1645 1684 1705 1715 1	
1623 1645 1684 1705 1715 1	
retinoid acid Strategene NTRO01 5-8 78 268-269 277 383 431	506
induced 623 677 731 999-1000 1199	1425-
neuronal cells 1426 1547	
neuronal cells Strategene NTU001 29 65-66 80 82 110 119 146	
166 174 181-185 198 227-22	
284 309 325 332 334 336-33 391 393 406 414-416 454 46	
470 488 503 506 510-512 51	
540 572-574 597 602 607 62	
661 700 702 716 743 771 79	2 858
904 948 954 977 1000 1005-	1006
1025 1064 1068 1122 1148 1	
1219 1226 1234 1246 1271 1	
1295-1296 1311 1317-1320 13	
1330 1350 1355 1365-1366 13 1383-1384 1400 1412 1445 19	
1539 1547 1578 1647 1656 16	
1690 1738 1749 1783-1784	,03
pituitary Clontech PIT004 311 314 379 408 419 430 456	1055
gland 1095-1096 1272-1273 1312 13	320
1378 1652 1671 1720 1725 1	736
1741 1755	
placenta Clontech PLA003 5-8 124 208 277 370 843 906	907
1280 1317-1319 1369 1609 16	21
prostate Clontech PRT001 9 46 57 71 107 147 171 177	197
201 229 231 242-243 274 280	
307 310 317 330 358 373 382	-383
400 430 434-436 461-462 469	477
489 497 500 505-506 513 521	
531-533 547 618 649 657-658	
664 710 729 767 771 789 820 871 874 890-891 905 938 945	
964 988-989 1002 1025 1033	1045
1061 1095-1096 1112 1125 11	42
1196 1198 1202 1232-1233 12	
1258 1272-1273 1287 1295 13	13
1333 1341 1344 1349 1360 13	62-
1363 1367 1437 1442 1447 14	
1478-1479 1482 1489 1513 15	17
1527 1531 1536 1598-1599 16 1636 1657 1680-1681 1687-16	
1717 1738 1743-1744	°8
rectum Invitrogen REC001 17-18 29 33 62-63 71 73-74	83 86
113 126 146 153 158 167-169	195
200 206 261 309 312 341 344	368
373 388 395 408 414 420 430	441-
442 446 448 464 468 483 517	
540 547 567 585 589 602 623	
629 632 645-647 651 657-658	
717-719 721 725-726 738 748 756 762-763 766 770 774 790	
825 843 849 851 881 903 909	
949 960 986 996 1020 1023 1	
1034 1064 1067 1070 1075 10	
1108-1109 1113 1130 1139 11	
1159 1172 1178 1185 1187-11	
1205 1220 1225 1240 1244 12	
1317-1320 1323 1334-1335 133	50-
1351 1355 1369 1373 1375 14	25-

		14	CEO TO NOC
Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
		January Hame	1426 1436 1439 1469 1474 1477
			1482 1546 1587-1588 1592 1596
			1610 1622 1627 1644 1658 1662
[1665-1666 1669 1675-1677 1749
			1786
salivary gland	Clontech	SAL001	10 55 97 103 110 140 149 152 158
			198 217-218 242-243 256 301 308
			312 321 333 351 354 360 410 437
		•	448 473 487 494 496 501 535 555
		:	569-570 572-573 590-591 624 636
}			809 826 848 865 879 906-907 925
(933 963 1016 1020 1025 1040 1046
			1055 1066 1103 1150 1172 1181
			1234 1281-1282 1288-1289 1298
			1315 1320 1333 1336-1337 1346
			1359 1373 1379 1424 1447 1449
(1474 1482 1492 1494 1498 1511
		,	1523-1524 1537 1554 1596 1626-
			1627 1636 1652-1655 1658 1665
	· · · · · · · · · · · · · · · · · · ·		1671-1672 1691-1692
salivary gland	Clontech	SALs03	158 326 1423 1463-1464
skin	ATCC	SFB001	1320 1400
fibroblast			200 500 1055
skin	ATCC	SFB002	262 736 1025 1253
fibroblast	3,000	SFB003	709 1119 1350 1631 1653
skin fibroblast	ATCC	258003	709 1119 1330 1631 1633
small	Clontech	SIN001	25 142 146-147 151 155 198 203
intestine	CIONLECII	5111001	244 260 271 280-281 286 288 298
ancestane			301-302 308 312 334 340 371 398
			408 412 414 416 423 426-427 430
	•		434-435 445 452 454 478 503 516
			519 521 523 543 547 549 555 559
		ľ	563 569-570 585 592 604 611 626
		}	628-629 632 650 659 681 710 714
			718 750 764 780 798 829 842 857
			859 866 887 892 894-895 901 904 906-907 912 919 935 997-998 1000
		}	1007-1008 1026-1028 1044 1055
		[1089 1097 1116-1117 1131 1148
		}	1169 1199 1219 1234 1247 1264
			1279 1316 1320 1326 1341 1343
			1349 1351 1374 1387 1398 1400
		1	1403 1407 1423 1428 1468 1498
			1501 1521 1550 1556 1585 1597
	1	1	1636 1638-1639 1645 1653 1656
	ļ	1	1662 1671 1675 1684 1691-1692
1	{	1	1704 1711 1717 1719 1722 1725-
			1726 1729 1733-1734 1743-1744 1762 1767 1780 1785
	Clartach	SKM001	18 20-21 82 84 101 118 134 148
skeletal muscle	Clontech	SWINDT	151 153 166 225-226 258 274 277
muscre			289 329 361 412 414 424 440 452
	İ		459 470 488 503-504 537-540 647
	}	j	660 673-675 715 773 780 786 830
	1		905 922 950 963 982 990 992 1020
	1	1	1047 1063 1115-1117 1121 1134
	l		1228 1268 1284 1298 1321 1329
			1336-1337 1343 1409 1413-1414
			1509 1599 1624 1644 1653 1712
skeletal	Clontech	SKM002	168 1683 1712
muscle			1025 006 1406
skeletal	Clontech	SKMs03	235-236 1409
muscle	01		1225 226
skeletal	Clontech	SKMs04	235-236
muscle spinal cord	Clontech	SPC001	4 9 11 17 30-31 35-36 43 46 60
	LIONLECH	, 320001	1 2 2 TT T1 20-2T 20-20 42 40 00

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	CEQ ID NOD!
	 		82 85 92 94 108 110 116 139 157
1			167 198 204-205 210 215 229 256
1	1		259 277 280-281 300-302 304 315
			317 372 379 387 392 419 426-427
1			430 433 448 467 473 487 489 506
			509 513 519 524 526 537-540 543
,	ĺ		547 549 551 559 567 569-570 593
	<u>}</u>		607 616-617 623 625 637 649-650
,			652 657-658 670-671 673 679 681- 682 709 711 715 719 728-729 734
			749-750 753 775-777 781 789 791
	•		809 820 832 834-836 847-849 854-
			855 858 861 864 871-872 875 884
			898 906-908 917 919 924 934 942
	!		944 970 985 990 992-993 998 1013
			1039 1053 1059 1065 1072 1075
	1		1077 1082 1085 1097 1103 1109
			1116-1117 1128 1134 1151 1170
]		1174 1192-1194 1215 1225 1241
1			1243 1283 1294 1307 1312 1320
]]	Ť	1323 1327 1330 1350 1353-1354
			1356 1359 1368 1375 1400 1406~
			1407 1423 1429 1437 1443 1448
			1454 1470 1482 1492 1501 1508
			1511 1529 1538 1548-1549 1565
	ļ		1571 1578 1598 1600 1614 1625
			1627 1630 1639 1646 1651-1652
			1670 1686 1696 1740 1751 1755
			1771
adult spleen	Clontech	SPLc01	117 312 326 348 424 426-427 431
			845 866 1320 1330 1333 1344
		,	1355-1357 1371 1387 1397 1446
	67		1538 1579 1669 1686 1739 1767
stomach	Clontech	ST0001	10 15-16 61 68-69 100 117 149
j			197 201 227-228 231 249 273 280-
			281 287 291-292 302 312 358 362
, i			426-427 430 446 462 475 479 535
			597 620 630 651 662-664 722 739 780 782 785 846 919 960 964 966-
			967 976 1008 1012 1032 1042 1063
1	:		1071 1135 1170 1208 1234-1235
	·		1259 1277 1280-1281 1322 1349
			1359 1369 1449 1468 1474 1478
1			1487 1493 1498 1557-1559 1622
, i	4		1634 1651 1653 1729
thalamus	Clontech	THA002	
{ :		1121002	9 11 25 85 87 112 137 146 180
	j	1112002	9 11 25 85 87 112 137 146 180 190 198 206 210 212-213 235-236
.		112002	9 11 25 85 87 112 137 146 180 190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325
·		1111002	190 198 206 210 212-213 235-236
		1121002	190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325
		1121002	190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379
		112002	190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458
		112002	190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606
		112002	190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736
		112002	190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891
		112002	190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004
		112002	190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145
		112002	190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177 1193-1194 1208 1220 1249 1280 1305 1345 1355 1369 1434-1435
		112002	190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177 1193-1194 1208 1220 1249 1280
		ALEXO Z	190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177 1193-1194 1208 1220 1249 1280 1305 1345 1355 1369 1434-1435 1440-1441 1454 1496 1546 1549 1562 1572 1578 1590 1594 1613-
		112002	190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177 1193-1194 1208 1220 1249 1280 1305 1345 1355 1369 1434-1435 1440-1441 1454 1496 1546 1549 1562 1572 1578 1590 1594 1613- 1614 1640 1651-1652 1671 1687-
		ALCOUZ	190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177 1193-1194 1208 1220 1249 1280 1305 1345 1355 1369 1434-1435 1440-1441 1454 1496 1546 1549 1562 1572 1578 1590 1594 1613- 1614 1640 1651-1652 1671 1687- 1688 1703 1743-1744 1746-1747
			190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177 1193-1194 1208 1220 1249 1280 1305 1345 1355 1369 1434-1435 1440-1441 1454 1496 1546 1549 1562 1572 1578 1590 1594 1613-1614 1640 1651-1652 1671 1687-1688 1703 1743-1744 1746-1747 1753
thymus	Clontech	THM001	190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177 1193-1194 1208 1220 1249 1280 1305 1345 1355 1369 1434-1435 1440-1441 1454 1496 1546 1549 1562 1572 1578 1590 1594 1613- 1614 1640 1651-1652 1671 1687- 1688 1703 1743-1744 1746-1747 1753
thymus	Clontech		190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177 1193-1194 1208 1220 1249 1280 1305 1345 1355 1369 1434-1435 1440-1441 1454 1496 1546 1549 1562 1572 1578 1590 1594 1613- 1614 1640 1651-1652 1671 1687- 1688 1703 1743-1744 1746-1747 1753 44-45 54 57-58 62-64 79 104 123 126 134 153 193 212-213 218 242-
thymus	Clontech		190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177 1193-1194 1208 1220 1249 1280 1305 1345 1355 1369 1434-1435 1440-1441 1454 1496 1546 1549 1562 1572 1578 1590 1594 1613- 1614 1640 1651-1652 1671 1687- 1688 1703 1743-1744 1746-1747 1753 44-45 54 57-58 62-64 79 104 123 126 134 153 193 212-213 218 242- 243 258 274 277 279 297 301 307
thymus	Clontech		190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177 1193-1194 1208 1220 1249 1280 1305 1345 1355 1369 1434-1435 1440-1441 1454 1496 1546 1549 1562 1572 1578 1590 1594 1613- 1614 1640 1651-1652 1671 1687- 1688 1703 1743-1744 1746-1747 1753 44-45 54 57-58 62-64 79 104 123 126 134 153 193 212-213 218 242- 243 258 274 277 279 297 301 307 327 330 333 342 351 358 371 410
thymus	Clontech		190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177 1193-1194 1208 1220 1249 1280 1305 1345 1355 1369 1434-1435 1440-1441 1454 1496 1546 1549 1562 1572 1578 1590 1594 1613- 1614 1640 1651-1652 1671 1687- 1688 1703 1743-1744 1746-1747 1753 44-45 54 57-58 62-64 79 104 123 126 134 153 193 212-213 218 242- 243 258 274 277 279 297 301 307

	RNA Source	Vycea	SEQ ID NOS:
Tissue Origin	NA SOUTCE	Hyseq Library Name	_
			540 546 548 554 567 584 586 590-
	·		591 604 612 621 638-640 645-647 649 656 660 665 670 698 710 720
			728 735 739 746 759 762 766-767
			775-777 780 784-785 800 802 809
			824 826 828 845 851 858-859 864
	l i		866 870-871 878 884 887 892 899-
	!		900 927 930-931 967 983 986 990
			992 999 1014 1029-1030 1033 1059 1066 1073 1103 1107 1113 1116-
			1117 1119 1140-1142 1158 1163
			1172 1177 1195 1206 1209 1213
	}		1216 1218-1219 1221-1222 1227
		1	1271 1277 1282 1320 1329 1349
			1367 1369 1383-1384 1417 1419
			1423 1425-1427 1448 1477 1488 1493 1536 1554 1620 1644 1646
	1		1649 1654-1655 1661-1662 1669-
			1670 1674 1676-1677 1685-1688
			1707 1711 1731-1732 1737
thymus	Clontech	THMc02	5-9 15-21 25 33 35-36 43-45 48
<u> </u>	Ť		50-51 54-55 60 75 83 87 89 93
		(98-100 102 105 112 117 135-137 141 143 146 157 167 169 192 196
			211 217-219 222 224 229 233 235-
		{	236 240-241 244 251-252 256 261-
		}	262 268-269 286 288 290 295 297
1			301-302 309-310 315-317 321 324
,		}	327 334 342 350 352-353 360 370-
			373 382 384 400 403 410 414-416 424 430-431 436 445 454-456 461
		1	464-467 470 472 474-476 483 488
	•		497 500 504 506 513 516 519-520
			524 526 530-531 534 537-540 549
			554-555 565-566 569-570 572-573
			575-577 586-587 595 603-604 606
		ł	612 630-632 634 636 647 650 657-
	1		700 703 708 720 725-726 731 738-
	1		739 743-744 750-753 757 759 763-
	}	:	765 767 772-779 787 789-790 798
		ļ	800 810 823 829 834-836 841 848
			854-856 859 861 864 870-871 881 890-891 898 908-909 913 928 933
			941 949 958 961 963 967 969 975
		1	981 986 988-990 992 999 1007-
		1	1008 1014 1016 1039 1041 1073-
			1074 1079 1089 1097 1109 1114-
			1117 1122 1131 1140-1141 1144- 1145 1163 1172 1175-1177 1186
			1196 1198 1206 1211 1216 1220
1		ł	1223 1227 1234-1243 1261-1262
	1	1	1267 1271 1280-1281 1284 1290
-			1308 1317-1320 1322 1324-1325
		1	1327 1330 1334-1335 1339 1346
1			1350-1351 1355 1357 1360 1370 1374 1377-1379 1386 1389-1390
	1	1	1374 1377-1379 1386 1389-1390
	1		1417 1423 1425-1427 1440-1441
ì	{		1466 1474 1477 1483 1493 1498
			1504 1506 1525 1536 1545 1549
l	1		1566 1594 1598-1600 1608 1611
		Į	1614 1621 1623 1625 1632 1639 1641 1644 1647 1649 1653-1656
	1		1641 1644 1647 1649 1653-1656
	1		1681 1686-1688 1693 1705 1707
			1711 1717-1718 1726-1727 1731-
1			1733 1737-1738 1743-1745 1758-
1		\	1761 1771-1772 1779 1786

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
thyroid gland	Clontech	THR001	4 9-10 20-21 37-39 48 50-51 54-
	ļ		57 60-61 65-66 71 83 94-96 98-
			100 102 104 110 112 115-117 119
	1		123 127 133 136-137 140 149 152- 153 155-158 163-164 168-169 171
			186 190-192 197 201-203 219-220
	(229 233-237 246-247 253 256 258
1			262 265-266 268-269 277 280-281
			284-286 288-289 298-299 302 309- 311 317 321 326 332 335 341-342
1			344 348 350 354 358-359 363 368
			371-373 382-383 385 394 398 400-
			401 411 414-415 421 424 430-431
			433-436 443-446 450-452 454-455
			458 472-474 476-478 482 484-485 487-488 490-494 496-497 500-501
Î			503-504 506 509-513 516-517 519
j			524 526-527 529 535-540 547 549
			562 564 569-570 575-576 588 594-
1	1		595 601-602 604 606 610 612 615-
			617 619-623 628-630 634-635 642 647 649-651 660 662-665 668 670
	į i		681 690-694 696 698 700 709 721
]		727-729 732 734 738 740-741 743
		•	745 750 759 761 763 765 770 773
	1		780 785 795-796 798 802 804 823- 824 826 828 833 838 841-845 847
			849 857-860 867 874-875 878 880-
	1		881 887-888 890-892 894-895 898
			908 910-911 913-914 922-923 926-
			927 929 932-934 937 939 941-942
	}		948 953 957 961 963-964 966 978- 979 981-982 987 990 992 1001
			1004-1006 1010 1014 1020 1024
	[1033 1038-1039 1044 1047 1050
	1		1052-1054 1056 1058 1068 1070-
			1071 1077-1079 1088 1094-1097
	1	i	1105-1106 1112-1113 1116-1117 1124 1126 1128-1129 1131 1134
	1		1136-1137 1142-1143 1146-1147
		•	1149-1150 1156 1161-1164 1167
			1170-1173 1177-1181 1190 1192
	.	ļ	1197 1200 1204 1208-1209 1214 1217 1219 1222 1230 1232-1233
1	i		1235 1241 1245 1247 1254 1257-
	}		1258 1260 1262 1271-1273 1283
	[1286-1289 1299 1306 1314 1320
1		•	1330-1332 1334-1335 1342 1345
}]		1349 1365-1367 1370-1372 1374 1381 1394 1407 1419 1428 1436-
	[1	1437 1440-1441 1443 1446-1449
			1454 1459 1461-1462 1468 1470-
			1471 1475 1477 1479 1482 1491
		Ì	1497-1498 1504-1505 1507 1513 1522 1524-1526 1528 1531 1534
			1536-1537 1548 1550 1553 1555-
	.		1559 1562 1567 1578 1590-1591
)		1597 1599-1601 1612 1614 1616
	[1619-1620 1622 1624-1626 1628
	1		1631-1632 1634 1636 1639 1644- 1645 1648 1651 1653-1656 1658
	İ	ļ	1660 1662-1663 1667 1669 1671
		1	1675 1678-1681 1683-1686 1689
)	1691-1692 1703 1709-1711 1717
ļ	Ì	1	1724-1726 1729 1734 1737-1738
1		l	1740 1743-1744 1749 1753 1759- 1761 1770 1777 1786
trachea	Clontech	TRCOOL	9 29-31 46 48 87 104 107 110 135
			158 222 262 266 286 301 318 331
			

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	
			352 372 377 384 414 424 445-446
			454 472 474 491 496 560 579 588
			593 597 607 612 626 681 702 719
į			810 859 866 878 894-895 912 916
)		922 932 935 1046 1075 1080 1099-
1			1102 1113 1208 1215 1232-1233
ł		ł	1237 1281 1312 1385 1387 1405
	ł		1414 1424 1430 1437 1447 1505
1	ĺ		1569 1579 1586 1600 1641 1653
}		1	1667 1671 1676-1677 1683 1691-
			1692 1711 1717 1726 1772
uterus	Clontech	UTR001	17 19 25 41 46 57-58 61 89 104
	Į.	}	108 139 152 174 198 200-201 206
	Ì		263-265 274 290 387 408 420 438
	1		446 448 452 473 491 493 499 503
	}	}	506 513 519 522 526 530 542-543
		Ì	560 601 610 632 659 665 720 751 773 780 833 845 857 872 877 912
	1	Ì	929 934 937 996 1009 1011 1018
		}	1 1050 1075 1107 1124 1170 1219
			1258 1279 1287 1310 1320 1323
			1343-1344 1375 1437 1451-1452
		·	1478 1481 1498 1519 1521 1536
	1		1552 1579 1597 1602 1606 1620
	1		1626-1627 1649 1652 1661 1670
1	1		1719 1722-1723
1	l	<u> 1 </u>	1/10 1/65 1/65

TRADOCS:1416191.1(%CQN01!.DOC)

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	\$ IDENTITY
NO:	Y41736	Homo	Human PRO1114 protein	SCORE 1398	100
-		sapiens	sequence.		
2	Y66656	Homo sapiens	Membrane-bound protein PRO943.	2389	99
3	AF113136	Homo sapiens	IL-1 receptor-associated- kinase-M; IRAK-M	3043	100
4	AF017806	Mus musculus	Zn-15 transcription factor	6351	77
5	X02761	Homo sapiens	fibronectin precursor	10535	98
6	X02761	Homo sapiens	fibronectin precursor	8990	89
8	X02761	Homo sapiens	fibronectin precursor Rab6 GTPase activating	12564 5251	99
9	AJ011679		protein, GAPCenA		
10	W88501	Homo sapiens	Human stomach carcinoma clone HP10415-encoded protein.	2381	100
11	AF117754	Homo sapiens	thyroid hormone receptor- associated protein complex component TRAP240	11336	98
12	297630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G)))	896	100
13	Y58620	Homo sapiens	Protein regulating gene expression PRGE-13.	1894	98
14	AF213457	Homo sapiens	triggering receptor expressed on myeloid cells 2	1238	100
16	AF233453	Homo sapiens	RACK-like protein PRKCBP1	3124	99
17	AF201303	Homo sapiens	dhfr oribeta-binding protein RIP60	3130	98
18	AF064205	Homo sapiens	dynactin 1 p150 isoform	6377	100
19	U00059	Saccharomyce s cerevisiae	Yhr121wp	174	26
20	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1801	99
21	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1485	99
22	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	3083	99
23	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	2300	99
24	AJ289131	Homo sapiens	chondroitin 4-0- sulfotransferase	2211	99
25	U33460	Homo sapiens	DNA-directed RNA polymerase I, largest subunit	8777	98
26	Y44488	Homo sapiens	ACRP30R2 variant protein.	1387	100
27	U43701	Homo sapiens	ribosomal protein L23a	791	100
28	U02032	Homo sapiens	ribosomal protein L23a	767	97
29	Y41324	Homo sapiens	Human secreted protein encoded by gene 17 clone HNFIY77.	1083	99
30	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	715	90
31	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	631	82
32	AF231917	Homo sapiens	long-chain 2-hydroxy acid oxidase HAOX2	1811	100
33	Z29481	Homo sapiens	3-hydroxyanthranilic acid dioxygenase	1507	99
34	AB001451	Homo sapiens	Sck	2869	100
35	Y00644	Homo sapiens	precursor polypeptide (AA -34 to 287)	1667	99
36	Y00644	Homo sapiens	precursor polypeptide (AA -34 to 287)	1104	98
37	¥78795	Homo sapiens	Human antizuai-2 (AZ-2) amino acid sequence.	3586	78
38	¥78795	Homo sapiens	Human antizuai-2 (AZ-2) amino	4726	99

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:	Y78795	Homo sapiens	Human ancizuat-z (Az-z) william	3556	77
			acid sequence.	3747	100
0	U93121		M-Duase Onosphoprocerr -	795	100
1	Y42750		Human calcium binding protein 1 (CaBP-1).		100
2	AF282626	Homo sapiens	latexin	1189	I
3	G02150	Homo sapiens	Human secreted protein, SEQ	384	94
		1	Elf-1	2724	88
14	U19617	Mas mas dazas	Elf-1	2062	86
15	U19617	Man management	osteoinductive factor OIF	1538	100
16	AF100758	220.00	Human SPROUTY-1 protein, SEQ	1737	99
17	Y87591	Homo sapiens	TD NO-24	942	99
49	X04145	Homo sapiens	T3 gamma precursor (aa -22 to 160)		
-1	X63547	Homo sapiens	oncogene	5845	99
51	M94043	Rattus	rab-related GTP-binding	1089	96
52	M24043	norvegicus	protein		1
	L31783	Mus musculus	uridine kinase	917	71
53		Homo sapiens	transcription factor	4486	98
54	X83973	Homo sapiens	chloride channel protein 7	4128	99
55	AF224741		Human secreted protein	1491	100
56	W74805	Homo sapiens	encoded by gene 77 clone		1.00
57	250907	Homo sapiens	Human TBC-1 cDNA from second transcript.	4824	100
58	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	6089	99
59	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	4014	91
60	Y59738	Homo sapiens	Human normal ovarian tissue	601	100
61	AB031069	Homo sapiens	derived protein 15. protein containing CXXC	1390	100
62	¥66660	Homo	domain 1 Membrane-bound protein	2492	99
	Y66660	sapiens Homo	PRO783. Membrane-bound protein	1709	99
63	_	sapiens	PRO783. tricarboxylate carrier	895	55
64	S70011	Rattus sp.	tricarboxylate carrier	178	24
65	AF139518	Rattus norvegicus	A-kinase anchor protein		
66	W29666	Homo sapiens	Homo sapiens DH1308_1 clone secreted protein.	157	30
		Homo sapiens	claudin-15	1206	100
67 68	AJ245738 AF099138	Rattus	GLUT4 vesicle protein	4183	87
69	AF099138	norvegicus Rattus	GLUT4 vesicle protein	4906	86
\	1	norvegicus Caenorhabdit	Similarity to Drosophila ring	1285	44
70	Z82059	is elegans	canal protein comes from this gene		
L				1282	100
71	AF224278	Homo sapiens		1809	100
72 73	AF126426 Y41652	Homo sapiens	neurotrimin Human MEK2 protein sequence.	2065	99
1	Y41652	sapiens	Human MEK2 protein sequence.	1207	100
74		sapiens		1485	74
75	AF188622	Mus musculus	embryonic epithelia protein-1		100
76	AE000406	Escherichia coli	putative DNA topoisomerase		100
77	X99302	Homo sapiens	Pop1	655	
78	AL136538	Schizosaccha romyces		210	31
		pombe	•		99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID NO:	NUMBER	J. Bellis	BESCRIFTION	WATERMAN	IDENTITY
80	AL096768	Homo sapiens	dJ858B16.2	2033	100
	1		(phosphatidylserine	l	1
	ľ	1	decarboxylase (PSSC, EC		ŧ
	<u> </u>	<u> </u>	4.1.1.65))		ļ
81	AL096768	Homo sapiens	dJ858B16.2	1220	96
			(phosphatidylserine		ł
			decarboxylase (PSSC, EC		
		<u> </u>	4.1.1.65))	<u> </u>	<u> </u>
82	X57351	Homo sapiens	1-8D	677	98
83	AC005594	Homo sapiens	R26984_1	2700	98
85	X73113 AF097330	Homo sapiens	fast MyBP-C H1 chloride channel; p64H1;	5959	99
65	AF09/330	Homo saptens	CLIC4	1305	99
86	AB018423	Mus musculus	SH2 domain-containing protein	1360	78
87	AF272151	Homo sapiens	adaptor protein CIKS	3084	99
88	AF196329	Homo saptens	triggering receptor expressed	1214	100
	111 230323	sapiens	on monocytes I	1214	100
89	AB016879	Arabidopsis	contains similarity to pre-	634	36
		thaliana	mRNA splicing	1 051	50
			factor-gene_id:MRB17.2		
90	AJ133721	Mus musculus	homeodomain protein	654	57
91	AJ242864	Mus musculus	phtf protein	619	61
92	A61971	unidentified	MCSP	11676	99
93	Y99365	Homo sapiens	Human PRO1250 (UNQ633) amino	3890	100
	-	_	acid sequence SEQ ID NO:86.	1	-
94	Y87231	Homo sapiens	Human signal peptide	1031	100
		1	containing protein HSPP-8	1	ł
			SEQ ID NO:8.		
95	AF227741	Rattus	protein kinase WNK1	2428	95
	<u></u>	norvegicus	<u> </u>	<u> </u>	
96	AF227741	Rattus	protein kinase WNK1	1961	94
		norvegicus		L	
97	Y92513	Homo sapiens	Human OXRE-10.	1626	100
98	AL021366	Homo sapiens	cICK0721Q.3 (Kinesin related	3423	100
99	AC005783	Vome condens	protein) R33083 1	 	
100	Y95293	Homo sapiens	Human GEF containing NEK-like	1974	99
100	195295	Homo saprens	kinase substrate sGNK.	4092	99
101	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	1509	100
		Liouio Bupieno	(translation of the cDNA	1 1309	1 100
			DKFZp566A0946, Em:AL050069))		ì
102	AJ006267	Homo sapiens	ClpX-like protein	3233	100
103	AF100753	Homo sapiens	ancient ubiquitous 46 kDa	2042	96
		_	protein AUP1	-	1
104	AB015982	Homo sapiens	serine/threonine kinase	4718	100
105	AF151074	Homo sapiens	HSPC240	831	64
106	M35522	Canis	GTP-binding protein (rab7)	354	50
		familiaris			
107	R99800	Homo sapiens	NTII-1 nerve protein,	2337	93
			facilitates regeneration of		
			nerve cells.	<u> </u>	
108	AF125533	Homo sapiens	NADH-cytochrome b5 reductase	1290	93
			isoform		
109	AC005614	Homo sapiens	F23269_2	3369	99
110	AF064729	Homo sapiens	RAN binding protein 16	3285	100
111	X52425	Homo sapiens	interleukin 4 receptor	4496	100
112	Y41686	Homo	Human PRO274 protein	2285	100
	123.550.5	sapiens	sequence.	 	
113	W15506	Homo sapiens	Mitogen activating protein	1991	100
110	¥71071		kinase ERK1.		
114	¥71071	Homo sapiens	Human membrane transport	1190	99
115	NT OA OE A C	Uomo	protein, MTRP-16.		
	AL049548	Homo sapiens	dJ398G3.1 (ortholog of rat	3497	99
116	AF189817	Mus musculus	CPG2) evectin-2		-
	ENC 10701/	musculus (CACCETII-S	1124	90
117	W30891	Homo	Human cytostatin III protein.	715	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	8
ID	NUMBER			WATERMAN	IDENTITY
NO:		_]		SCORE	
		sapiens			1.00
118	AF116618	Homo sapiens	PRO1038	1469	100
119	Y08915	Homo sapiens	alpha 4 protein	1748	39
120	AF098070	Drosophila melanogaster	Lis1 homolog	192	
121	AF052432	Homo sapiens	katanin p80 subunit	181	37
122	Y70743	Homo sapiens	PSEQ-1 protein encoded by	2637	98
		-	NSEQ gene associated with matrix remodelling.		
123	AF083246	Homo sapiens	HSPC028	2132	100
124	Y27096	Homo sapiens	Human viral receptor protein (ACVRP).	833	99
125	M63109	Leishmania major	glycoprotein 96-92	172	27
126	U75467	Drosophila melanogaster	Atu	935	36
		Caenorhabdit	Similarity to Human ADP/ATP	438	43
127	Z68220	is elegans	carrier protein		
120	AF095927	Rattus	protein phosphatase 2C	1927	94
128	AFU95927	norvegicus	bracem buashmana as		(
129	W92958	Homo sapiens	Human zsig44 protein.	463	100
130	AF115391	Lactobacillu	ribokinase RbsK	508	37
T30	WETTOOD	s sakei]	
131	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	1250	100
132	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	916	87
133	W52811	Homo sapiens	Human DBI/ACBP -like protein (DBIH).	705	97
134	Y84444	Homo sapiens	Amino acid sequence of a	3230	100
134	104444	Nome Dapage	human RNA-associated protein.		
135	M69181	Homo sapiens	non-muscle myosin B	189	20
136	W74882	Homo sapiens	Human secreted protein	480	100
730	W/4502	noo	encoded by gene 154 clone HE6FL83.		
137	W78200	Homo sapiens	Human secreted protein	855	99
137	W78200	110/110 Bapters	encoded by gene 75 clone		
	1	Homo sapiens	dJ349A12.1 (similar to	424	39
138	AL033520	HOMO Sapiens	KIAA0701 protein)		
139	AF020261	Santalum	proline rich protein	119	30
140	X70394	Homo sapiens	zinc finger protein	1634	100
141	Y06439	Homo sapiens	Human protease HUPM-8.	936	100
141	Z68493	Caenorhabdit	predicted using Genefinder	365	42
143	AB018107	is elegans Arabidopsis	ADP-ribosylation factor-like	596	65
		thaliana	protein		
144	AF161483	Homo sapiens	HSPC134	580	51
145	Y84902	Homo sapiens	A human proliferation and apoptosis related protein.	480	100
146	AB004906	Ipomoea purpurea	transposase	146	20
147	AC007357	Arabidopsis thaliana	F3F19.18	647	31
148	W75155	Homo sapiens	Human secreted protein encoded by gene 41 clone HNTME13.	1494	98
149	AF056490	Homo sapiens	cAMP-specific phosphodiesterase 8A	3710	99
150	Y58171	Homo sapiens	Human hydrolase homologue HHH-7.	785	99
151	U10397	Saccharomyce s cerevisiae	Yhrl48wp	515	53
152	X73478	Homo sapiens		1719	99
			,		99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	8
ID	NUMBER	1		WATERMAN	IDENTITY
NO:	<u> </u>			SCORE	<u> </u>
			similar to arginyl-tRNA)		
154	AF169802 X94703	Homo sapiens	cytochrome b5 reductase b5R.2	1455	99
155	1	Homo sapiens	rab28	1126	99
156	Y25716	Homo sapiens	Human secreted protein	1471	100
158	W77404	Home comicans	encoded from gene 6.	1000	
128	W / /404	Homo sapiens	Secreted salivary polypeptide zsiq32.	937	100
159	Y17248	Homo sapiens	Human protein kinase	383	100
133	11,240	nomo saprens	inhibitor-2 (PKI-2).	363	100
160	J04970	Homo sapiens	carboxypeptidase M precursor	2395	100
161	W54040	Homo sapiens	Human interferon-inducible	484	98
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	nome bapacins	protein, HIFI.	404	30
162	AL022724	Homo sapiens	dJ413H6.1.1 (hamster	1357	100
			Androgen-dependent Expressed	1 -55.	
	Ì		Protein LIKE PUTATIVE	1	ì
	ļ		protein) (isoform 1)	1	
163	AF125535	Homo sapiens	pp21 homolog	193	45
164	G03632	Homo sapiens	Human secreted protein, SEQ	463	97
			ID NO: 7713.	1	
165	AJ250839	Homo sapiens	serine/threonine protein	1442	71
			kinase	<u>l</u>	j
166	L09649	Zymomonas	zm2	173	37
		mobilis			
167	Y73337	Homo sapiens	HTRM clone 1944530 protein	1204	100
			sequence.		L
168	W88645	Homo sapiens	Secreted protein encoded by	1084	100
169	30034003		gene 112 clone HUKFC71.		
170	AF214731 AE000871	Homo sapiens	ATP-dependent RNA helicase	4402	100
170	AE0008/1	Methanobacte rium	conserved protein	166	27
		thermoautotr		1	l
		ophicum			
171	¥27684	Homo sapiens	Human secreted protein	821	100
1/1	12/004	nomo saprens	encoded by gene No. 118.	821	100
172	AF226044	Homo sapiens	HSNFRK	2904	100
173	AJ245946	Homo sapiens	neuroglobin	779	100
174	D43949	Homo sapiens	This gene is novel.	3202	100
175	¥07923	Homo sapiens	GTP-binding protein	1205	100
176	W90338	Homo	Human DP1 homologue protein.	966	100
	ĺ	sapiens	<u> </u>		
177	Y41675	Homo sapiens	Human channel-related	1122	100
			molecule HCRM-3.		
178	Y41674	Homo sapiens	Human channel-related	936	99
			molecule HCRM-2.		
179	AF220492	Homo sapiens	krueppel-like zinc finger	4100	99
			protein HZF2		
180	X03084	Homo sapiens	Clq B-chain precursor	1240	100
181	U57344	Mus musculus	Meis3	1813	89
183	U57344	Mus musculus	Meis3	1743	86
184	U57344	Mus musculus	Meis3	1070	86
185	AF033120	Homo sapiens	p53 regulated PA26-T2 nuclear	1389	58
100	A 17000050		protein		
186	AF200357	Mus musculus	pantothenate kinase 1 beta	1605	82
187	W75058	Homo sapiens	Human secreted protein	1188	99
			encoded by gene 2 clone		
188	AJ292529	17	HLDBG33.		
190	X54134	Homo sapiens	suppressor of sterile four 1	2424	100
191	Y22203	Homo sapiens	protein-tyrosine phosphatase	3705	100
+21	124203	Homo sapiens	Human calcium-binding	1083	99
l		l	phosphoprotein, CBPP-1,		1
i i	W63692	Homo	protein sequence.	1075	100
192	407027		Human secreted protein 12.	1975	100
192	ì	eaniene l		1	
	พลวววว	sapiens	Human serum alucocontinuid	2605	00
192	W87772	sapiens Homo sapiens	Human serum glucocorticoid- regulated kinase (H-SGK2)	2605	99

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	identity
NO: 194	AF084259		bromodomain-containing protein BP75	693	54
195	Y00752	Rattus norvegicus	serine dehydratase (AA 1 - 327)	994	61
196	W95349	Homo sapiens	Human foetal brain secreted protein fh170_7.	2596	100
197	AB028859	Homo sapiens	hDj9	1890	100
198	W95633	Homo sapiens	Homo sapiens secreted protein gene clone hm236_1.	1614	100
199	¥44277	Homo sapiens	Human nucleic acid methylase-	2096	99
200	AB030039	Homo sapiens	hPACPL1	2258	100
201	X54162	Homo sapiens	64 Kd autoantigen	2918	99
202	G02061	Homo sapiens	Human secreted protein, SEQ ID NO: 6142.	558	99
203	X13885	Nicotiana tabacum	extensin (AA 1-620)	185	33
204	J04204	Bos taurus	32 kd accessory protein	1837	100
	J04204 J04204	Bos taurus	32 kd accessory protein	1101	100
205 207	Y87283	Homo sapiens	Human signal peptide containing protein HSPP-60 SEQ ID NO:60.	1318	100
208	Y02860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	936	98
209	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in AL023803))	694	54
		<u> </u>	NPD007	1345	76
210	AF226732	Homo sapiens	Clg C chain	970	73
211	X66295	Mus musculus	Ubiquitin-conjugating enzyme	966	100
212	Z29328	Homo sapiens	UbcH2	542	98
213	Z29328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2		100
214	AJ002030	Homo sapiens	progresterone binding protein	1163	100
215	X70649	Homo sapiens	member of DEAD box protein family	3933	99
216	AF250558	Homo sapiens	claudin-2	1169	
217	AL021453	Homo sapiens	dJ821D11.1 (PUTATIVE protein)	259	100
218	Y08565	Homo sapiens	UDP-GalNAc:polypeptide N- acetylgalactosaminyltransfera se	3331	99
219	Y94452	Homo sapiens	Human inflammation associated protein	l	100
220	AL035521	Arabidopsis thaliana	putative protein	315	42
221	AL031786	Schizosaccha romyces pombe	putative proline-trna synthetase	811	41
222	AL109736	Schizosaccha romyces pombe		626	40
223	X52493	Glycine max	DNA-directed RNA polymerase	136	23
224	AL035659	Homo sapiens		5199	98
225	AB032401	Mus musculus		1761	92
226	AB032401	Mus musculus		1988	92
227	X83502	Saccharomyce s cerevisiae	J1007	112	26
228	X83502	Saccharomyce s cerevisiae	J1007	79	25
229	AF143723	Homo sapiens		2557	99
230	Y66677	Homo sapiens	Membrane-bound protein PRO828.	982	100
1000	700000	Homo sapiens		1756	99
231	AB027466	Homo sapiens	Homo sapiens secreted	1391	100
232	W95634	1 -		ł	1
<u> </u>	W95634 W00365	sapiens Homo sapiens	protein.	2218	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
			designated RAQ.		
235	Z50749	Homo sapiens	yeast sds22 homolog	1800	100
236	Z50749	Homo sapiens	yeast sds22 homolog	1754	98
237	AB026491	Homo sapiens	PICK1	2137	100
238	AJ270205	Entodinium	putative	114	37
		caudatum	phosphatidylinositol-4- phosphate 5-kinase		
239 ·	AB030189	Mus musculus	contains transmembrane (TM)	710	93
240	W56538		region and ATP binding region		
		Homo sapiens	Human hedgehog interacting protein (HIP).	3785	99
241	W56538	Homo sapiens	Human hedgehog interacting protein (HIP).	3436	99
242	AF155107	Homo sapiens	NY-REN-37 antigen	996	99
243	AF155107	Homo sapiens	NY-REN-37 antigen	1005	100
244	AL031320	Homo sapiens	dJ20N2.1 (novel protein	763	99
			similar to yeast and bacterial cytosine)
			deaminase)		
245	บ37026	Rattus	sodium channel beta 2 subunit	162	30
		norvegicus			
246	AL078599	Homo sapiens	dJ991C6.1 (novel protein	2391	98
			similar to C. elegans F55A12.9 (Tr:P91086))		
247	U32274	Coophana		191	<u> </u>
		Saccharomyce s cerevisiae	Ydr386wp; CAI: 0.12		37
248	Y41719	Homo sapiens	Human PRO864 protein sequence.	1879	100
249	AB029434	Homo sapiens	ghrelin precursor	611	100
250	X97831	Rattus	carnitine/acylcarnitine	246	38
		norvegicus	carrier protein	l	
251	W80993	Homo sapiens	Human RIP-interacting factor RIF.	1724	100
252	Y94873	Homo	Human protein clone HP02632.	1876	100
253	W59878	sapiens Homo sapiens	Amino acid sequence of the	765	100
254	AL354533	Leishmania	cDNA clone AIF-2 (HEBGM49). possible adenylate kinase	265	34
		major		265	34
255	AF233322	Mus musculus	zinc transporter like 2	1916	95
256	¥78113	Homo sapiens	Human cytokine signal regulator CKSR-1 SEQ ID NO:1.	2247	99
257	AL035539	Arabidopsis	putative amino acid transport	390	27
		thaliana	protein		<u> </u>
258	W74787	Homo sapiens	Human secreted protein encoded by gene 58 clone HHFHN61.	1171	100
259	AL035689	Homo sapiens	dJ187J11.1 (novel protein similar to protein kinase C	974	100
260	AE000909	Methanobacte	inhibitors) serine/threonine protein	363	30
200	AEGGGGG	rium	kinase related protein	363	30
		thermoautotr	kinase relaced procein		ł
		ophicum		1	
261	AL050131	Homo sapiens	handthatianl	636	100
262	AF019661		hypothetical protein	626	100
		Mus musculus	zeta proteasome chain; PSMA5	1214	100
263	AL035593	Homo sapiens	dJ310J6.1 (novel protein)	821	100
264	AL022318	Homo sapiens	bK150C2.3 (PUTATIVE novel protein similar to APOBEC1)	1072	100
265	AF205940	Homo sapiens	endomucin	1289	100
266	AL023583	Homo sapiens	dJ500L14.1 (novel protein)	789	100
267	AL034548	Homo sapiens	dJ1103G7.3 (novel protein kinase domains containing protein similar to	1888	99
			phosphoprotein C8FW)		

149

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
268	AF161470	Homo sapiens	HSPC121	1884	98
269	AF161470	Homo sapiens	HSPC121	1232	96
270	X90763	Homo sapiens	HHa5 hair keratin type I intermediate filament	2190	99
271	AF207600	Homo sapiens	ethanolamine kinase	1952	100
272	M32334	Homo sapiens	intercellular adhesion molecule 2	1436	100
273	AF161483	Homo sapiens	HSPC134	663	61
274	Y53052	Homo sapiens	Human secreted protein clone df202 3 protein sequence SEQ ID NO:110.	587	100
276	¥77576	Homo sapiens	Human cytoskeletal protein (HCYT) (clone 2195418).	762	100
277	AF077042	Homo sapiens	30S ribosomal protein S7 homolog	1269	100
278	Y94907	Homo sapiens	Human secreted protein clone cal06_19x protein sequence SEQ ID NO:20.	1619	98
279	Y68788	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-20.	2801	.99
280	Z75134	Canis familiaris	red transducin	1816	100
281	Z75134	Canis familiaris	rod transducin	1718	96
282	AF249873	Homo sapiens	muscle-specific protein	1395	100
283	AL050007	Homo sapiens	hypothetical protein	405	98
284	AF201931	Homo sapiens	DC1	1859	99
285	AF156102	Homo sapiens	ELL complex EAP30 subunit	1318	99
286	¥35897	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 146.	1250	99
287	U88964	Homo sapiens	HEM45	923	100
288	AL050143	Homo sapiens	hypothetical protein	598	100
289	AJ011098	Homo sapiens	telethonin	574	100
290	¥66724	Homo sapiens	Membrane-bound protein PRO836.	2321	100
291	AF034801	Homo sapiens	liprin-alpha4	2565	98
292	AF034801	Homo sapiens	liprin-alpha4	2590	100
293	AL049851	Homo sapiens	dJ889J22B.1 (novel protein (isoform 1))	1738	100
294	Y73348	Homo sapiens	HTRM clone 839651 protein sequence.	1245	99
295	L11672	Homo sapiens	zinc finger protein	1694	44
296	AL035423	Homo sapiens	carrier protein-1 (BMCP1))	1024	79
297	AF198532	Homo sapiens	lymphoid enhancer binding factor-1	2173	100
298	AF161417	Homo sapiens	HSPC299	1147	85
299	AF159141	Homo sapiens	suppressor 1	1236	99
300	U26397	Rattus norvegicus	inositol polyphosphate 4- phosphatase	160	30
301	AF036145	Homo sapiens	5	3458	100
302	Z82022	Homo sapiens	GlcNac-1-P transferase	2067	99
303	AF269232	Mus musculus	BUTR-1	271	50
304	AJ222644	Arabidopsis thaliana	asparaginyl-tRNA synthetase	659	50
305	AF054180	Homo sapiens	hematopoietic cell derived zinc finger protein	351	79
306	AJ272079	Homo sapiens		3056	100
308	Y44486	Homo sapiens	Human GPRW receptor polypeptide.	1721	100
309	AJ131891	Homo sapiens	DNA polymerase mu	2598	100

SEO	ACCESSION	SPECIES	DECORT DETON	T 03/2	
ID	NUMBER	SPECIES	DESCRIPTION	SMITH-	8
NO:	Nonbek	Ì		WATERMAN	IDENTITY
310	AF293335	Homo sapiens	p30 DBC	SCORE	
311	AF176525	Mus musculus		1248	92
312	X57802	Homo sapiens	F-box protein FBL12	1501	93
312	A5/802	Homo eabrens	immunoglobulin lambda light	959 .	81
333-	826926	 	chain		
313	Z36715	Homo sapiens	Net	2048	98
314	AF161532	Homo sapiens	HSPC047	727	100
315	AF208068	Homo sapiens	kelch-like protein KLHL3a	3046	100
316	Y66666	Homo	Membrane-bound protein	1166	100
	<u> </u>	sapiens	PRO1013.	_	
317	Y29666	Homo sapiens	Human Ras protein RAPR-1.	1253	98
318	AJ387747	Homo sapiens	sialin	2614	99
319	AF161362	Homo sapiens	HSPC099	224	40
320	Y68773	Homo sapiens	Amino acid sequence of a	2243	99
			human phosphorylation		
			effector PHSP-5.		
321	AJ238379	Homo sapiens	putative TH1 protein	3013	100
322	AB040812	Homo sapiens	protein kinase PAK5	3792	99
323	Y95013	Homo sapiens	Human secreted protein	913	100
	1	1	VC48_1, SEQ ID NO:66.		
324	Y13381	Homo sapiens	Amino acid sequence of	1976	100
		•	protein PRO271.		
325	Y94944	Homo sapiens	Human secreted protein clone	2305	98
			bf157 16 protein sequence	2303] 50
			SEQ ID NO:94.	i	
326	¥76884	Homo sapiens	Retinoblastoma binding	6728	99
			protein-7sequence.	0720	"
327	AF198532	Homo sapiens	lymphoid enhancer binding	2173	100
			factor-1	21/3	100
328	278013	Caenorhabdit	Similarity to Drosophila	569	
	270013	is elegans	Cadherin-related tumor	209	33
		13 Cregans	suppressor		
329	AF212921	Mus musculus	MMTV receptor variant 1	484	
330	Z75330	Homo			94
330	273330	sapiens]	nuclear protein SA-1	6492	99
		>R65207			
		R65207 02-			
]	MAR-1995 27-]	
	i .	AUG-1993			
	} .	Human			}
	ļ				
		ctromplin_1			
		stromalin-1.			
		[Homo			
331	AT.008583	[Homo sapiens	dT227776 2 /aumanted b.	2122	
331	AL008583	[Homo	dJ327J16.3 (supported by	2133	99
		[Homo sapiens Homo sapiens	GENSCAN, FGENES and GENEWISE)	l	
331	AL008583 Y36104	[Homo sapiens	GENSCAN, FGENES and GENEWISE) Extended human secreted	2133	99
		[Homo sapiens Homo sapiens	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO.	l	
332	Y36104	[Homo sapiens Homo sapiens Homo sapiens	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489.	310	41
332	Y36104 AJ271669	[Homo sapiens Homo sapiens Homo sapiens	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease	310	100
332 333 334	Y36104 AJ271669 AF156598	[Homo sapiens Homo sapiens Homo sapiens Mus musculus	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3	310 1747 997	100
332	Y36104 AJ271669	[Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the	310	100
333 334 335	Y36104 AJ271669 AF156598 M99058	[Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria maxima	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Eimeria tenella gene et100	310 1747 997 154	100 64 26
332 333 334	Y36104 AJ271669 AF156598	[Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Eimeria tenella gene et100 Human homologue of UNC-53	310 1747 997	100
333 334 335 336	Y36104 AJ271669 AF156598 M99058 Y85564	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria maxima Homo sapiens	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Eimeria tenella gene et100 Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	310 1747 997 154	100 64 26
333 334 335	Y36104 AJ271669 AF156598 M99058	[Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria maxima	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Eimeria tenella gene et100 Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53	310 1747 997 154	100 64 26
333 334 335 336	Y36104 AJ271669 AF156598 M99058 Y85564 Y85564	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria maxima Homo sapiens Homo sapiens	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Bimeria tenella gene et100 Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	310 1747 997 154 3386	100 64 26
333 334 335 336	Y36104 AJ271669 AF156598 M99058 Y85564	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria maxima Homo sapiens	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Eimeria tenella gene et100 Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53	310 1747 997 154 3386	100 64 26
333 334 335 336 337	Y36104 AJ271669 AF156598 M99058 Y85564 Y85564	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria maxima Homo sapiens Homo sapiens	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Bimeria tenella gene et100 Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	310 1747 997 154 3386 2602	100 64 26 97
333 334 335 336	Y36104 AJ271669 AF156598 M99058 Y85564 Y85564	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria maxima Homo sapiens Homo sapiens	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Eimeria tenella gene et100 Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53	310 1747 997 154 3386 2602	100 64 26 97
333 334 335 336 337	Y36104 AJ271669 AF156598 M99058 Y85564 Y85564 Y85564	[Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria maxima Homo sapiens Homo sapiens	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Bimeria tenella gene et100 Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Similarity to Human rab13	310 1747 997 154 3386 2602	100 64 26 97 94
333 334 335 336 337	Y36104 AJ271669 AF156598 M99058 Y85564 Y85564 Y85564	[Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria maxima Homo sapiens Homo sapiens Caenorhabdit	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Eimeria tenella gene et100 Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	310 1747 997 154 3386 2602	100 64 26 97 94
333 334 335 336 337	Y36104 AJ271669 AF156598 M99058 Y85564 Y85564 Y85564	[Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria maxima Homo sapiens Homo sapiens Caenorhabdit	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Bimeria tenella gene et100 Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Similarity to Human rab13 protein (PIR Acc. No. A49647).	310 1747 997 154 3386 2602 3447 716	100 64 26 97 94 98
333 334 335 336 337 338	Y36104 AJ271669 AF156598 M99058 Y85564 Y85564 Y85564 Z66561	[Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria maxima Homo sapiens Homo sapiens Caenorhabdit is elegans	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Bimeria tenella gene et100 Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Similarity to Human rab13 protein (PIR Acc. No. A49647). gonadotropin inducible	310 1747 997 154 3386 2602	100 64 26 97 94
333 334 335 336 337 338	Y36104 AJ271669 AF156598 M99058 Y85564 Y85564 Y85564 Z66561	[Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria maxima Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Bimeria tenella gene et100 Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Similarity to Human rab13 protein (PIR Acc. No. A49647). gonadotropin inducible transcription repressor-3	310 1747 997 154 3386 2602 3447 716	100 64 26 97 94 98 34
333 334 335 336 337 338 339	Y36104 AJ271669 AF156598 M99058 Y85564 Y85564 Y85564 Z66561 AB021643	[Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria maxima Homo sapiens Homo sapiens Caenorhabdit is elegans Homo	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Bimeria tenella gene et100 Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Similarity to Human rab13 protein (PIR Acc. No. A49647). gonadotropin inducible transcription repressor-3 Human secreted protein, SEQ	310 1747 997 154 3386 2602 3447 716	100 64 26 97 94 98
333 334 335 336 337 338 339	Y36104 AJ271669 AF156598 M99058 Y85564 Y85564 Y85564 Z66561 AB021643	[Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Eimeria maxima Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens	GENSCAN, FGENES and GENEWISE) Extended human secreted protein sequence, SEQ ID NO. 489. putative sialoglycoprotease p53-regulated DDA3 em100 gene is homologous the Bimeria tenella gene et100 Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Human homologue of UNC-53 (Hs-UNC-53/1) sequence. Similarity to Human rab13 protein (PIR Acc. No. A49647). gonadotropin inducible transcription repressor-3	310 1747 997 154 3386 2602 3447 716	100 64 26 97 94 98 34

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:	NUMBER			SCORE	ł
NO:	 		VDJ region		
44	U10281	Sus scrofa	gastric mucin	279	24
44	AK000404	Homo sapiens	unnamed protein product	1177	99
45	L22557	Rattus	calmodulin-binding protein	1949	84
46	122557	norvegicus			
47	L22557	Rattus norvegicus	calmodulin-binding protein	2363	91
48	AL049481	Arabidopsis thaliana	AIG1-like protein	316	30
50	AJ251516	Mus musculus	cysteine and histidine-rich protein	1460	99
51	AK024477	Homo sapiens	FLJ00070 protein	1773	100
52	U50133	Homo sapiens	ankyrin	502	33
53	AK000625	Homo sapiens	unnamed protein product	721	100
54	AF161420	Homo sapiens	HSPC302	2623	97
55	AJ010014	Homo sapiens	M96A protein	1269	47
	AF151029	Homo sapiens	HSPC195	941	91
56	AL022327	Homo sapiens	dJ355C18.1 (KIAA0027)	1911	100
57	W78128	Homo sapiens	Human secreted protein	1117	100
358	W78128	Homo sapiens	encoded by gene 3 clone HOSBI96.		
359	X03414	Drosophila melanogaster	Kr polypeptide	316	45
360	AF151079	Homo sapiens	HSPC245	643	100
361	Y53886	Homo sapiens	A suppressor of cytokine	530	41
301	133830	nome suprem	signalling protein designated HSCOP-6.		
362	AF254741	Drosophila melanogaster	Centaurin Gamma 1A	681	46
363	AF213465	Homo sapiens	dual oxidase	2016	100
364	AF181562	·Homo sapiens	prosaas	1319	100
365	AF181562	Homo sapiens	prosaas	1024	99
366	U73200	Mus musculus	pl16Rip	884	82
367	AF263744	Homo sapiens	erbb2-interacting protein ERBIN	4973	99
368	U37501	Mus musculus	laminin alpha 5 chain	5867	72
369	AF043695	Caenorhabdit	similar to the protein	549	36
307	Ar 043695	is elegans	phosphates 2c family		
370	Y73440	Homo sapiens	Human secreted protein clone yj23_1 protein sequence SEQ ID NO:102.	1484	99
271	AF272833	Homo sapiens		2869	97
371 372	AF272833 AF198454	Homo sapiens	epithelial protein lost in	3927	100
			neoplasm beta	273	80
373	Y73345	Homo sapiens	sequence.	2717	98
374	AF169017	Homo sapiens	cyclodeaminase		
375	A95106	unidentified	.1	1202	99
376	W74828	Homo sapiens	Human secreted protein encoded by gene 100 clone HLOAB52.	1012	99
377	Y32131	Homo sapiens		3556	99
	M14912	Homo sapiens		132	86
378		Homo sapiens		382	100
379	AF090934			2499	100
380	X66363	Homo sapiens	kinase Human PRO703 protein	2362	100
381	Y41699	Homo sapiens	sequence.	7008	98
382	AF174498	Homo sapiens	phosphatase	L	36
383	U64608	Caenorhabdit is elegans	yk173c12.5	246	
384	U50133	Homo sapiens	ankyrin	502	33
385	AJ238520	Homo sapiens	putative transcription	4123	97
		• •	factor-like nuclear regulator	1	1

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	d.
ID NO:	NUMBER			WATERMAN	IDENTITY
387	AF208845	Homo sapiens	BM-003	1375	99
389	X57821	Homo sapiens	immunoglobulin lambda light	797	76
			chain		
390	AF182404	Homo sapiens	mitochondrial uncoupling protein 1	1670	99
391	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3386	97
393	AF178432	Homo sapiens	SH3 protein	3700	100
394	AF229928	Drosophila melanogaster	cytoplasmic protein 89BC	1616	62
395	AF181721	Homo sapiens	RU2S	2254	100
396	Y69197	Homo sapiens	Amino acid sequence of a human betaIV-spectrin protein.	1626	98
397	U48238	Mus musculus	zinc finger protein neuro-d4	749	60
398	AL390137	Homo sapiens	hypothetical protein	263	51
399	AF217525	Homo sapiens	Down syndrome cell adhesion molecule	5337	60
400	AL022599	Schizosaccha	WD repeat protein	447	27
		romyces			1
401	AC004859	Homo sapiens	similar to 2-oxoglutarate dehydrogenase ; similar to Q02218 (PID:g1352618)	4176	78
402	AB010266	Mus musculus	tenascin-X	10246	62
403	AL133288	Homo sapiens	dJ671D7.1 (similar to D.melanogaster CG5986	761	100
			protein)	l	
404	Z68753	Caenorhabdit is elegans	ZC518.3b	888	48
405	Z78013	Caenorhabdit is elegans	Similarity to Drosophila Cadherin-related tumor suppressor	569	33
406	AB031230	Homo sapiens	protein containing CXXC domain 2	1196	97
407	AF155106	Homo sapiens	NY-REN-36 antigen	1168	100
408	Y57945	Homo sapiens	Human transmembrane protein HTMPN-69.	1538	99
409	Z18361	Ovis aries	trichohyalin	184	30
410	AF249744	Homo sapiens	RhoGEF	2733	100
411	AF176529	Mus musculus	F-box protein FBX13	2072	94
412	AF210842	Homo sapiens	HARP	4880	100
413	AL031658	Homo sapiens	dJ310013.7 (novel protein similar to H. roretzi HRPET- 3)	776	98
414	X57398	Homo sapiens	pm5 protein	6131	99
415	AB029826	Homo sapiens	3-methylcrotonyl-CoA carboxylase biotin-containing subunit	2961 .	99
416	U43503	Saccharomyce s cerevisiae	Lph1p	115	42
417	AL160493	Leishmania major	possible t26f17.21	239	35
418	Y08100	Homo sapiens	Human PRO331 protein.	330	29
119	U15131	Homo sapiens	p126	2228	54
120	AF117946	Homo sapiens	Link guanine nucleotide exchange factor II	2363	100
121	AF190635	Drosophila melanogaster	ankyrin 2	755	30
422	AF302150	Homo sapiens	phosphoinositol 3-phosphate- binding protein-2	1962	100
123	AL137530	Homo sapiens	hypothetical protein	433	94
124	X63753	Homo sapiens	son-a	7269	100
125	AB027249	Homo sapiens	MAPKK like protein kinase	1693	100
426	AF279144	Homo sapiens	tumor endothelial marker 7	1084	55
		•	precursor	i .	

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:	AF279144		tumor endothelial marker 7	1259	56
28	AE003683	Drosophila melanogaster	CG8312 gene product	149	29
20	Y07829	Homo sapiens	RING finger protein	2201	99
30	AF096897		pushover	4442	47
	U41387	Homo sapiens	Gu protein	4021	99
31 32	AF023674	Homo sapiens	nephrocystin	3783	100
133	AF146760	Homo sapiens	septin 2-like cell division control protein	2284	100
434	AB006697	Arabidopsis thaliana	cleft lip and palate associated transmembrane protein-like	886	42
437	Y94247	Homo sapiens	Human calcium binding protein hCBP.	1704	100
438	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N- acetylgalactosaminyltransfera se	1075	63
439	AF105228	Bos taurus	tuftelin .	285	33
440	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	3073	99
441	X14971	Mus musculus	alpha-adaptin (A) (AA 1-977)	4897	98
442	X53773	Rattus norvegicus	alpha-c large chain (AA 1- 938)	3979	81
443	Y66689	Homo sapiens	Membrane-bound protein PRO1136.	3299	33
444	AC067754	Arabidopsis thaliana	unknown protein; 20348-23707	2077	93
445	AF229032	Mus musculus	piL	2662	85
446	AF056035	Rattus norvegicus	s-nexilin	478	51
447	AF132484	Mus musculus	unknown	528	45
448	W89024	Homo sapiens	Polypeptide fragment encoded by gene 156.	1606	100
449	AF161445	Homo sapiens	HSPC327	951	49
450	Z68753	Caenorhabdit is elegans	ZC518.3b Human partial complement	155	32
451	W39160	Homo sapiens	factor H protein fragment 3. Novel protein (Clone		99
452	W85727	Homo sapiens	BM46_10). A bone marrow secreted	2810	100
453	Y53629	Homo sapiens	protein designated BMS115. Similar to a C.elegans	4069	100
454	D87438	Homo sapiens	protein in cosmid C14H10	3687	100
455	AF240468	Homo sapiens Homo sapiens	CENP-E	13305	99
456 457	Z15005 M59216	Homo sapiens	gamma-aminobutyric acid receptor beta-1 subunit	2477	100
458	¥73467	Homo sapiens		966	100
459	W67824	Homo sapiens	Human secreted protein encoded by gene 18 clone HSLFM29.	535	100
460	AF163151	Homo sapiens	precursor	279	19
461	D87446	Homo sapiens	protein encoded in cosmid C27F2 (U40419)	9196	99
462	G04044	Homo sapiens		486	93
463	AC002398	Homo sapiens		1018	100
464	AF064856		7acomp protein	1845	99
465	AF223408		B99	3686	

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
466	AF223408	Homo sapiens	B99	2878	87
467	AF104415	Mus musculus	gene trap locus-13	6336	91
468	U53450	Rattus norvegicus	Jun dimerization protein 1 JDP-1	196	49
469	AL031297	Homo sapiens	dJ97P20.1 (novel gene)	3564	99
470	AF257077	Homo sapiens	eukaryotic translation initiation factor EIF2B subunit 3	1274	95
471	L28125	Podospora anserina	beta transducin-like protein	284	38
472	Y84903	Homo sapiens	A human proliferation and apoptosis related protein.	2337	100
473	AF144237	Homo sapiens	LOMP protein	252	44
474	Y71213	Homo sapiens	Human irritable bowel disease related polypeptide IMX39.	838	100 .
475	Y95006	Homo sapiens	Human secreted protein vel3 1, SEQ ID NO:52.	3411	100
476	D38549	Homo sapiens	hal025 is new	6533	99
477	AF241230	Homo sapiens	TAK1-binding protein 2	3656	100
478	AL031534	Schizosaccha romyces pombe	putative asparagine synthase	482	40
479	L28125	Podospora anserina	beta transducin-like protein	233	26
480	AF161544	Homo sapiens	HSPC059	434	77
481	AJ238248	Homo sapiens	centaurin beta2	3986	99
482	Z38061	Saccharomyce s cerevisiae	mal5, sta1, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	295	23
483	AF161381	Homo sapiens	HSPC263	1404	100
484	AF223468	Homo sapiens	AD021 protein	1314	100
486	X57527	Homo sapiens	alpha 1(VIII) collagen	4166	99
487	Y19062	Homo sapiens	39k3 protein	2475	100
488	¥73373	Homo sapiens	HTRM clone 921803 protein sequence.	555	56
489	AL021918	Homo sapiens	b3418.1 (Kruppel related Zinc Finger protein 184)	4184	100
490	X53773	Rattus norvegicus	alpha-c large chain (AA 1- 938)	4675	97
491	U52426	Homo sapiens	GOK	1459	59
492	AL359773	Leishmania major	possible threonine synthase	702	45
493	AF226614	Homo sapiens	ferroportin1	2929	100
494	Z93241	Homo sapiens	dJ222E13.1 (novel protein with some similarity to Drosophila KRAKEN)	513	96
495	AF036977	Homo sapiens	unknown	1812	100
496	U93564	Homo sapiens	p40	133	45
497	Y91405	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:126.	357	100
498	AF069781	Drosophila melanogaster	Bem46-like protein	653	43
499	Y16601	Homo sapiens	Human cell-cycle phosphoprotein CECYF-2.	1658	98
500	X70944	Homo sapiens	PTB-associated splicing factor	3883	100
501	AF027503	Mus musculus	putative membrane-associated guanylate kinase 1	205	36
502	AF282874	Homo sapiens	nectin 3; PRR3	2856	99
503	AJ249732	Homo sapiens	G8 protein	669	100
504	AF208861	Homo sapiens	BM-019	1629	100
505	L09708	Homo sapiens	complement component C2	4022	100
507	X66285	Mus musculus	HC1 ORF	115	43
508	D00189	Rattus norvegicus	Na+,K+-ATPase alpha-subunit	5227	99

155

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
509	¥94971	Homo sapiens	Human secreted protein clone fal71 1 protein sequence SEQ ID NO:148:	2176	100
	22010020	Homo sapiens	beta-1,4 mannosyltransferase	781	77
10	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1347	100
11	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1520	99
12	AB019038	•	phosphorylase kinase	5729	99
513	X84908	Homo sapiens	peptidylprolyl isomerase	650	76
514	X52851	Homo sapiens	epidermal growth factor	3046	99
15	AF186084	Homo sapiens	repeat containing protein Human secreted protein, SEQ	505	99
516	G03602	Homo sapiens	ID NO: 7683.		77
517	U04706	Bos taurus	50 kDa protein	1749	1
518	G00653	Homo sapiens	Human secreted protein, SEQ ID NO: 4734.	530	100
519	AF161475	Homo sapiens	HSPC126	1368	100
520	Y99366	Homo sapiens	Human PRO1475 (UNQ746) amino acid sequence SEQ ID NO:88.	3394	97
521	AF266852	Homo sapiens	PTPLA	1295	100
522	AE000995	Archaeoglobu s fulgidus	chromosome segregation protein (smc1)	153	20
523	AF062249	Homo sapiens	immunoglobulin heavy chain variable region	605	97
524	AJ223830	Rattus norvegicus	ARE1	2950	98
525	W01535	Homo sapiens	Cellular homologue of the SV40 large T antigen.	1276	83
526	AF145658	Drosophila melanogaster	BcDNA.GH10229	320	33
527	AF112213	Homo sapiens	putative Rab5-interacting protein	524	79
528	D49387	Homo sapiens	NADP dependent leukotriene b4 12-hydroxydehydrogenase	1616	100
529	Y30819	Homo sapiens	Human secreted protein encoded from gene 9.	328	32
530	AL079335	Homo sapiens	dJ132F21.3 (72.1 KDa protein (DKFZP564A032, SBB188) similar to mouse IFN-gamma induce MG11.)	1059	99
531	Y91506	Homo sapiens	Human secreted protein sequence encoded by gene 56 SEQ ID NO:179.	1159	98
532	X76116	Caenorhabdit is elegans	carrier protein (c2)	576	50
533	X76116	Caenorhabdit is elegans	carrier protein (c2)	506	50
534	X12966	Homo sapiens	3-oxoacyl-CoA thiolase propeptide (424 AA)	1972	100
535	¥09267	Homo sapiens	1 2 2	2486	100
		Homo sapiens		2201	99
536	Z11773			4741	99
537	D84224	Homo sapiens		3887	99
538	D84224	Homo sapiens		2933	96
539	D84224	Homo sapiens		4529	99
540	D84224	Homo sapiens	H+ ATPase 31kDa subunit (EC	848	77
541	J03244	Bos taurus	3.6.1.3)		99
542	Y92514	Homo sapiens		2301	
543	AF221712	Homo sapiens	Smad- and Olf-interacting zinc finger protein	2151	61
544	AE000919	Methanobacte rium thermoautotr ophicum	_	207	38
545	A06669	synthetic	preTGF-betal	2070	99

SEO	ACCESSION	OPPOTES		7	
ID NO:	NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	# IDENTITY
546	Y02698	Homo sapiens	encoded by gene 49 clone	854	98
547	AF112205	Homo sapiens	HTPCS60. WSB-1 protein	2275	
548	X60271	Mus musculus	c-rel	2275	100 74
549	AC016827	Arabidopsis	putative GTPase	810	42
550	¥70400	thaliana	Human cell-signalling	429	
330	170400	sapiens	protein-2.	429	68
551	AB048365	Homo sapiens	NEDD4-like ubiquitin ligase 1	8290	99
552	Y57880	Homo sapiens	Human transmembrane protein HTMPN-4.	1112	95
553	AF119855	Homo sapiens	PRO1847	265	67
554	M17236	Homo sapiens	MHC HLA-DQ alpha precursor	1332	100
555	AL078468	Arabidopsis thaliana	putative protein	540	40
556	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	515	44
557	AK024487	Homo sapiens	FLJ00086 protein	1623	98
558	M12140	Homo sapiens	pol gene protein; Xxx	117	48
559	W74825	Homo sapiens	Human secreted protein encoded by gene 97 clone HAQBF73.	225	56
560	X56681	Homo sapiens	junD protein	373	88
561	AF003136	Caenorhabdit is elegans	contains weak similarity to an AMP-binding motif	2926	54
562	AL109839	Homo sapiens	dJ1069P2.3.1 (novel PABPC1 (poly(A)-binding protein)	877	100
563	AF181640	Drosophila melanogaster	BcDNA.GH09817	289	42
564	AF052723	Feline leukemia virus	gag-pol precursor polyprotein gPr80	1547	43
565	AF161472	Homo sapiens	HSPC123	439	44
566	Y28817	Homo sapiens	pt326_4 secreted protein.	3338	100
567	U09848	Homo sapiens	zinc finger protein	1738	100
569 570	AF155113 AF155113	Homo sapiens	NY-REN-55 antigen	3603	93
571	AF155113	Homo sapiens	NY-REN-55 antigen dJ55C23.1 (vanin 1)	3951	99
572	M69181	Homo sapiens	non-muscle myosin B	1821 7350	98 99
573	M69181	Homo sapiens	non-muscle myosin B	7311	98
574	Y59678	Homo sapiens	Secreted protein 108-008-5-0- E6-PL.	772	100
575	AL365234	Arabidopsis thaliana	putative protein	788	40
576	AL365234	Arabidopsis thaliana	putative protein	788	40
577	X06745	Homo sapiens	DNA polymerase alpha-subunit (AA 1 - 1462)	7619	99
578	AB041642	Homo sapiens	PAR-6	1342	100
579	D86984	Homo sapiens	similar to yeast adenylate cyclase (S56776)	2446	100
580	AF165124	Homo sapiens	gamma-aminobutyric acid A receptor gamma 2	2499	99
581	W88812	Homo sapiens	Polypeptide fragment encoded by gene 58.	2339	99
582	U82319	Homo sapiens	novel ORF	342	100
583	P92219	Homo sapiens (human)	CR1 protein.	11425	99
584	AJ223948	Homo sapiens	RNA helicase	6608	99
585	Y08612	Homo sapiens	88kDa nuclear pore complex protein	3874	99
586	Y42384	Homo sapiens	Amino acid sequence of lv310 7.	1007	37
587	AF129756	Homo sapiens	BAT4	1873	98

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:			Unknown	1929	99
588	AF131775	Homo sapiens	TESS 2	2348	100
589	AJ250865	Homo sapiens	dJ522J7.2 (bromodomain-	4167	100
591	Z98885	Homo sapiens	containing 1 (similar to peregrin, BR140))		
592	Б 76571	Homo sapiens	nuclear hormone receptor	1355	100
593	AF091622	Homo sapiens	PHD finger protein 3	9054	100
594	X56807	Homo sapiens	desmocollin type 2a	4443	100
595	AL137802	Homo sapiens	dJ798A10.1 (novel protein)	212	55
596	AL022329	Homo sapiens	bK407F11.2 (adrenergic, beta, receptor kinase 2)	3653	100
597	AF226048	Homo sapiens	GL003	2009	99
598	AJ278112	Homo sapiens] >Y49635 Y49635 21-	putative cell cycle control protein	335	23
		OCT-1999 15- APR-1998 Human sdp3.5 protein. [Homo sapiens			
599	Y59741	Homo sapiens	Human normal ovarian tissue derived protein 18.	1574	99
600	L36531	Homo sapiens	integrin alpha 8 subunit	5386	99
601	¥38458	Homo sapiens	Human secreted protein encoded by gene No. 20.	895	100
602	AF218584	Homo sapiens	GGA1	3265	100
603	Y13115	Homo sapiens	serine/threonine protein kinase	5071	99
604	AL132776	Homo sapiens	dJ393D12.1 (KIAA0776)	2413	99
605	AL034452	Homo sapiens	dJ682J15.1 (novel Collagen triple helix repeat containing protein)	1979	100
606	Y14494	Homo sapiens	aralar1	3465	99
607	AJ001981	Homo sapiens	OXA1L	2603	100
608	X86098	Homo sapiens	binds directly to adenovirus type 5 ElA protein	3069	100
610	AF163572	Homo sapiens	Forssman glycolipid synthetase	1865	99
611	AF161503	Homo sapiens	HSPC154	1261	97
612	L41834	Ensis minor	nuclear protein	345	30
613	Y91954	Homo sapiens	protein 9 (CYSKP-9).	3668	100
614	AL022327	Homo sapiens	dJ355C18.1 (KIAA0027)	361	94
615	X85786	Homo sapiens		3203	100
616	Y08319	Homo sapiens	kinesin-2	3487	99
617	D12644	Mus musculus	KIF2 protein	3609	97
618	U28789	Mus musculus	PACT	5936	89
619	Y35914	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 163.	1684	99
620	AB046382	Mus musculus	testis-abundant finger	199	23
621	Y00062	Homo sapiens	to 1120)		99
622	AF068286	Homo sapiens		861	100
623	X98248	Homo sapiens		4436	99
624	X61100	Homo sapiens	dehydrogenase precursor	3734	99
625	S58544	Homo sapiens	sperm protein	2125	99
626	AF151027	Homo sapiens	HSPC193	582	93
627	X14968	Homo sapiens	RII-alpha subunit (AA 1-404)	2079	100
628	Y50911	Homo sapiens	Human fetal brain cDNA clone vb7_1 derived protein	1983	100

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	- E
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
629	Y50911	Homo sapiens	Human fetal brain cDNA clone vb7_1 derived protein	1694	100
630	AF098786	Homo sapiens	17 beta-hydroxysteroid dehydrogenase type VII	1754	100
631	AL034555	Homo sapiens	dJ134019.3 (zinc finger protein 151 (pHZ-67))	4273	100
632	W74826	Homo sapiens	Human secreted protein encoded by gene 98 clone HAQBT94.	794	96
633	AF288288	Homo sapiens	HPT protein	2236	.100
634	AF041429	Homo sapiens	pRGR1	823	99
635	X66357	Homo sapiens	serine/threonine protein kinase	1589	100
636	Y11284	Homo sapiens	AFX1	2571	98
637	AB004884	Homo sapiens	PKU-alpha	3718	99
638	AJ002303	Homo sapiens	synaptogyrin 1c	1020	100
639	AJ002304	Homo sapiens	synaptogyrin 1b	1002	100
640 641	AJ002303 D87682	Homo sapiens Homo sapiens	synaptogyrin 1c similar to a C.elegans protein encoded in cosmid	933 2676	100
			T26A5.	<u> </u>	
642	M14660	Homo sapiens	ISG-K54	2473	99
643 644	X06661 AF119900	Homo sapiens	calbindin (AA 1-261)	1358	100
645	AB031048	Drosophila	PRO2822 microtubule associated-	185 738	76 27
646	AF250842	melanogaster Drosophila	protein orbit multiple asters	834	29
		melanogaster	_		
647	X86691 U67934	Homo sapiens	Mi-2 protein	10110	99
		Homo sapiens	44.9 kDa protein C18B11 homolog	827	96
649	AF236061	Oryctolagus cuniculus	RING-finger binding protein	3830	91
650	AL034553	Homo saplens	dJ914P20.2 (KIAAO784 protein similar to Mus musculus activity-dependent neuroprotective protein (Adnp))	5708	100
653	X14766	Homo sapiens	GABA-A receptor alpha 1 subunit	2388	99
654	AC004614	Homo sapiens	similar to f-spondin proteins AB006086 (PID:g2529225)	3026	99
655	¥57908	Homo sapiens	Human transmembrane protein HTMPN-32.	608	99
656	Z34975	Homo sapiens	ldlCp	3733	100
658	AL050306	Homo sapiens	dJ475B7.2 (novel protein)	1942	99
659	W76734	Homo sapiens	Human mDia Rho targeting protein.	781 .	34
660	AF202724	Homo sapiens	Sad1 unc-84 domain protein 1	2172	100
661	Z21966	Homo sapiens	mPOU homeobox protein	1529	100
662 663	AJ242954	Mus musculus	dysferlin	4752	59
665	AF182316 AL161516	Homo sapiens Arabidopsis thaliana	myoferlin hypothetical protein	6232 209	30
667	X59303	Homo sapiens	valyl-tRNA synthetase	3393	99
668	Y13355	Homo sapiens	Amino acid sequence of protein PRO220.	3692	100
669	AB010692	Arabidopsis thaliana	contains similarity to endo- beta-N-acetylglucosaminidase gene	611	52
671	X56123	Mus musculus	talin	4474	76
672	AB039371	Homo sapiens	mitochondrial ABC transporter	2902	99
673	AF269223	Homo sapiens	TCP11	806	42
674	AF229633	Mus musculus	groucho-related protein 4	4053	99
675	L14463	Rattus	'transducin	3619	92

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	8
ID	NUMBER			WATERMAN	IDENTITY
NO:	Ì			SCORE	
		norvegicus			
76	AC005757	Homo sapiens	R32611_1	2779	100
77	861069	Homo sapiens	reverse transcriptase	252	65
			homolog=pol {retroviral element}		
78	AF271388	Homo sapiens	CMP-N-acetylneuraminic acid synthase	2273	100
79	X79066	Homo sapiens	ERF-1	1783	100
80	AF118566	Mus musculus	hematopoietic zinc finger protein	769	50
681	Y51415	Homo sapiens	Human wild type pKe83 . protein.	2621	99
	AL133545	Homo sapiens	bA386N14.1 (novel protein	700	68
582	WP133242	Homo sapiens	similar to a dual specificity phosphatase)		
		Homo sapiens	Nuclear transport protein	5888	99 .
683	Y86214	Homo sapiens	clone hfb341 protein sequence.	1	
	704050	Homo sapiens	Human secreted protein clone	354	98
684	¥94952	HOMO Sabrens	fh116_11 protein sequence SEQ ID NO:110.		
	77.001.000	Homo sapiens	dJ257I20.4 (transcription	154	67
685	AL021878	nomo sapiens	factor 20 (AR1) (KIAA0292) (isoform 2))		
686	AE000198	Escherichia	orf, hypothetical protein	628	100
		coli	synapsin I	3730	99
687	M58378	Homo sapiens	antigen NY-CO-31	508	98
688	AF039697	Homo sapiens	protein phosphatase 2Al B	2356	99
689	U09355	Oryctolagus cuniculus	gamma subunit	265	50
690	AF155106	Homo sapiens	NY-REN-36 antigen	1542	100
691	AC004774	Homo sapiens	Dlx-5	1926	99
692	X90530	Homo sapiens	ragB	1405	199
693	X90530	Homo sapiens	ragB	1590	85
694	X90530	Homo sapiens	ragB Human secreted protein, SEQ	330	100
695	G01563	Homo sapiens	ID NO: 5644.	669	52
696	AC011810	Arabidopsis thaliana	Putative methionine aminopeptidase		98
697	AJ250425	Rattus norvegicus	Collybistin I	2455	
698	AB037901	Homo sapiens	gene amplified in squamous cell carcinoma-1	5364	99
699	Y99401	Homo sapiens	Human PRO1327 (UNQ687) amino acid sequence SEQ ID NO:218.	1386	100
701	AF221712	Homo sapiens	Smad- and Olf-interacting zinc finger protein	6705	100
702	X83573	Homo sapiens	ARSE	3184	99
702	AJ243274	Homo sapiens	AP-2rep protein	2078	99
704	Y71262	Homo sapiens		1697	94
705	Y71262	Homo sapiens		1736	99
706	¥41257	Homo sapiens	1 -	1060	100
707	AL022237	Homo sapiens		2030	100
700	AJ006266	Homo sapiens		5942	100
708 709	G01571	Homo sapiens		777	99
	V00000	Homo sapiens		2849	98
710 711	Y08698 Y68770	Homo sapiens		754	99

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
712	U93574	Homo sapiens	putative p150	799	59
713	AC004531	Homo sapiens	Gene with similarity to DEAD box helicases	2715	99
714	D89016	Homo sapiens	Neuroblastoma	538	48
715	Y92175	Homo sapiens	Human cardiovascular system associated protein tyrosine phosphatase 2.	734	98
716	AL137013	Homo sapiens	bA311P8.3 (probable uracil phosphoribosyltranferase)	862	100
717	AB035123	Mus musculus	GD1 alpha/GT1a alpha/GQ1b alpha synthase	1696	93
718	Y96290	Homo >P40254 P40254 25- OCT-1984 09- APR-1983 Human IgD. [Homo sapiens	Human IGFAM-2 immunoglobulin.	2345	85
719	X07979	Homo sapiens	integrin beta 1 subunit precursor	4347	99
720	AJ224819	Homo sapiens	tumor suppressor	2149	99
721	Y07595	Homo sapiens	transcription factor TFIIH	2373	100
722	W41565	Homo sapiens] >W41564 W41564 08- OCT-1997 05- APR-1996 Human calpain. [Homo sapiens	Human calpain.	1591	99
723	AF161341	Homo sapiens	HSPC078	1097	98
724	AF187318	Homo sapiens	F-box protein Fbx2	1607	100
725	AC006708	Caenorhabdit is elegans	contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)	1143	46
726	AC006708	Caenorhabdit is elegans	contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)	988	46
727	AC024818	Caenorhabdit is elegans	contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3	950	44
728	AJ005897	Homo sapiens	JM5	831	47
729	Y45377	Homo sapiens	Human secreted protein fragment encoded from gene 27.	908	97
730	G03931	Homo sapiens	Human secreted protein, SEQ ID NO: 8012.	578	100
731	AB012720	Oncorhynchus masou	GTP-binding protein	3865	76
732	W73404	Homo sapiens	Human secreted protein encoded by Gene No. 8.	862	97
733	G02650	Homo sapiens	Human secreted protein, SEQ ID NO: 6731.	644	97
734	AC024813	Caenorhabdit is elegans	Hypothetical protein Y54F10AL.a	152	24
735	AL035461	Homo sapiens	dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase	1562	98
			family member protein)		
736	U00033	Caenorhabdit is elegans	family member protein) similar to S. cerevisiae YJU2 protein arginine-tRNA-protein	605	99

161

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:		Homo sapiens	nucleolar RNA-helicase	2793	100
38	AJ131712	1101110 011-	TSC-22-like protein	2054	99
39	AJ133115	and the same	TSC-22-11ke protein	953	100
40	X98258	Homo sapiens	M-phase phosphoprotein 9		74
41	X98258	Homo sapiens	M-phase phosphoprotein 9	564	1
42	U97191	Caenorhabdit	strong similarity to the YPT1	960	85
42	09/191	is elegans	sub-family of RAS proteins		
			phosphomannose isomerase	2191	100
743	X76057	Homo sapiens	phospholiatinose racinerase	496	98
744	G03209	Homo sapiens	Human secreted protein, SEQ	430	100
		1	ID NO: 7290.		
	X97064	Homo sapiens	Sec23 protein	4034	99
745		Homo sapiens	Human regulatory molecule	994	100
746	W93946	Homo sapiens	HRM-2 protein.		1
		l	HRW-2 process.	1565	99
747	Y73388	Homo sapiens	HTRM clone 3376404 protein	1202	"
73.	1.020	-	sequence.		
		Sus scrofa	follistatin A	1906	98
748	M19529			183	28
749	AJ249457	Trichomonas	centrin, putative	1 -00	1
		vaginalis			
750	AC004410	Homo sapiens	fos39554 1	2094	100
		Homo sapiens	p47ING3 protein	2167	100
751	AF074968		transcription specificity	4005	100
752	AF252284	Homo sapiens	cranscription specificity	1	1
			factor Sp1		1.50
753	AB049629	Homo sapiens	phospholysine	1375	99
155	ABUNDUZS		phosphohistidine inorganic	1	
		1	pyrophosphate phosphatase	1	ļ
	1		pyrophosphate phosphataet	160	77
754	D79205	Homo sapiens	ribosomal protein L39		
755	AB00B430	Homo sapiens	CDEP	142	29
		Homo sapiens	transcription factor	574	80
758	L32162		RING zinc finger protein	295	54
759	AF037204	Homo sapiens	RING ZING TINGEL DIOCETH	625	100
760	Y44250	Homo	Human cell signalling	625	1 -00
, , ,		sapiens	protein-13.		
		Homo sapiens	Cide-b	1136	100
761	AF218586	Homo sapiens		625	97
762	U38934	Gallus	histone H2A	1 020	
	i	gallus			
763	AF226053	Homo sapiens	HSKM-B	606	32
		Homo sapiens	Oct-1 protein (AA 1 - 743)	3626	100
764	X13403		Similar to a C.elegans	568	38
765	D87446	Homo sapiens	protein encoded in cosmid C27F2 (U40419)		
766	AT-023828	Caenorhabdit	Y17G7B.14	200	27
, 50	122020	is elegans	1		
	<u> </u>	15 cregans	Human chordin related protein	2551	99
767	Y82777	Homo sapiens			1
			(Clone dw665_4).	1 2 4 2 2	100
768	X92475	Homo sapiens	ITBA1	1429	
	Y42752	Homo sapiens		1426	100
769	146/36		3 (CaBP-3).	ł	1
				2641	97
770	X51416	Homo sapiens		1	1
		1	521)	1703	100
771	AJ006591	Homo sapiens	cysteine-rich protein	1793	
	A08695	Homo sapiens		935	100
772				2970	100
773	Z12173	Homo sapiens			
1	1		sulphatase	FC5	43
774	Y91950	Homo sapiens	Human cytoskeleton associated	565	*3
l · · · ^	1	<u> </u>	protein 5 (CYSKP-5).		
	77.000.700	Homo sapiens		855	56
776	AL023799			855	56
777	AL023799	Homo sapiens	0110	849	98
778	G01880	Homo sapiens	Human secreted protein, SEQ	043	1 -
	1		ID NO: 5961.		
	- 13 TOTO COA	Homo sapiens	glucose 1-dehydrogenase	4155	99
779	AJ012590			1321	68
780	AL078582	Homo sapiens	G QUISUE4.2 (KIAAU/36)	384	34
781	275955	Caenorhabdit		384	J.
'31		is elegans	carrier protein		
L			dJ1121G12.2 (SCAN domain-	900	100
782	AL109965	Homo	QUITAIDIA. A COMP COMMENT		ĺ
i .	1	sapiens	containing 1 protein)	12216	83
	7.0001000	Mus	semaF cytoplasmic domain	1316	1 02
793	Arubizez				
783	AF061262	musculus	associated protein 2 B Human secreted protein, SEQ	_	95

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID	NUMBER	SPECIES	DESCRIPTION		TOWNSTAN
	NUMBER			WATERMAN	IDENTITY
NO:		ļ		SCORE	
505	70444	<u> </u>	ID NO: 7954.		
785	Y84441	Homo sapiens	Amino acid sequence of a	2074	100
	1		human RNA-associated		ŀ
		<u></u>	protein.		<u> </u>
786	Y00918	Homo sapiens	Human Rab protein, RABP-1,	1048	99
			protein sequence.		
787	Z97029	Homo sapiens	ribonuclease HI large subunit	1548	99 ·
788	AB035384	Homo sapiens	SRp25 nuclear protein	962	94
789	AF024631	Homo sapiens	ANG2	2644	100
790	AJ006710	Rattus	phosphatidylinositol 3-kinase	4508	97
		norvegicus	1		
792	V00638	bacteriophag	reading frame eal0	600	100
		e lambda	1 2000 2000	***	= "
793	AF049103	Homo sapiens	Huntingtin interacting	819	100
,,,,	Aroquios	nomo saprens	protein	1 023	100
795	Z26317	Homo sapiens	desmoglein 2	4810	99
	.1	1		1	1
796	¥76884	Homo sapiens	Retinoblastoma binding	5080	99
			protein-7sequence.		
797	U15155	Gallus	trypsinogen	372	37
		gallus	<u> </u>		J
798	U97189	Caenorhabdit	strong similarity to thw	227	28
	1	is elegans	P13/P14 family of kinases	İ	
799	AF112201	·Homo sapiens	neuronal protein NP25	1053	100
800	AF234765	Rattus	serine-arginine-rich splicing	958	63
		norvegicus	regulatory protein SRRP86	1	
801	AF267852	Homo sapiens	placental protein 13-like	743	99 .
	}		protein	}	
802	AF208851	Homo sapiens	BM-009	766	80 .
803	Z81097	Caenorhabdit	Similarity to Human	152	27
003	201037	is elegans	retinoblastoma-binding		"
		is elegans	protein RBAP46 yk662d12.5		:
		1	comes from this gene	ł	ł
804	G02113	77		100	
804	G02113	Homo sapiens	Human secreted protein, SEQ	496	98
		<u> </u>	ID NO: 6194.		<u> </u>
805	AL121673	Homo sapiens	bA305P22.1 (novel protein)	1160	100
806	AC013483	Arabidopsis	putative GTPase activator	264	30
·		thaliana	protein		
807	AC013483	Arabidopsis	putative GTPase activator	264	30
	<u> </u>	thaliana	protein	<u> </u>	
808	AB013885	Homo sapiens	beta-ureidopropionase	1494	100
809	AF078842	Homo sapiens	HOTTL protein	1581	99
810	AF161421	Homo sapiens	HSPC303	2134	96
811	AF261689	Homo sapiens	DNA polymerase epsilon p17	734	100
		· .	subunit	1	1
812	274029	Caenorhabdit	Similarity to C.elegans	610	71
		is elegans	alcohol dehydrogenase comes		1
	•			1	
			from this gene		I .
813	Z73497	Homo sapiens	from this gene cU240C2.2 (Core histone	324	100
813	273497	Homo sapiens	cU240C2.2 (Core histone	324	100
			CU240C2.2 (Core histone H2A/H2B/H3/H4)		L
813	Z73497 W87689	Homo	cU240C2.2 (Core histone	1484	99
814	W87689	Homo sapiens	CU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide.	1484	99
		Homo sapiens Homo	CU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide. zinc finger protein (217 AA)		L
814	W87689 X16282	Homo sapiens Homo sapiens	CU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide. zinc finger protein (217 AA) (1 is 2nd base in codon)	1484	99
814	W87689	Homo sapiens Homo sapiens Mycobacteriu	CU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide. zinc finger protein (217 AA)	1484	99
814	W87689 X16282	Homo sapiens Homo sapiens Mycobacteriu	CU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide. zinc finger protein (217 AA) (1 is 2nd base in codon)	1484	99
814 815 816	W87689 X16282 Z92539	Homo sapiens Homo sapiens Mycobacteriu m tuberculosis	CU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide. Zinc finger protein (217 AA) (1 is 2nd base in codon) pth	1109	99
814 815 816	W87689 X16282 Z92539 AB030483	Homo sapiens Homo sapiens Mycobacteriu m tuberculosis Mus musculus	CU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide. zinc finger protein (217 AA) (1 is 2nd base in codon) pth B9	1484 1109 300	99 99 36
814 815 816 818 819	W87689 X16282 Z92539 AB030483 AL117555	Homo sapiens Homo sapiens Mycobacteriu m tuberculosis Mus musculus Homo sapiens	cU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide. zinc finger protein (217 AA) (1 is 2nd base in codon) pth B9 hypothetical protein	1109	99
814 815 816	W87689 X16282 Z92539 AB030483	Homo sapiens Homo sapiens Mycobacteriu m tuberculosis Mus musculus	CU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide. zinc finger protein (217 AA) (1 is 2nd base in codon) pth B9	1484 1109 300	99 99 36
814 815 816 818 819	W87689 X16282 Z92539 AB030483 AL117555	Homo sapiens Homo sapiens Mycobacteriu m tuberculosis Mus musculus Homo sapiens Homo sapiens	CU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide. zinc finger protein (217 AA) (1 is 2nd base in codon) pth B9 hypothetical protein R26660_2, partial CDS	1484 1109 300 197 321	99 99 36 27 94
814 815 816 818 819 820	W87689 X16282 Z92539 AB030483 AL117555 AC005328	Homo sapiens Homo sapiens Mycobacteriu m tuberculosis Mus musculus Homo sapiens	cU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide. zinc finger protein (217 AA) (1 is 2nd base in codon) pth B9 hypothetical protein	1484 1109 300 197 321 865	99 99 36 27 94 97
814 815 816 818 819 820	W87689 X16282 Z92539 AB030483 AL117555 AC005328	Homo sapiens Homo sapiens Mycobacteriu m tuberculosis Mus musculus Homo sapiens Homo sapiens	CU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide. zinc finger protein (217 AA) (1 is 2nd base in codon) pth B9 hypothetical protein R26660_2, partial CDS Human secreted protein, SEQ ID NO: 8032.	1484 1109 300 197 321 865 700	99 99 36 27 94 97
814 815 816 818 819 820 821	W87689 X16282 Z92539 AB030483 AL117555 AC005328 G03951	Homo sapiens Homo sapiens Mycobacteriu m tuberculosis Mus musculus Homo sapiens Homo sapiens Homo sapiens	CU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide. zinc finger protein (217 AA) (1 is 2nd base in codon) pth B9 hypothetical protein R26660_2, partial CDS Human secreted protein, SEQ	1484 1109 300 197 321 865	99 99 36 27 94 97
814 815 816 818 819 820 821	W87689 X16282 Z92539 AB030483 AL117555 AC005328 G03951 L34807	Homo sapiens Homo sapiens Mycobacteriu m tuberculosis Mus musculus Homo sapiens Homo sapiens Homo sapiens Musca domestica	CU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide. zinc finger protein (217 AA) (1 is 2nd base in codon) pth B9 hypothetical protein R26660_2, partial CDS Human secreted protein, SEQ ID NO: 8032. transposase	1484 1109 300 197 321 865 700	99 99 36 27 94 97 99
814 815 816 818 819 820 821	W87689 X16282 Z92539 AB030483 AL117555 AC005328 G03951	Homo sapiens Homo sapiens Mycobacteriu m tuberculosis Mus musculus Homo sapiens Homo sapiens Homo sapiens	CU240C2.2 (Core histone H2A/H2B/H3/H4) Human HTXFT19 polypeptide. zinc finger protein (217 AA) (1 is 2nd base in codon) pth B9 hypothetical protein R26660_2, partial CDS Human secreted protein, SEQ ID NO: 8032.	1484 1109 300 197 321 865 700	99 99 36 27 94 97

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	8
ID	NUMBER			WATERMAN	IDENTITY
NO:	1			SCORE	
		romyces	protein 1		ļ
		pombe		603	68
325	AJ006692	Homo sapiens	ultra high sulfer keratin	693 3406	90
326	U23037	Oryctolagus	eIF-2Bepsilon	3406	30
	1	cuniculus		464	100
827	G03412	Homo sapiens	Human secreted protein, SEQ	404	1 ***
			ID NO: 7493.	113	44
328	Y30827	Homo sapiens	Human secreted protein	113	3.7
			encoded from gene 17.	1012	100
329	Y32199	Homo sapiens	Human receptor molecule (REC)	1012	100
			encoded by Incyte clone	l	
	·		2022379. Fragment of human secreted	1264	99
830	W78279	Homo sapiens	protein encoded by gene 33.	1204	"
				2097	100
832	AB011542	Homo sapiens	MEGF9	223	70
833	G02639	Homo sapiens	Human secreted protein, SEQ	223	'
			ID NO: 6720. transcriptional regulator	1574	100
834	AF119664	Homo sapiens	protein HCNGP	1	
			transcriptional regulator	1144	89
835	AF119664	Homo sapiens	protein HCNGP		1
			transcriptional regulator	1448	94
836	AF119664	Homo sapiens	protein HCNGP	1	
		77	C protein (AA 1-159)	918	100
837	X12517	Homo sapiens	linotte protein	164	24
838	U32865	Drosophila melanogaster	Tinocce procesn		
***	7000000	Homo sapiens	TLS-associated protein TASR-2	631	56
839	AF067730	Homo sapiens	striatum-enriched phosphatase	2840	98
840	U27831	Homo sapiens	CamKI-like protein kinase	1796	100
841	AF286366	1	Human secreted protein, SEQ	278	98
842	G02309	Homo sapiens	ID NO: 6390.	1	
	78007615	Drosophila	ade3 gene product	113	48
843	AE003615	melanogaster	ades gene product		
	200 250	Homo sapiens	Human secreted protein, SEQ	629	100
844	G01350	HOWO Bapiens	ID NO: 5431.		
845	U27838	Mus musculus	glycosyl-phosphatidyl-	3305	96
845	027030	Mas mascaras	inositol-anchored protein	ļ	ļ
			homolog	1	}
847	Y87788	Homo sapiens	Human RBP-26 protein.	2026	100
848	AF164794	Homo sapiens	Diff33 protein homolog	2398	100
849	U41315	Homo sapiens	ZNF127-Xp	2458	93
850	AF192784	Homo sapiens	makorin 1	2062	97
851	Y58628	Homo sapiens	Protein regulating gene	1548	100 .
927	130020	1101110 20220112	expression PRGE-21.		
852	Z22968	Homo sapiens	M130 antigen	6205	100
853	Z22971	Homo sapiens	M130 antigen extracellular	6380	100
033	222711	nome paparet	variant	- }	
854	G03362	Homo sapiens	Human secreted protein, SEQ	330	96
034	003302		ID NO: 7443.	1	
855	G03362	Homo sapiens		203	100
000	003302		ID NO: 7443.		
856	AF285118	Homo sapiens	CGI-203	452	100
857	AC006069	Arabidopsis	putative cleavage and	1383	55
037	1	thaliana	polyadenylation specifity	ļ	
			factor		
858	AL021546	Homo sapiens	Cytochrome C Oxidase	593	100
	1		Polypeptide VIa-liver		
			precursor (EC 1.9.3.1)		
859	L02956	Xenopus	ribonucleoprotein	1664	85
	1	laevis			
860	AF201947	Homo sapiens	MEK binding partner 1	616	100
861	L31783	Mus musculus		1266	92
862	AF161472	Homo sapiens	HSPC123	602	73
863	Z49068	Caenorhabdit		370	43
		is elegans			
864	AF154108	Homo sapiens	tumor necrosis factor type 1	3559	99

No:	SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
Ref		NUMBER	l		WATERMAN SCORE	IDENTITY
B66 X57807 Homo sapiens Immunoglobulin lambda light chain				receptor associated protein		
Chain	865	AE001530		putative	230	32
RRAB box protein with 18 C2Hz type Zinc finger domains 100	866	X57807	Homo sapiens		699	91
AF192968 Homo sapiens high-glucose-regulated protein 37	867	AL031673	Homo sapiens	KRAB box protein with 18 C2H2 type Zinc finger domains)	4066	99
Process	868		1		1	1
### ### ##############################	869	AF192968	Homo sapiens	protein 8	3041	99
872	870	AB020648	Homo sapiens	KIAA0841 protein	3237	99
B73		AL031427			1608	100
elegans UNC-93 (protein 1, C46F11.1) LIKE protein) 100			Homo sapiens		1866	100
### ### ### ### ### ### ### ### ### ##			_	elegans UNC-93 (protein 1, C46F11.1) LIKE protein)		
Second Comparison Compari			1 -		1	
Secretisize	875	AL117334	Homo sapiens	(part of translation of cDNA	306	100
ch834 1 protein sequence SEQ DNO:8.	876	X79489		E-925 protein	446	35
879 X79417 Sus scrofa 40S ribosomal protein S12 687 100	877	Y53001	Homo sapiens	dn834_1 protein sequence SEQ	811	100
Record R	878	AF281064	Homo sapiens	CHMP1.5	957	100
S cerevisiae	879	X79417		40S ribosomal protein S12	687	100
Containing protein HSPP-52 SEQ ID NO:52. SEQ ID NO:52.	880	AF001317		Soilp	478	28
Record R	881	Y87275	-	containing protein HSPP-52	2547	100
Phospholipase A2	882	M14036		C1-inhibitor	598	77
885 Y10936 Homo sapiens hypothetical protein 1104 99	883	AB041261	Homo sapiens	phospholipase A2	2903	100
Ref	884	1 .	Mus musculus		1	84
1			Homo sapiens	hypothetical protein	1104	99
### HTMPN-17. #### Reference of the protein and protein are september of the protein sequence, SEQ ID NO.		AF073997		<u> </u>	866	36
### Record ### Re			_	HTMPN-17.		
transporter family member GLUT9						<u></u>
Protein sequence, SEQ ID NO.	889	AF210317	Homo sapiens	transporter family member	2046	99
Note	890	Y36031	Homo sapiens	protein sequence, SEQ ID NO.	583	100
892 AF237631 Homo sapiens ubiquitous tropomodulin U- Tmod 893 AF090929 Homo sapiens PR00477p 653 99 894 AL031228 Homo sapiens dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1) 895 AL031228 Homo sapiens dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1) 896 AF171102 Homo sapiens retinal degeneration B beta 1302 95 897 AE003551 Drosophila CG18176 gene product 633 33	891	Y36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO.	192	57
893 AF090929 Homo sapiens PR00477p 653 99 894 AL031228 Homo sapiens dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1) 895 AL031228 Homo sapiens dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1) 896 AF171102 Homo sapiens retinal degeneration B beta 1302 95 897 AE003551 Drosophila CG18176 gene product 633 33	892	AF237631	Homo sapiens	ubiquitous tropomodulin U-	1798	100
894 AL031228 Homo sapiens dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1) 895 AL031228 Homo sapiens dJ1033B10.2 (WD40 protein 2825 96 BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1) 896 AF171102 Homo sapiens retinal degeneration B beta 1302 95 897 AE003551 Drosophila CG18176 gene product 633 33	893	AF090929	Homo sapiens		653	99
895 AL031228 Homo sapiens dJ1033B10.2 (WD40 protein 2825 96 BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1) 896 AF171102 Homo sapiens retinal degeneration B beta 1302 95 897 AE003551 Drosophila CG18176 gene product 633 33	894	AL031228		dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta	3196	100
897 AE003551 Drosophila CG18176 gene product 633 33	895	AL031228	Homo sapiens	dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YBR082C, M. sexta	2825	96
	896	AF171102	Homo sapiens		1302	95
melanogaster	897	AE003551			633	33

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY \$
NO:	AJ237946	Homo sapiens	DEAD Box Protein 5	2443	100
898		Homo sapiens	HKE2	624	100
399	Z97184		HKE2	409	98
000	Z97184	Homo sapiens	Kruppel-type zinc finger	1942	100
901	AJ245587	Homo sapiens	GTP-binding protein RAB22A	1011	100
902	AF091034	Homo sapiens	GTP-binding protein RABZZA	414	96
903	R95953	Homo sapiens	Eukaryotic cell growth inhibiting factor.		
904	L04733	Homo sapiens	kinesin light chain	1936	72
905	AE003540	Drosophila melanogaster	CG10984 gene product	446	33
906	M55542	Homo sapiens	guanylate binding protein isoform I	2993	98
907	M55542	Homo sapiens	guanylate binding protein isoform I	2901	96
908	W84085	Homo sapiens	Human membrane fusion protein WDProl.	1889	100
909	AF168676	Homo	TNF intracellular domain- interacting protein	647	100
		sapiens	KRAB zinc finger protein	2196	100
910	AB029150	Homo sapiens	HFB101L		
911	G02871	Homo sapiens	Human secreted protein, SEQ ID NO: 6952.	521	100
912	G03162	Homo sapiens	Human secreted protein, SEQ ID NO: 7243.	387	87
913	AJ243721	Homo sapiens] >Y92508 Y92508 13- APR-2000 06- OCT-1998 Human OXRE- 5. [Homo	dTDP-4-keto-6-deoxy-D-glucose 4-reductase	1710	
914	U24189	sapiens Caenorhabdit	hypothetical protein 1207-1;	244	41
711	021103	is elegans	Method: conceptual translation supplied by authors	1	
915	Y02591	Homo sapiens	A human progesterone receptor complex p23-like protein.	843	99
916	AE000984	Archaeoglobu s fulgidus	dinitrogenase reductase activating glycohydrolase	171	26
918	M23159	Cricetus	(draG) DHFR-coamplified protein	163	30
910	M23139	cricetus			
919	L12018	Caenorhabdit is elegans	putative	1232	41
020	AF102177	Homo sapiens	tumor antigen SLP-8p	1260	97
920 921	AF102177 AL096712	Homo sapiens	dJ744124.2 (similar to a novel human gene mapping to Activator)	1017	78
922	AL161495	Arabidopsis thaliana	putative WD-repeat protein	866	42
923	AL161495	Arabidopsis thaliana	putative WD-repeat protein	442	36
924	U97001	Caenorhabdit	similar to Schizosaccharomyces pombe	605	51
		is elegans		1503	95
925 926	X71978 M92288	Mus musculus Drosophila	beta-spectrin	290	51
927	Y27575	melanogaster Homo sapiens	Human secreted protein	1392	100
			encoded by gene No. 9.	2249	100
928	Y22499	Homo sapiens	sequence clone mh703_1.	912	100
930	AJ224326	Homo sapiens	epimerase	660	55
		Caenorhabdit			

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	क्ष
ID	NUMBER		j .	WATERMAN	IDENTITY
NO:	1			SCORE	1
		is elegans	cm21c7		†
932	AL080065	Homo sapiens	hypothetical protein	210	25
933	G01884	Homo sapiens	Human secreted protein, SEQ	767	98
			ID NO: 5965.		
934	AJ276485	Homo sapiens	integral membrane transporter	1200	100
			protein	<u> </u>	1.
935	AL035681	Homo sapiens		1142	80
			similar to drosophila		Ì
			transcriptional repressor)		
936	AB026808	Mus musculus	synaptotagmin XI	2142	95
937	AB015345	Homo sapiens	HRIHFB2216	2601	99
938	X65724	Homo sapiens	ORF2	498	100
939	W89024	Homo sapiens	Polypeptide fragment encoded	1487	100
			by gene 156.	1	İ
940	G04047	Homo sapiens	Human secreted protein, SEQ	117	100
			ID NO: 8128.		<u> </u>
941	AF094583	Homo sapiens	putative HIV-1 infection	452	100
043	70004000	-	related protein		L
942	AC024200	Caenorhabdit	contains similarity to	350	69
		is elegans	several zinc finger proteins		
		ł	but not to the zinc finger domains	ŀ	
943	AF129756	Vone need need	GSC		
944	M23765	Homo sapiens	1	273	100
J44	1723/65	Rattus norvegicus	alpha-tropomyosin	133	96
945	AC009917	Arabidopsis	G		
945	AC009917	thaliana	Contains similarity to	583	47
946	AF223468		2001		<u> </u>
947	AF055473	Homo sapiens	AD021 protein	551	44
948	X75756	Homo sapiens	GAGE-8	273	51
948		Homo sapiens Mus musculus	protein kinase C mu	2019	68
950	AF143956		coronin-2	2300	93
950	Y36729	Homo	Human PG1 protein sequence.	1861	99
951	W49041	sapiens			
331	M43041	Homo sapiens	Human low density lipoprotein	282	67
952	AB016881	Arabidopsis	binding protein LBP-2. gene_id:MXC17.7~	202	<u> </u>
	ABUTUUUT	thaliana	gene_id:MACI/./~	203	46
953	Y01785	Homo sapiens	Human ubiquitin-conjugating	365	100
	1 :-	110 NO Bapiens	enzyme >Y25341 Y25341 01-JUL-	303	100
			1999 12-AUG-1998 Human NCE-2	ł	
i	'		protein.		
954	AF145615	Drosophila	BcDNA.GH03377	823	46
		melanogaster	303111. G1103377	023	30
955	U09410	Homo sapiens	zinc finger protein ZNF131	2483	99
956	U09410	Homo sapiens	zinc finger protein ZNF131	1853	99
957	AF195623	Homo sapiens	cholinephosphotransferase 1	2126	99
_		Japacina	alpha		,,,
958	X94917	Drosophila	head-elevated expression in	155	32
- 1	· ·	melanogaster	0.9 kb	122	3.5
959	U54807	Rattus	GTP-binding protein	1167	97
		norvegicus			1 - '
960	AF058807	Bos taurus	GTP-binding protein rah	606	97
961	G03244	Homo sapiens	Human secreted protein, SEQ	471	100
			ID NO: 7325.		
	AF078850	Homo sapiens	steroid dehydrogenase homolog	583	40
962			transient receptor potential-	317	30
	AP001754	HOMO Bablene		1	30
		Homo sapiens		ĺ i	
962 963		Homo sapiens	related channel 7, a novel		
			related channel 7, a novel putative Ca2+ channel protein	1129	100
963	AP001754	Homo sapiens	related channel 7, a novel putative Ca2+ channel protein dJ1100H13.1 (putative novel	1129	100
963	AP001754	Homo sapiens	related channel 7, a novel putative Ca2+ channel protein dJ1100H13.1 (putative novel protein)		
963	AP001754 AL035419	Homo sapiens	related channel 7, a novel putative Ca2+ channel protein dJ1100H13.1 (putative novel	1129	100
963 964 965	AP001754 AL035419	Homo sapiens Rattus rattus	related channel 7, a novel putative Ca2+ channel protein dJ1100H13.1 (putative novel protein) interferon-induced protein	202	46
963 964 965	AL035419 X61381	Homo sapiens Rattus rattus Homo	related channel 7, a novel putative Ca2+ channel protein dJ1100H13.1 (putative novel protein) interferon-induced protein inositol 1,4,5-trisphosphate		
963	AL035419 X61381	Homo sapiens Rattus rattus	related channel 7, a novel putative Ca2+ channel protein dJ1100H13.1 (putative novel protein) interferon-induced protein	202	46

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
ID	NUMBER	1		· SCORE	
NO:				611	100
68	บ79275	Homo sapiens	unknown	2752	99
69	AJ011306	Homo	guanine nucleotide exchange	2752	} 33
		sapiens	factor (long isoform)		100
70	AF281134	Homo sapiens	exosome component Rrp46	1186	
771	U53336	Caenorhabdit	weak similarity over a short	536	23
		is elegans	region to myosin heavy chain		
972	AC018749	Leishmania	L8840.12	589	53
712	ACOLOTA	major			<u> </u>
	AF188504	Mus musculus	LNV	544	85
973		Homo sapiens	Taxl binding protein	852	98
74	U25801		huntingtin-interacting	1390	97
975	AF049523	Homo sapiens	protein HYPA/FBP11	}	1
			HSPC182	1040	100
976	AF161530	Homo sapiens	Human secreted protein, SEQ	626	100
977	G04020	Homo sapiens		020	
			ID NO: 8101.	908	100
978	AF164797	Homo sapiens	ribosomal protein L17 isolog	795	97
979	U94991	Xenopus	transcription factor XLMO1	/ 75	1 "
-	1 '	laevis			1200
980	S73775	Homo sapiens	calmitine; calsequestrine	2029	100
981	Y94888	Homo	Human protein clone HP01462.	2501	100
30 L	154000	sapiens		1	<u></u>
000	AJ243191	Homo sapiens	heat shock protein	827	96
982		Bos taurus	PSST subunit of the NADH:	964	85
983	X65020	DOS LAUTUS	ubiquinone oxidoreductase	1	1
	1	[complex		1
			putative racemase	351	43
984	AJ249207	Rhodococcus	pucative racemase	1	1
		sp. AD45	to the factor 2	1576	99
985	Z30093	Homo sapiens	basic transcription factor 2,	12370	1
			35 kD subunit	4697	99
986	AB030835	Homo sapiens	contains two glutamine rich	4697	1 23
	}	,	domains, three zinc-finger		1
		1	domains, and matrin 3		l l
			homologous domain 3 (MH3)	1	
987	AF227258	Bos taurus	RPGR-interacting protein-1	1262	38
	AL022238	Homo sapiens	dJ1042K10.2 (supported by	4048	99
988	AL022236	NOMO SEPTEMS	GENSCAN, FGENES and GENEWISE)		- (
		Homo sapiens	dJ1042K10.2 (supported by	2321	99
989	AL022238	Homo saptens	GENSCAN, FGENES and GENEWISE)		1
			HSPC308	448	92
990	AF161426	Homo sapiens		448	92
991	AF161426	Homo sapiens	HSPC308	453	92
992	AF161426	Homo sapiens	HSPC308	172	42
993	AL023859	Schizosaccha	trna-splicing endonuclease	1/2	12
		romyces	subunit		i
		pombe			
994	AL049631	Homo sapiens	dJ513M9.1 (novel Homeobox	241	47
7,3		1	domain protein)		
995	AC005253	Homo sapiens		902	100
	AF265206	Homo sapiens		974	100
996		Pyrococcus	sarcosine oxidase, subunit	195	28
997	AJ248285		beta (soxB)	1	
		abyssi	BG:DS00941.3 gene product	218	58
998	AE003641	Drosophila		1	1
		melanogaster	Secreted protein of clone	1340	98
999	W69343	Homo	<u> </u>		1
1		sapiens	CR930_1.	1543	100
1000	AY007135	Homo sapiens	similar to bovine ADP/ATP	1243	1 100
		İ	translocase T1 mRNA with	1	l l
1		1	GenBank Accession Number	1	
		1	M24102.1		
1001	Y73381	Homo sapiens	HTRM clone 1877278 protein	1668	100
1 1001	1,3301		sequence.		
L	10000044	Homo sapiens		428	100
1002	AF208844		hypothetical protein	134	35
1003	AE004944	Pseudomonas	HAbornectest brocern		1
1		aerugiņosa		2058	100
1004	AL031431	Homo sapiens	dJ462023.2 (novel protein)	1949	100
1004			l	レフサブ	,
1004	S45367	Canis familiaris	centractin	1 -7 -7	1

SEO	ACCESSION	SPECIES	DESCRIPTION	SMITH-	9-
ID	NUMBER	SPECIES	DESCRIPTION	WATERMAN	IDENTITY
NO:	NOMBER			SCORE	IDENTITY
1006	S45367	Canis	centractin	1315	98
1000	343307	familiaris	Centractin	1313	30
1007	AB022158	Mus	chaperonin containing TCP-1	2649	96
		musculus	epsilon subunit		
1008	Y76332	Homo sapiens	Fragment of human secreted	1282	97
1		1	protein encoded by gene 38.	1	,
1009	AB011414	Homo sapiens	Kruppel-type zinc finger	1671	58
	<u> </u>		protein	1	
1010	Z68218	Caenorhabdit	K01H12.1	269	67
		is elegans			
1011	AB011414	Homo sapiens	Kruppel-type zinc finger	1671	58
			protein	L	
1012	Z14000 G02841	Homo sapiens	RING1	2017	100
1013	G02841	Homo sapiens	Human secreted protein, SEQ	332	93
1014	AF145659	Drosophila	ID NO: 6922. BcDNA.GH10333	1244	52
1014	Ar 145659	melanogaster	BCDNA.GHIU333	1244	52
1015	Y02860	Homo sapiens	Fragment of human secreted	664	67
1013	102880	HOMO Sapiens	protein encoded by gene 65.	004	67
1016	Y02591	Homo sapiens	A human progesterone receptor	772	97
		noo bapaono	complex p23-like protein.	' ' -	-
1017	Y99448	Homo sapiens	Human PRO1759 (UNQ832) amino	2323	100
			acid sequence SEQ ID NO:374.		
1018	X67250	Rattus	n-chimaerin	1710	97
		norvegicus			
1019	AF183417	Homo	microtubule-associated	631	100
		sapiens	proteins 1A/1B light chain 3		
1020	AF164795	Homo sapiens	sex-regulated protein janus-a	674	100
1021	AF190625	Coturnix	qdgl-1	638	96
		coturnix		L	
1022	AL133363	Arabidopsis	putative protein	155	37
<u> </u>		thaliana			
1023	AB034912	Homo sapiens	WD-repeat like sequence	2483	100
1024	AY007091	Homo sapiens	similar to Homo sapiens mammalian inositol	2243	100
			hexakisphosphate kinase 2		
ļ			(IP6K2) mRNA with Ge	}	
1025	X69910	Homo sapiens	P63 protein	2958	99
1026	U80736	Homo sapiens	CAGF9	1657	100
1027	AB029333	Halocynthia	HrPET-1	1048	54
		roretzi			1
1028	AB032931	Homo sapiens	ubiquitin-conjugating enzyme	1,045	100
		_	isolog		
1029	G01797	Homo sapiens	Human secreted protein, SEQ	749	98
			ID NO: 5878.		
1030	G01797	Homo sapiens	Human secreted protein, SEQ	749	98 .
			ID NO: 5878.		
1031	AF193795	Homo sapiens	vacuolar sorting protein	960	100
1020	7700000	W	VPS29/PEP11	L	<u> </u>
1032 1033	AJ222968	Mus musculus	L-periaxin	120	30
1033	281317	Schizosaccha romyces	DNA2-NAM7 helicase family	685	31
		romyces	protein		
1034	Y41519	Homo sapiens	Fragment of human secreted	1321	99
		Tomo Baptens	protein encoded by gene 75.	****]
1035	AJ276004	Mus musculus	Paxneb protein	1709	77
1036	AF025459	Caenorhabdit	H14A12.3 gene product	190	30
		is elegans			-
1037	U37251	Homo sapiens	Description: KRAB zinc finger	196	43
			protein; this is a splicing		
			supplied by author		
103B	W74580	Homo	Human membrane protein	1921	97
		sapiens	BA0306.	ĺ	
1039	U88173	Caenorhabdit	weak similarity to	331	80
1039	[
1033		is elegans	Arabidopsis thaliana ubiquitin-like protein 8		

TABLE 2

Note Note	SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
196730 1	NO: L040	AF290204	Homo sapiens	- -		99
AP140683	.041	¥96730	120	PRO539, a Costal-2 homologue.	162	
103 AF151023 Some sapiens BSFC189 1104 100	042	AF140683		F-box protein FWD2	2397	1
					1104	100
1045 107985	044		Drosophila		204	
No. No.	1045	¥77985		sequence.		
1047 AB035863 Homo sapiens AFF specific succinyl CoA 2324 99 8 8 8 8 8 8 8 8	1046	AJ243972	Homo sapiens	6-phosphogluconolactonase		
ALO34550 Homo sapiens Similar to nucleolar protein A (NOLA) (NOLD)	1047	AB035863		synthetase beta subunit precursor		
1050 AF201949 Homo sapiens 668 100 1051 AF190624 Mus musculus mdgl-1 236 85 1052 AF003529 Drosophila melanogaster 160 160 44 160	1048	AL034550		similar to nucleolar protein 4 (NOL4) (NOLP))		
1050 AF201949 Homo sapiens Solog Sol	1049	AF163825		pre-B lymphocyte protein 3		
1051	1050	AF201949		isolog		
Drosophila Drosophila Drosophila Drosophila Drosophila Homo sapiens Drosophila Homo sapiens Drosophila	1051	AF190624			1	
ID NO: \$272.	1052	AE003529	melanogaster			
Nelseria Nelseria	1053	G01191		ID NO: 5272.		
1055	1054		meningitidis	amidotransferase subunit A		
S	1055		norvegicus	associated protein		
1057	1056 5	U89649	s	light chain		
1058	1057	AF159141	Homo sapiens	suppressor 1		
1060	1058	AF230929	1	protein pemphaxin		
1050 AF224263 Heterodontus francisci fragment	1059	AJ270952				1
1061 X63417 Homo sapiens Name	1060	AF224263				
1062 AL079345 Streptomyces coelicolor	1061	X63417	Homo sapiens			
1064	1062	AL079345	coelicolor	hypothetical protein		
1064	1063	Y71112	_	(HYDRL-10).		1
1065 Y13356	1064	AF263614				
1066 AC006153 Homo sapiens GTP-binding protein; similar to AE000771 (PID:g2984292) 1067 Y18930 Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus sapiens Sulfolobus solfataricus Sulfolobus solfataricus Sulfolobus sapiens Sulfolobus solfataricus Sulfolobus sapiens Sulfolobus solfataricus Sulfolobus sapiens Sulfolobus solfataricus Sulfolobus sapiens Sul		Y13356		Amino acid sequence of protein PRO221.		
1067 Y18930 Sulfolobus Sulfolobus Solfataricus Solfata	1066	AC006153	Homo sapiens	GTP-binding protein; similar to AE000771 (PID:g2984292)		
1068 R65969 Homo sapiens Hom	1067	Y18930				
1070 AF177476 Rattus fragment 1995 86 1071 AF245505 Homo sapiens adlican 3109 99 1072 U92794 Mus musculus alpha glucosidase II, beta 147 36 1073 G03889 Homo sapiens Human secreted protein, SEQ 698 98 1074 U15779 Homo sapiens p70 380 28	1068	R65969	sapiens T98G	polypeptide.		
1070 AF177476 Rattus norvegicus protein 1071 AF245505 Homo sapiens adlican 3109 99 1072 U92794 Mus musculus alpha glucosidase II, beta 147 36 1073 G03889 Homo sapiens Human secreted protein, SEQ 698 98 1074 U15779 Homo sapiens p70 380 28	1069	Y07964	Homo sapiens	fragment		
1071 AF245505 Homo sapiens addition 1072 U92794 Mus musculus alpha glucosidase II, beta 147 36 subunit 1073 G03889 Homo sapiens Human secreted protein, SEQ 698 98 ID NO: 7970. 1074 U15779 Homo sapiens p70 380 28	1070		norvegicus	protein		
1072 U92794 Mus musculus alpha glucosidase 17, 2004 subunit 1073 G03889 Homo sapiens Human secreted protein, SEQ 698 98 ID NO: 7970. 380 28	1071	l — — —		adlican		
1073 G03889 Homo sapiens Human secreted protein, 512 10 No: 7970. 1074 U15779 Homo sapiens p70 380 28	1072	U92794		subunit		
1074 U15779 Homo sapiens pro	1073			ID NO: 7970.		
	1074	U15779	_			

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	<u> </u>
ID	NUMBER			WATERMAN	IDENTITY
NO:	ł	1		SCORE	
			protein PRO328.		
1076	AF161457	Homo sapiens	HSPC339	571	100
1077	Y79509	Homo sapiens	Human carbohydrate-associated	2151	98
		l	protein CRBAP-5.		
1078	AF223466	Homo sapiens	HT015 protein	831	66
1079	AL132965	Arabidopsis	putative WD-40 repeat-protein	286	29
		thaliana			<u> </u>
1080	AB024937	Homo sapiens	LUNX	1284	100
1081	Y14768	Homo sapiens	V-ATPase G-subunit like	579	100
1082	AF016416	Caenorhabdit	protein F29A7.4 gene product		
1002	VL 010410	is elegans	F29A7.4 gene product	141	31
1083	L13291	Homo sapiens	ADP-ribosylarginine hydrolase	802	45
1084	AB041541	Mus musculus	unnamed protein product	151	44
1085	G01922	Homo sapiens	Human secreted protein, SEQ	202	97
1			ID NO: 6003.	202	1 3 '
1086	AB030814	Homo sapiens	H-REV107 protein homolog	833	100
1087	AF151638	Homo sapiens	phosphatidylcholine transfer	1142	100
}	i		protein		
1088	Y84432	Homo sapiens	Amino acid sequence of a	2783	100
1		·	human RNA-associated		J
			protein.	İ	
1089	Y94867	Homo	Human protein clone HP10563.	613	100
	<u> </u>	sapiens		L	
1090	AK023982	Homo sapiens	unnamed protein product	130	49
1091	AB041586	Mus musculus	unnamed protein product	1103	81
1092	Y71277	Homo sapiens	Human Zlipo3 protein.	606	100 🔥
1093	U34973	Mus musculus	protein tyrosine phosphatase-	1131	95
1094	Y66677	Homo	† ======	622	<u> </u>
1074	1000//	sapiens	Membrane-bound protein PRO828.	522 .	56
1095	Y87276	Homo sapiens	Human signal peptide	1029	99
		110mo Bapiens	containing protein HSPP-53	1029	33
			SEQ ID NO:53.		}
1096	Y87276	Homo sapiens	Human signal peptide	863	98
ļ		-	containing protein HSPP-53		
1	ļ		SEQ ID NO:53.		
1097	AF161455	Homo sapiens	HSPC337	742	98
1098	U80029	Caenorhabdit	similar to thioredoxin	242	39
		is elegans			
1099	AJ005866	Homo sapiens	Sqv-7-like protein	1321	99
1100	AJ005866	Homo sapiens	Sqv-7-like protein	1118	99
1101	AJ005866	Homo sapiens	Sqv-7-like protein	891	99
1102	AJ005866	Homo sapiens	Sqv-7-like protein	1016	99
1103 1104	AL110244	Homo sapiens	hypothetical protein	299	31
TT0#	AF242194	Drosophila melanogaster	brakeless-B	147	52
1105	AL031010	Homo sapiens	dJ422F24.1 (PUTATIVE novel	968	100
	122031010	nomo saprens	protein similar to C. elegans	965	100
	:		C02C2.5)		
1106	U28016	Mus musculus	parathion hydrolase	1624	87
			(phosphotriesterase) -related	2021	
			protein		
1107	AJ278150	Homo sapiens	putative lipid kinase	2207	99
1108	G03733	Homo sapiens	Human secreted protein, SEQ	495	98
		_	ID NO: 7814.		1
1109	AF217287	Drosophila	G protein RhoBTB	834	54
		melanogaster			
1110	Y28921	Homo	Human regulatory protein	941	48
		sapiens	HRGP-7.		
1111	Y28921	Homo	Human regulatory protein	1331	51
	N 0 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	sapiens	HRGP-7.		
1112	AF176704	Homo sapiens	F-box protein FBX9	2027	99
1113	AF182076	Homo	glioma tumor suppressor	2418	100
1114	G04039	sapiens Homo sapiens	candidate region protein 2 Human secreted protein, SEQ	- 	
	30-033	sabiens	man secreted protein, SEO	475	96

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY *
NO:	NO. IDER			SCORE	<u> </u>
			ID NO: 8120.		
115	AF229439	Mus musculus	zinc finger protein 289	1697	91
116	L40357	Homo sapiens	thyroid receptor interactor	509	100
117	L40357	Homo sapiens	thyroid receptor interactor	404	85
118	A12155	Homo sapiens	Human X5L cDNA.	1673	100
119	AL161542	Arabidopsis thaliana	isomerase like protein	607	53
120	AL023754	Homo sapiens	dJ272L16.1 (Rat Ca2+/Calmodulin dependent Protein Kinase LIKE protein)	2341	98
.121	Y57901	Homo sapiens	Human transmembrane protein HTMPN-25.	321	36
1122	Z14122	Xenopus laevis	XLCL2	455	77
123	AF225418	Homo sapiens	lipase	1531	97
124	Y06518	Homo sapiens	Zen GTPase interacting protein ZIP.	3227	100
	77.005.600	Homo sapiens	dJ202I21.1 (novel protein)	952	100
1125	AL035690	Homo sapiens	CLIC2	1286	99
126	AJ000217		UBE-1c2	1069	79
1127	AB030505 Y73375	Mus musculus Homo sapiens	HTRM clone 1427838 protein	874	100
1129	¥78941	Homo sapiens	sequence. Cyclophilin-type peptidyl prolyl cis/trans isomerase amino acid sequence.	877	100
1130	AL023553	Homo sapiens	dJ347H13.4 (novel protein)	557	100
1131	Y91945	Homo sapiens	Human chaperone protein 6 (HCHP-6).	1408	100
1132	Z68197	Schizosaccha romyces	putative nuclear pore protein	596	39
1133	Z68197	pombe Schizosaccha romyces pombe	putative nuclear pore protein	389	35
1134	AF180681	Homo sapiens	guanine nucleotide exchange	3597	100
1135	AF079765	Mus musculus	enhancer of polycomb	264	41
1136	M62419	Mus musculus	clathrin-associated protein	2189	99
1137	AJ006219	Drosophila melanogaster	clathrin-associated protein	1254	78
1138	Y76218	Homo sapiens	Human secreted protein encoded by gene 95.	440	98
1139	W88104	Homo sapiens	A Rab protein designated HRABS-2.	1065	99
1140	Y13401	Homo sapiens	Amino acid sequence of protein PRO339.	3979	98
1141	W85026	Chimeric - Homo sapiens	Green fluorescent protein-	3309	100
1142	Y13402	Homo sapiens		1694	99
1143	G03875	Homo sapiens	<u> </u>	660	99
1144	¥12917	Homo sapiens		750	98
1145	Y12917	Homo sapiens	Amino acid sequence of a	1096	100
1146	AL022157	Homo sapiens		1233	100
1147	AL022157	Homo sapiens		1233	100
1148	G02548	Homo sapiens	(PROTEIN DXF34)) Human secreted protein, SEQ	370	98
1149	Y73338	Homo sapiens		1492	100
	W74841	Homo sapiens	sequence. Human secreted protein	228	55

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	ફ
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	
			HEAAR60.		
1151	AF044201	Rattus	neural membrane protein 35;	1570	92
1152	AF156774	norvegicus Homo	NMP35 lysophosphatidic acid	3055	99
1152	AF156//4	sapiens	acyltransferase-gammal	1855	99
1153	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	872	64
1133	ABLIOSOL	nomo sapiens	(translation of the cDNA	0/2	64
		ļ	DKFZp566A0946, Em:AL050069))	1	
1154	AF131852	Homo sapiens	Unknown	473	100
1155	Y41705	Homo	Human PRO352 protein	1381	97
		sapiens	sequence.		1 - '
1156	G04036	Homo sapiens	Human secreted protein, SEQ	607	99
		_	ID NO: 8117.		
1157	AF112444	Lupinus	L-asparaginase	287	43
	<u></u>	luteus			
1158	AF151848	Homo sapiens	CGI-90 protein	232	32
1159	AJ272267	Homo sapiens	choline dehydrogenase	2449	100
1160	AB001773	Ciona	PEM-6	196	33
3363	Vogana	savignyi		1245	1
1161	¥87330	Homo sapiens	Human signal peptide	746	83
			containing protein HSPP-107 SEQ ID NO:107.	1	
1162	Y87330	Homo sapiens	SEQ ID NO:107. Human signal peptide	746	83
	107330	TOWN Babiens	containing protein HSPP-107	/30	1 03
		•	SEQ ID NO:107.		
1163	AF113534	Homo sapiens	HP1-BP74 protein	2723	96
1164	AF232226	Danio rerio	Dedd1	191	41
1165	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	1051	71
		•	(translation of the cDNA		
			DKFZp566A0946, Em:AL050069))		
1166	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	945	76
		:	(translation of the cDNA		
			DKFZp566A0946, Em:AL050069))		
1167	AF187733	Homo sapiens	syntaphilin	831	42
1168	AB019435	Homo sapiens	phospholipase	951	55
1169	AF064604	Homo sapiens	KE03 protein	324	33
1170	Y01164	Homo sapiens	Polypeptide fragment encoded	1191	100
1171	L03188	Saccharomyce	by gene 6. putative	180	22
11/1	103100	s cerevisiae	pucacive	180	
1172	AF113751	Mus musculus	nuclear pore membrane	3941	81
			glycoprotein POM210	3332	
1173	AJ245417	Homo sapiens		794	100
1174	AL022238	Homo sapiens	dJ1042K10.3 (novel protein)	1285	100
1175	U41278	Caenorhabdit	F33G12.3 gene product	332	28
•		is elegans	[1	
1176	M35617	Homo sapiens	T-cell receptor V-alpha-J-	284	83
			alpha region		
1177	AC012680	Arabidopsis	putative protein phosphatase	209	37
		thaliana	2C; 55455-56414		
1178	G01345	Homo sapiens	Human secreted protein, SEQ	692	99
	110000		ID NO: 5426.		
1179	AL096767	Homo sapiens	dJ579N16.3 (novel protein	1342	100
			similar to worm, Arabidopsis		
1180	AF039716	Caenorhabdit	and pine proteins)	106	
7700	AE035/16	is elegans	similar to ATP synthase B chain	496	55
1181	Y11710	Homo sapiens	collagen type XIV	1048	97
1182	X82240	Homo sapiens	T cell leukemia/lymphoma 1	617	100
	1.022.30	sapiens]	T CETT TEMVENITA\TAMBHOMY I	31,	100
		>R94974			•
]	R94974 09-			
		MAY-1996 27-			-
		OCT-1994			
		Human TCL-1		1	
	1	polypeptide.		1	

173

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		[Homo sapiens			
183	U42841	Caenorhabdit is elegans	short region of weak similarity to collagen	161	33
185	AJ131613	Homo sapiens	dicarboxylate carrier protein	1470	99
186	L27645	Danio rerio	growth-associated protein	130	36
187	Y02738	Homo sapiens	Human secreted protein	636	100
107	102730	2.0	encoded by gene 89 clone		
188	AF217544	Xenopus laevis	ornithine decarboxylase-2	1459	60
189	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)	182 .	33 .
700	X89602	Homo sapiens	rTSbeta	197	100
190	U32828	Haemophilus influenzae Rd	ribosomal protein S6 modification protein (rimK)	268	31
192	AF154831	Rattus norvegicus	PV-1	1403	60
1193	¥50926	Homo sapiens	Human fetal brain cDNA clone vc16_1 derived protein.	918	100
1194	AF026530	Rattus norvegicus	stathmin-like-protein splice variant RB3''	1093	97
1195	U35244	Rattus norvegicus	vacuolar protein sorting homolog r-vps33a	2981	96
1196	¥70470	Homo sapiens	Human p53 target molecule, PRG3 protein.	1680	100
1197	AF157318	Homo sapiens	AD-017 protein	912	47
1198	AF125443	Caenorhabdit is elegans	contains similarity to S. pombe phosphatidyl synthase (GB: Z28295)	460	39
1199	AF201934	Homo sapiens	DC12	1649	88
1200	AL031775	Homo sapiens	dJ30M3.3 (novel protein similar to C. elegans Y63D3A.4)	1902	100
1201	M21103	Ovis aries	BIIIB4 high-sulfur keratin	484	82
1202	Z85986	Homo sapiens	dJ108K11.3 (similar to yeast suppressor protein SRP40)	1143	75
1203	U18762	Rattus	retinol dehydrogenase type I	890	52
1204	U35730	Mus musculus	jerky	2235	76
1205	AB002327	Homo sapiens	KIAA0329	151	24
1206	AB019233	Arabidopsis thaliana	ubiquinone/menaquinone biosynthesis methyltransferase-like	762	56
1207	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)	742	100
1208	AF207989	Homo sapiens	orphan G-protein coupled receptor	2326	100
1209	297630	Homo sapiens		181	44
4040	U21549	Mus musculus		1280	68
1210 1211	Y27700	Homo sapiens		1267	100
1010	AF117814	Mus musculus		945	66
1212	AF117814 AF277233	Naegleria fowleri	calcineurin B	222	39
1214	D14849	Mus musculus	structural protein 1	1950	77
1215	G03022	Homo sapiens	Human secreted protein, SEQ ID NO: 7103.	590	100
l	272510	Caenorhabdit		634	49

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	- a -
ID NO:	NUMBER	SPECIES	DESCRIPTION	WATERMAN SCORE	IDENTITY
		is elegans	protein (Swiss Prot accession yk677hll.5 comes from this		
			gene		
1217	Z49703	Saccharomyce s cerevisiae	unknown	134	22
1218	AC013430	Arabidopsis thaliana	F3F9.18	199	29
1219	L10910	Homo sapiens	splicing factor	1026	71
1220	Z70750	Caenorhabdit	similar to vanadate	965	58
		is elegans	resistance protein transmembranous comes from this gene		
1221	AL163815	Arabidopsis thaliana	putative protein	653	61
1222	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
1223	J05071	Bos taurus	GTP-binding regulatory protein gamma-6 subunit	356	100
1224	¥73364	Homo sapiens	HTRM clone 2765991 protein sequence.	1169	99
1225	AL050170	Homo sapiens	hypothetical protein	714	100
1226	X64002	Homo sapiens	RAP74	2661	99
1227	X04085	Homo sapiens	catalase	2846	100
1228	AJ005620	Mus musculus	skeletal muscle-specific gene	1416	90
1229	AF045564	Rattus norvegicus	development-related protein	1715	93
1230	X97571	Mus musculus	HCMV-interacting protein	479	96
1231	L08239	Homo sapiens	located at OATL1	2274	100
1232	AF121863	Homo sapiens	sorting nexin 14	1964	100
1233	AF121863	Homo sapiens	sorting nexin 14	1203	84
1234	AC024805	Caenorhabdit is elegans	contains similarity to TR:004595	744	31
1235	AC006634	Caenorhabdit is elegans	contains similarity to Saccharomyces cerevisiae probable membrane protein YLR418c (GB:U20162)	357	33
1236	Y18101	Mus musculus	macrophage actin-associated- tyrosine-phosphorylated protein	1559	87
1237	AB042646	Homo sapiens	TGIF2	1224	100
1238	AB026264	Homo sapiens	IMPACT	1694	100
1239	AB026264	Homo sapiens	IMPACT	1123	100
1240	G00429	Homo sapiens	Human secreted protein, SEQ ID NO: 4510.	324	100
1241	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	1363	53
1242	AL035602	Arabidopsis thaliana	putative protein	499	28
1243	X76483	Gallus gallus	Yes-associated protein (65kDa)	574	48
1244	AF220186	Homo sapiens	uncharacterized hypothalamus protein HT012	503	100
1245	AL021453	Homo sapiens	dJ821D11.3 (PUTATIVE protein)	856	100
1246	AJ276003	Homo sapiens	GAR1 protein	1216	100
1247	Y57910	Homo sapiens	Human transmembrane protein HTMPN-34.	1369	98
1248	AC004874	Homo sapiens	similar to N- acetylgalactosaminyltransfera se; similar to Q07537 (PID:g1171989)	957	100
1249	AF199597	Homo sapiens	A-type potassium channel modulatory protein 1	1139	100
1250	Y13148	Rattus norvegicus	PAG608	1350	88
1251	M24852	Rattus	neuron-specific protein PEP-	124	46

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY %
NO: 1252	AF146738	Rattus norvegicus	testis specific protein	771	83
1253	G02725	Homo sapiens	Human secreted protein, SEQ ID NO: 6806.	419	97
1254	W44375	Homo sapiens	Human ubiquitin-conjugating enzyme polypeptide.	1045	99
1255	AC006538	Homo sapiens	BC41195 1	831	78
1256	AB004316	Bos taurus	mitochondrial methionyl-tRNA transformylase	1556	88
1257	235094	Homo sapiens	SURF-2	1354	97
1258	Y13362	Homo sapiens	Amino acid sequence of	2383	100
1259	AC006014	Homo sapiens	protein PRO214. similar to RFP transforming	1299	100
1239	Acousti	none supreme	protein; similar to P14373 (PID:g132517)		
1260	AC005099	Homo sapiens	match to AI222572 (NID:g3804775)	469	100
1261	V00507	Homo sapiens	coding sequence of DHFR (1 is 1st base in codon) (561 is 3rd base in codon)	984	100
1262	X15443	Rattus sp.	gamma-glutamyltranspeptidase (AA 1-568)	697	32
1263	AF173871	Mus musculus	neuronal PAS3	977	94
1264	AF178983	Homo sapiens	Ras-associated protein Rap1	433	97
1265	Y70473	Homo sapiens	Human cyclic nucleotide- associated protein-1 (CNAP- 1).	2785	99
1266	Y41738	Homo sapiens	Human PRO541 protein sequence.	1622	100
1267	AF061346	Mus musculus	Edpl protein	1077	64
1268	U97006	Caenorhabdit is elegans	C13F10.4 gene product	154	23
1269	AF233582	Mus musculus	GTPase Rab37	942	95
1270	AF195951	Homo sapiens	signal recognition particle 68	3127	98
1271	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	1150	55
1272	AF201933	Homo sapiens	DC11	650	100
1273	AF201933	Homo sapiens	DC11	346	98
1274	AL021710	Arabidopsis thaliana	putative protein	348	49
1275	AC004449	Homo sapiens	R33683_3	556	100
1276	Y86295	Homo sapiens	Human secreted protein HL2AG87, SEQ ID NO:210.	1920	100
1277	Y71111	Homo sapiens	Human Hydrolase protein-9 (HYDRL-9).	1576	99
1278	S94421	Homo sapiens	T cell receptor eta-exon	478	100
1279	Y66695	Homo sapiens	Membrane-bound protein PRO1344.	1909	
1280	AF161380	Homo sapiens		772 779	100
1281	Y48610	Homo sapiens	associated protein 71.		
1282	AC015446	Arabidopsis thaliana	Similar to AIG1 protein	406	35
1283	AK024432	Homo sapiens		403	35
1284	W96153	Homo sapiens	protein (FIP).	1825	81
1285	AJ001019	Homo sapiens		1301	100
1286	AE003823	Drosophila melanogaster	CG13178 gene product	195	29
1287	AF178632	Homo sapiens	FEM-1-like death receptor binding protein	3261	100
1288	AC006033	Homo sapiens	similar to MLN 64; similar to I38027 (PID:g2135214)	_	100
1289	AC006033	Homo sapiens	similar to MLN 64; similar to I38027 (PID:g2135214)		93
	AB023811	Homo sapiens	TU3A	351	54

1 1	SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	T
No.			SPECIES	DESCRIPTION		IDENTITY
1291 273424 Caenorhabdit Selegans Human protein clone HP02551. 1222 100 sapiens Sapiens Human protein clone HP02551. 1222 100 Sapiens Human protein clone HP02551. 1222 100 Sapiens Human secreted protein, SEQ 110 1295 AF180425 Homo sapiens Fetinoblastoma-associated 489 29 protein RAP140 1294 G03856 Homo sapiens Human secreted protein, SEQ 538 799 1295 AF133670 Mus musculus ARL-6 interacting protein-2 367 51 1296 A734735 Homo sapiens ARL-6 interacting protein-2 367 51 1297 X57560 Caenorhabdit Goded for by C. elegans cDNA 200 2		1.0.1221				IDENTITI
1998 1948/1 Home Human protein clone HP02551. 1222 100		7.73424	Caenorhabdit	C44P9 1		36
1293 Y94871 Homo		-/		C44B3.1	233	36
Sapiens Homo sapiens Petinoblastoma-associated Protein RAP140 Protein RAP150 Protein RAP150 Protein RAP150 Protein RAP150 Protein RAP150 Protein RAP150 Protein RAP150 Protein RAP150 Protein RAP150 Protein RAP150 Protein RAP150 Protein RAP150 Protein RAP150 Protein RAP150 Protein RAP150 Protein RAP150 Pr	1292	Y94871		Human protein clone HP02551	1222	100
1293 AF180425 Homo sapiens retinoblastoma-associated protein RAP140		1		naman process orang measure.	1222	100
	1293	AF180425		retinoblastoma-associated	489	29
1294 G03856		1		1	1 .00	23
ID NO. 7937.	1294	G03856	Homo sapiens		538	99
1295						
1295	1295	AF133670	Mus musculus		367	51
1297 X57550 Sacherichia coli 1298 AP169284 Homo sapiens LIM and cysteine-rich domains 1997 100	1296	AJ249735				L
Coli	1297	X57560				_
1299 U41023 Caenorhabdit coded for by C. elegans cDNA yk61f1.3; coded for by C. yk109h8.5 yk61f1.3; coded for by C. yk109h8.5 yk61f1.3; coded for by C. yk109h8.5 yk			1	Popo promise		200
1299 U41023 Caenorhabdit coded for by C. elegans cDNA yk61f1.3; coded for by C. yk109h8.5 yk61f1.3; coded for by C. yk109h8.5 yk61f1.3; coded for by C. yk109h8.5 yk	1298	AF169284	Homo sapiens	LIM and cysteine-rich domains	1997	100
1309						-00
13 13 15 16 16 18 18 18 18 18 18	1299	U41023	Caenorhabdit		324	29
300						
1300						
1301 X55989	1300	AB024523	Homo sapiens		1206	100
Note	1301				1	
1302						1
1303 X52904 Escherichia Open reading frame (AA 1-65) 359 100	1302	AF007151	Homo sapiens		1481	100
1304	1303	X52904		open reading frame (AA 1-65)	359	100
1305 AF266508 Mus musculus NELF protein 1409 97]		coli	, , , , , , ,	1]
Coli	1304	U19577	Escherichia	galactonate dehydratase	242	93
1306 Y57901 Homo saplens Human transmembrane protein HTMPN-25. 100 HTMPN-25. 1307 U58750 Caenorhabdit is elegans carrier family 365 54 1308 AF044774 Homo saplens breakpoint cluster region 2681 99 protein 2 2 2 2 2 2 2 2 2		1	coli	1		1
1306 Y57901 Homo sapiens Human transmembrane protein HTMPN-25. 1307 U58750 Caenorhabdit is elegans Similar to the mitochondrial 365 54 1308 AF044774 Homo sapiens Dreakpoint cluster region 2681 99 Protein 2 2681 39 2681 310 268293 Homo sapiens dJ210B1.1 (KIAA0680) 267 34 311 262263 Caenorhabdit 15 elegans C47A4.1 283 35 262263 Caenorhabdit 15 elegans C47A4.1 283 35 262263 Caenorhabdit 15 elegans C47A4.1 283 35 262263 Caenorhabdit 15 elegans C47A4.1 283 35 262263 Caenorhabdit C47A4.1 283 35 262263 Caenorhabdit Sapiens	1305	AF266508	Mus musculus	NELF protein	1409	97
HTMPN-25.	1306	Y57901	Homo sapiens		932	100
1308 AF044774 Homo sapiens Dreakpoint cluster region 2681 99 1309 AL078593 Homo sapiens E48 antigen 620 96 1311 282263 Caenorhabdit is elegans C47A4.1 283 35 1312 AF131218 Homo sapiens Chromosome 16 open reading 1493 100 1314 AF196972 Homo sapiens Membrane-bound protein 1228 97 1316 AF153127 Gallus Sapiens SAPK interacting protein 1477 83 1319 AF153127 Gallus			<u>-</u>			
1308	1307	U58750	Caenorhabdit	similar to the mitochondrial	365	54
1309 AL078593 Homo sapiens dJ210B1.1 (KIAA0680) 267 34 1310 X82693 Homo sapiens E48 antigen 620 96 1311 Z82263 Caenorhabdit is elegans C47A4.1 283 35 1312 AF131218 Homo sapiens Chromosome 16 open reading 1493 100 1313 Y41763 Homo Human PRO938 protein 1636 100 1314 AF196972 Homo sapiens JM24 protein 2239 100 1315 AF053356 Homo Sapiens Insulin receptor substrate 228 97 1316 Y66695 Homo Membrane-bound protein 1909 100 1317 AF153127 Gallus SAPK interacting protein 2442 89 1318 AF153127 Gallus SAPK interacting protein 1477 83 1319 AF153127 Gallus SAPK interacting protein 1651 86 1320 X56932 Homo sapiens 23 kD highly basic protein 1044 100 1321 AF174605 Homo F-box protein Fbx25 467 70 AF174605 Homo F-box protein Fbx25 467 70 AF174605 Homo F-box protein Fbx25 467 70 AF174605 Homo Sapiens F-box protein FBP-18. IKomo Sapiens IKomo Sapiens IKomo Sapiens IKomo Sapiens IKomo Sapiens IKomo Sapiens IKomo Sapiens IKomo Sapiens IKomo Sapiens IKomo Sapiens IKomo Sapiens IKomo Sapiens IKomo Sapiens IKomo Sapiens IKomo Sapiens IKomo IKomo Sapiens IKomo IKom			is elegans	carrier family		
1309 AL078593 Homo sapiens dJ210B1.1 (KIAA0680) 267 34 1310	1308	AF044774	Homo sapiens	breakpoint cluster region	2681	99
1310 X82693	ł		·		ł	{
1311 282263 Caenorhabdit is elegans C47744.1 283 35 1312	1309	AL078593	Homo sapiens	dJ210B1.1 (KIAA0680)	267	34
1312	1310	X82693	Homo sapiens	E48 antigen	620	96
1312	1311	Z82263	Caenorhabdit	C47A4.1	283	35
1313 Y41763 Homo Human PR0938 protein 1636 100 1314 AF196972 Homo sapiens JM24 protein 2239 100 1315 AF053356 Homo sapiens Insulin receptor substrate 228 97 1316 Y66695 Homo Membrane-bound protein 1909 100 1317 AF153127 Gallus SAPK interacting protein 2442 89 1318 AF153127 Gallus SAPK interacting protein 1477 83 1319 AF153127 Gallus SAPK interacting protein 1651 86 1320 X56932 Homo sapiens 23 kD highly basic protein 1044 100 1321 AF174605 Homo F-box protein Fbx25 467 70 1321 AF174605 Homo F-box protein Fbx25 KBP			is elegans	i		
1313	1312	AF131218	Homo sapiens	chromosome 16 open reading	1493	100
Sapiens Sequence.						
1314	1313	Y41763			1636	100
1315						
1316 Y66695 Homo Membrane-bound protein 1909 100					2239	
1316 Y66695 Homo Membrane-bound protein 1909 100	1315	AF053356	Homo sapiens		228	97
Sapiens PRO1344.						
1317	1316	Y66695		-	1909	100
gallus			•			
1318	1317	AF153127		SAPK interacting protein	2442	89
gallus SAPK interacting protein 1651 86 1319			_			
1319 AF153127 Gallus gallus 1320 X56932 Homo sapiens 23 kD highly basic protein 1044 100 1321 AF174605 Homo sapiens]	1318	AF153127		SAPK interacting protein	1477	83
gallus 1320 X56932 Homo sapiens 23 kD highly basic protein 1044 100 1321 AF174605 Homo sapiens]	3336					
1320 X56932 Homo sapiens 23 kD highly basic protein 1044 100 1321 AF174605 Homo sapiens	1319	AF153127		SAPK interacting protein	1651	86
1321 AF174605 Homo sapiens] >Y83086 Y83086 09- MAR-2000 28- AUG-1998 F- box protein FBP-18. [Homo sapiens	1300	VECCOO				
sapiens] >Y83086 Y83086 09- MAR-2000 28- AUG-1998 F- box protein FBP-18. [Homo sapiens				,		
>Y83086 Y83086 09- MAR-2000 28- AUG-1998 F- box protein FBP-18. [Homo sapiens	1321	AF174605		F-box protein Fbx25	467	70
Y83086 09- MAR-2000 28- AUG-1998 F- box protein FBP-18. [Homo sapiens			_			
MAR-2000 28- AUG-1998 F- box protein FBP-18. [Homo sapiens		1				
AUG-1998 F- box protein FBP-18. [Homo sapiens						
box protein FBP-18. [Homo sapiens						
FBP-18. [Homo sapiens		1		•		
[Homo sapiens			-			
sapiens]				
]	• • • • •			
, ,, 1200a000a1a000000	1322	M61732		neuraminidase	214	24
cruzi	-				~ * *	44
1323 Y17013 porcine pol 304 64	1323	Y17013		pol	304	64
endogenous 501			-	E		I

				OLIZMY	
SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
ID	NUMBER			SCORE	I DEMILIE
NO:					
	7712000	retrovirus Arabidopsis	putative protein	1174	37
1324	AL138655	thaliana	burgerse brocern		
1325	AL138655	Arabidopsis	putative protein	946	35
1325	WDT30022	thaliana	pacacive process		
1326	AL133215	Homo sapiens	bA108L7.2 (novel protein	1322	99 3
1320	MD133213	HORO Bupions	similar to rat tricarboxylate		
			carrier)		
1327	AF161541	Homo sapiens	HSPC056	1357	99
1328	Y73346	Homo sapiens	HTRM clone 619699 protein	785	96
1320	173340	nome suprem	sequence.		
1329	L10910	Homo sapiens	splicing factor	912	82
1330	AF146568	Homo sapiens	MIL1 protein	1936	100
1331	W87772	Homo sapiens	Human serum glucocorticoid-	232	39
1331	1,07772		regulated kinase (H-SGK2)	Ì	1
			polypeptide.	1	
1332	Y41741	Ното	Human PRO704 protein	1860	100
		sapiens	sequence.		
1333	AF295096	Homo sapiens	zinc-finger protein ZBRK1	411	91
1334	Z82271	Caenorhabdit	Similarity to Mouse kinensin-	578	44
		is elegans	like protein KIF4 comes from	1	
		_	this gene		
1335	AE000810	Methanobacte	conserved protein	290 .	43
		rium		ļ	
		thermoautotr		1	İ
		ophicum			
1336	Y68779	Homo sapiens	Amino acid sequence of a	1019	91
			human phosphorylation		1
			effector PHSP-11.		
1337	AB027003	Mus musculus	protein phosphatase	378	84
1338	U64856	Caenorhabdit	weak similarity to TPR	215	40
i	1	is elegans	domains	1	29
1339	AE001394	Plasmodium	protein of the YMR7 family	170	29
		falciparum		204	89
1340	X76717	Homo sapiens	MT-11 protein	289	45
1341	AC011914	Arabidopsis	putative mutT protein; 68398-	289	43
		thaliana	67881	2122	100
1342	AJ276171	Homo sapiens	ASPIC myosin regulatory light chain	2303	99
1343	AF187016	Homo sapiens	interacting protein MIR	2303	"
	1	Homo sapiens	similar to Kelch proteins;	894	35
1344	AC006963	Homo sapiens	similar to Reich process,	1000	
	1		(PID:g4650844)		1
2245	AF257466	Homo sapiens	N-acetylneuraminic acid	1880	99
1345	AF25/466	HOMO Bapiens	phosphate synthase		
1346	Y25896	Homo sapiens	Human secreted protein	1148	100
1346	123030	nomo supremo	fragment encoded from gene]	
			64.		
1347	AJ272073	Torpedo	male sterility protein 2-like	1664	58
157'	122,20,3	marmorata	protein		1
1348	AF161548	Homo sapiens	HSPC063	1018	98
1349	W78128	Homo sapiens		1117	100
		1	encoded by gene 3 clone		1
1			HOSBI96.	<u> </u>	
1351	G02144	Homo sapiens	Human secreted protein, SEQ	418	100
	· · ·	1	ID NO: 6225.	1	
1352	D90869	Escherichia	similar to	2047	100
]	1	coli			
1353	A12029	Homo sapiens	MRP-14	613	100
1354	AC005328	Homo sapiens	R26660 1, partial CDS	870	74
1355	AC024876	Caenorhabdit		829	61
1		is elegans	SW:RPB1_CRIGR		
1		-	copine III	1876	64
1356	AF077226	Homo sapiens	COPING III		
1356	AF077226 AF217188	Mus musculus		801	63
			YIP1B ZNF234	801 3869 5035	63 100 99

SEQ ID NO:	ACCESSION	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		 	element binding and beta	SCORE	
			transducin family proteins		1
1362	Z48475	Homo sapiens	glucokinase regulator	3160	99
1363	Z48475	Homo sapiens	glucokinase regulator	2682	97
1364	AF195764	Homo sapiens	megakaryocyte-enhanced gene	2055	99 .
		noo papaono	transcript 1 protein; MEGT1	2033	,
1365	AF116609	Homo sapiens	PR00915	581	100
1366	AF116609	Homo sapiens	PRO0915	581	100
1367	AL117352	Homo sapiens	dJ876B10.3 (novel protein	2581	99
		nome supreme	similar to C. elegans T19B10.6 (Tr:Q22557))	2501	
1368	Y34124	Homo	Human potassium channel	1342	100
	1	sapiens	K+Hnov15.		
1369	AJ245621	Homo sapiens	CTL2 protein	3728	99
1370	AF008220	Bacillus	YtaG	429	45
	1	subtilis	1000	123	43
1371	X05562	Homo sapiens	alpha-2 chain precursor (AA - 25 to 1018) (3416 is 2nd base in codon)	5908	99
1372	298048	Homo sapiens	dJ408N23.4 (novel DnaJ domain protein)	1296	99
1373	AF154415	Homo sapiens	FLASH	10253	100
1374	U20286	Rattus	lamina associated polypeptide	1567	69
		norvegicus	1C		
1375	U53445	Homo sapiens	DOC1	1645	46
1376	AL117337	Homo	bA393J16.1 (zinc finger	250	60
		sapiens	protein 33a (KOX 31))	250	00
1377	AC005328	Homo sapiens	R26660 1, partial CDS	1126	100
1378	U35113	Homo sapiens	metastasis-associated gene	1823	69
1379	L15313	Caenorhabdit	putative	858	1
13/3	D13313	is elegans	putative	858	58
1380	Y25756	Homo sapiens	Human secreted protein encoded from gene 46.	1508	100
1381	AB037360	Homo sapiens	ANKHZN	5734	95
1382	AB037360	Homo sapiens	ANKHZN	959	97
1383	AF237676	Mus musculus	G beta-like protein GBL	1721	96
1384	AF237676	Mus musculus			1
1385	Y58793		G beta-like protein GBL	1043	70
1386	AF212162	Homo sapiens	Human calcium regulatory protein CaREG-1.	715	100
1385	AL031685	Homo sapiens	ninein	10369	99
1387	AC004890		dJ963K23.2 (novel protein)	337	33
	AC004890	Homo sapiens	similar to zinc finger proteins; similar to BAA24380 >W06316 W06316 03-OCT-1996 27-APR-1995 TRP-1 protein.	542	86
1389	AF187989	Homo sapiens	zinc finger protein ZNF223	2665	99
1390	AC035150	Homo sapiens	Zinc finger protein ZNF221	3459	100
1391	AF287894	Homo sapiens	PIST	1410	97
1392	AF282265	Homo sapiens	inner centromere protein INCENP	1794	99
1393	X90840	Homo sapiens	axonal transporter of synaptic vesicles	4584	99
1394	AF076249	Homo sapiens	zinc finger protein SBBIZ1	3208	99
1395	G02224	Homo sapiens	Human secreted protein, SEQ ID NO: 6305.	299	75
1396	AC004809	Arabidopsis thaliana	Similar to	130	34
1398	AF242519	Homo sapiens	zinc finger protein SBZF3	181	66
1399	AL133396	Homo sapiens	dJ1068H6.4 (prion protein like protein doppel)	962	100
1400	Y48611	Homo sapiens	Human breast tumour- associated protein 72.	817	99
1401	AC004472	Homo sapiens	P1.11659_5	280	54
1402	X91489	Saccharomyce s cerevisiae	putative HMG box	164	27

179

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:	¥79222		Human transferase TRNSFS-14.	2842	100
		sapiens		1010	99
404	X81058	LIGO MADO	tex261	194	29
405	AB012084	Mus musculus	ITM	3233	99
406	AB030251	Homo sapiens	GTPase activating protein		99
407	AJ010585	Rattus rattus	PTB-like protein	2684	
408	X75760	Drosophila melanogaster	LRR47	364	29
409	U76618	Mus musculus	N-RAP	804	48
410	AC005578	Homo sapiens	P20887_1, partial CDS	835	63
411	AE000284	Escherichia coli	orf, hypothetical protein.	360	100
1412	X01563	Escherichia coli	L5 (rplE) (aa 1-179)	911	100
1413	W78279	Homo sapiens	Fragment of human secreted protein encoded by gene 33.	1264	99
1414	AB031051	Homo sapiens	organic anion transporter OATP-E	3832	100
1415	M17466	Homo sapiens	coagulation factor XII	3455	100
1415	AF097994	Homo sapiens	L-kynurenine/alpha- aminoadipate aminotransferase	2202	99
	AF151077	Homo sapiens	HSPC243	1262	99
1417 1418	Y09945	Rattus norvegicus	putative integral membrane transport protein	1098	61
1419	U13152	Mesocricetus	guanine nucleotide-binding	2179	76
1420	AL162458	Homo sapiens	bA465L10.5 (KIAA1176 (novel protein, presumed ortholog of mouse K-Cl cotransporter	5696	100
1421	Y99426	Homo sapiens	KCC2)) Human PRO1604 (UNQ785) amino	152	29
1422	¥94923	Homo sapiens	acid sequence SEQ ID NO:308. Human secreted protein clone	4039	99
		-	qs14_3 protein sequence SEQ ID NO:52.	10748	99
1423	AF177388	Homo sapiens	cancer-amplified transcriptional coactivator ASC-2	10748	
1424	Y48517	Homo sapiens	Human breast tumour- associated protein 62.	1851	99
1465	1 NEOCOOAS	Homo sapiens	BM-006	1454	89
1425	AF208848	Homo sapiens	BM-006	853	79
1426 1427	AF208848 AF112886	Bos taurus	differentiation enhancing factor 1	4693	95
	1,,,,,,,,,	Homo sapiens	Gu protein	1372	63
1428	U41387	Homo sapiens		2853	78
1429	AF161534	Mus musculus		275	30
1430 1431	AF125043 Y66718	Homo sapiens	Membrane-bound protein PRO1106.	1886	100
1432	AF193613	Homo sapiens	cell recognition molecule Caspr2	568	100
1455	AB044560	Mus musculus		192	34
1434	R99800	Homo sapiens		707	51
1435	AF220530	Homo sapiens		2904	100
1436	X70944	Homo sapiens		1261	72
			factor	1282	100
1437	AF271732	Homo sapiens		595	98
1438	Y30811	Homo sapiens	encoded from gene 1.	628	97
1439	AJ293659	Homo sapiens	mucolipidin		100
1440	AF219138	Homo sapiens		3083	100
1441	AF219138	Homo sapiens	GGA3 long isoform	3346	1.00

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	8
ID	NUMBER	SPECIES	DESCRIPTION	WATERMAN	IDENTITY
NO:				SCORE	IDENTITI
1442	AB039669	Homo sapiens	ALEX3	1944	100
1443	AF237711	Drosophila	Diablo	191	27
	1	melanogaster		191	2'
1444	AJ011896	Homo sapiens	Nafl beta protein	439	39
1445	X73874	Homo sapiens	phosphorylase kinase	6233	98
1446	AF214114	Homo sapiens	breast carcinoma-associated	3999	99
1110	Merrina	nomo saprens	antiqen BCAA	3333	33
1447	AF003924	Homo sapiens	ANC 2H01	2645	99
1448	AF003136	Caenorhabdit	contains weak similarity to	2843	52
1110	A 005150	is elegans	an AMP-binding motif	2043	32
1449	AF155112	Homo sapiens	NY-REN-50 antigen	1184	89
1450	Y95004	Homo sapiens	Human secreted protein	985	100
1150	155004	nomo saprons	vc54 1, SEQ ID NO:48.	303	100
1451	AF107203	Homo sapiens	ataxin 2-binding protein	688	57
1452	AF107203	Homo sapiens	ataxin 2-binding protein	456	78
1453	Z38011	Mus musculus	DMR-N9	882	56
1454	X90568	Homo sapiens	Protein sequence and	510	28
1424	290300	HOLLO BADIELIS	annotation available soon via	310	20
			LABEIT@EMBL-Heidelberg.DE		
1455	AL035409	Homo sapiens	dJ564M11.3 (similar to	1356	100
1133	7000030700	nomo saprens	sialyltranferase)	1336	100
1456	D44480	Mus musculus	MATH-2 protein	272	100
1458	AF141326	Homo sapiens	RNA helicase HDB/DICE1	478	45
1459	AF242552	Gallus	retinovin	945	34
1437	AL 242332	gallus	Tecinovin	1 343	34
1460	U11036	Homo sapiens	Ibd1	724	84
1461	AB025258	Mus musculus	granuphilin-a	545	39
1462	Y08134	Homo sapiens	acid sphingomyelinase-like	2428	99
1402	100134	HOMO SAPTERS	phosphodiesterase	2428	99
1463	AC004997	Homo sapiens	match to ESTs Z43979	869	98
1403	ACOU4331	HOIRO SAPTERS	(NID:g573097), R19699	003	98
			(NID:93734333)	1	
1464	AC004997	Homo sapiens	match to ESTs 243979	869	98
	ACOUTSS	nomo sapiens	(NID:9573097), R19699	003	
			(NID:9774333)	1	
1465	U32743	Haemophilus	fucose operon protein (fucU)	315	50
		influenzae	racobe operom process (raco)	1 323	30
		Rd		1	
1466	Y09022	Homo sapiens	Not56-like protein	2342	100
1467	AC003034	Homo sapiens	Homolog of rat kidney-	1072	99
		Duplons	specific (KS) gene	2072	
1468	1				"
	AF071544	Spinacia		222	
100	AF071544	Spinacia oleracea	ribulose-1,5-bisphosphate	333	26
2.100	AF071544	Spinacia oleracea	ribulose-1,5-bisphosphate carboxylase/oxygenase small	333	
		oleracea	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I		26
1469	AF071544 Y57930		ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein	1053	
		oleracea	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54.	1053	26
1469	Y57930	oleracea (Homo sapiens	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein		26
1469	Y57930	oleracea (Homo sapiens Rattus norvegicus	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54.	1053	26
1469	Y57930 AF032666	oleracea (Homo sapiens	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel	1053	26
1469	Y57930 AF032666	oleracea (Homo sapiens Rattus norvegicus Homo sapiens	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel protein-17 (MECHP-17).	1053 4504 452	26 100 93
1469 1470 1471	Y57930 AF032666 Y70467	oleracea (Homo sapiens Rattus norvegicus	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel	1053	26
1469 1470 1471	Y57930 AF032666 Y70467	oleracea (Homo sapiens Rattus norvegicus Homo sapiens	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel protein-17 (MECHP-17). C321D2.1 (Ribosomal Large Subunit Pseudouridine	1053 4504 452	26 100 93
1469 1470 1471	Y57930 AF032666 Y70467	oleracea (Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel protein-17 (MECHP-17). C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein)	1053 4504 452 1694	26 100 93 74 100
1469 1470 1471 1472	Y57930 AF032666 Y70467 AL031033	Oleracea (Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel protein-17 (MECHP-17). C321D2.1 (Ribosomal Large Subunit Pseudouridine	1053 4504 452	26 100 93
1469 1470 1471 1472	Y57930 AF032666 Y70467 AL031033	oleracea (Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens Homo sapiens	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel protein-17 (MECHP-17). C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) genethonin 3 HTS1	1053 4504 452 1694 4026 1101	26 100 93 74 100
1469 1470 1471 1472 1473 1474	Y57930 AF032666 Y70467 AL031033 AF177292 S45936	Oleracea (Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel protein-17 (MECHP-17). C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) genethonin 3 HTS1 Human secreted protein	1053 4504 452 1694	26 100 93 74 100
1469 1470 1471 1472 1473 1474	Y57930 AF032666 Y70467 AL031033 AF177292 S45936 Y86241	oleracea (Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel protein-17 (MECHP-17). C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) genethonin 3 HTS1 Human secreted protein HOABR60, SEQ ID NO:156.	1053 4504 452 1694 4026 1101 1879	26 100 93 74 100 98 50 98
1470 1471 1472 1473 1474 1475	Y57930 AF032666 Y70467 AL031033 AF177292 S45936	oleracea (Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Fugu	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel protein-17 (MECHP-17). C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) genethonin 3 HTS1 Human secreted protein	1053 4504 452 1694 4026 1101	26 100 93 74 100
1470 1471 1472 1473 1474 1475	Y57930 AF032666 Y70467 AL031033 AF177292 S45936 Y86241 AJ010317	oleracea (Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel protein-17 (MECHP-17). C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) genethonin 3 HTS1 Human secreted protein HOABR60, SEQ ID NO:156. Sand	1053 4504 452 1694 4026 1101 1879	26 100 93 74 100 98 50 98
1469 1470 1471 1472 1473 1474 1475	Y57930 AF032666 Y70467 AL031033 AF177292 S45936 Y86241	oleracea (Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Caenorhabdit	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel protein-17 (MECHP-17). C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) genethonin 3 HTS1 Human secreted protein HOABR60, SEQ ID NO:156. Sand coded for by C. elegans cDNA	1053 4504 452 1694 4026 1101 1879	26 100 93 74 100 98 50 98
1469 1470 1471 1472 1473 1474 1475	Y57930 AF032666 Y70467 AL031033 AF177292 S45936 Y86241 AJ010317	oleracea (Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Tugu rubripes	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel protein-17 (MECHP-17). C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) genethonin 3 HTS1 Human secreted protein HOABR60, SEQ ID NO:156. Sand coded for by C. elegans cDNA yk99b4.3; similar to human	1053 4504 452 1694 4026 1101 1879	26 100 93 74 100 98 50 98
1469 1470 1471 1472 1473 1474 1475	Y57930 AF032666 Y70467 AL031033 AF177292 S45936 Y86241 AJ010317	oleracea (Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Caenorhabdit	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel protein-17 (MECHP-17). C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) genethonin 3 HTS1 Human secreted protein HOABR60, SEQ ID NO:156. Sand coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein	1053 4504 452 1694 4026 1101 1879	26 100 93 74 100 98 50 98
1469 1470 1471 1472 1473 1474 1475 1476	Y57930 AF032666 Y70467 AL031033 AF177292 S45936 Y86241 AJ010317 U42831	oleracea (Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Caenorhabdit is elegans	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel protein-17 (MECHP-17). C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) genethonin 3 HTS1 Human secreted protein HOABR60, SEQ ID NO:156. Sand coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157)	1053 4504 452 1694 4026 1101 1879 1278	26 100 93 74 100 98 50 98 68
1469 1470 1471 1472 1473 1474 1475	Y57930 AF032666 Y70467 AL031033 AF177292 S45936 Y86241 AJ010317	oleracea (Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Caenorhabdit	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I Human transmembrane protein HTMPN-54. rsec5 Human membrane channel protein-17 (MECHP-17). C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) genethonin 3 HTS1 Human secreted protein HOABR60, SEQ ID NO:156. Sand coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein	1053 4504 452 1694 4026 1101 1879	26 100 93 74 100 98 50 98

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:	AL078599	Homo sapiens	dJ991C6.1 (novel protein	1274	65
461	ALU 10555	NOMO BAPICIA	similar to C. elegans		
			F55A12.9 (Tr:P91086))		
400	Z98977	Schizosaccha	putative vacuolar protein	256	29
482	436377	romyces	Pacacato taranta p		1
					ļ
		pombe	JNK/SAPK-associated protein-1	4968	92
.483	AB005662	Mus musculus	hypothetical protein	716	100
484	AL050120	Homo sapiens	hypothetical protein	1006	53
485	M27878	Homo sapiens	DNA binding protein		1
486	Y69161	Homo sapiens	Amino acid sequence of a	575	99
		1	partial protein kinase.		
1487	X84156	Saccharomyce	ATH1	341	29
	ļ	s cerevisiae			<u> </u>
1488	AF038963	Homo sapiens	RNA helicase	446	34
1489	U56966	Caenorhabdit	coded for by C. elegans cDNA	620	42
1409	030300	is elegans	yk30b3.5; coded for by C.		j
	}	15 cregains	elegans cDNA yk30b3.3		
		Archaeoglobu	enoyl-CoA hydratase (fad-4)	533	46
1490	AE000989		enoy1-cox nyaracase (144 17		1
		s fulgidus	adenylyl cyclase type IV	707	95
1491	M80633	Rattus	adenatat cacrase cabe in	l	1
		norvegicus		3513	99
1492	Y73342	Homo sapiens	HTRM clone 2709055 protein	3213	""
	1		sequence.		
1493	Y17220	Homo sapiens	Human secreted protein (clone	462	37
		_	fj283-11).		
1494	AF133670	Mus musculus	ARL-6 interacting protein-2	701	97
1495	Y94897	Homo	Human protein clone HP10574.	1371	100
1433	194097	sapiens			
	1		dJ747H23.2 (novel protein)	1550	100
1496	AL049699	Homo sapiens	ribosomal S6 protein kinase	2427	100
1497	AF037447	Homo sapiens	ribosomai se procein kinase	269	35
1498	AL445067	Thermoplasma	putative target YPL207w of	209	133
		acidophilum	the HAP2 transcriptional		1
			complex related protein		
1499	AB039947	Homo sapiens	X11L-binding protein 51	227	36
1500	AJ277750	Homo sapiens	UBASH3A protein	3509	100
1501	AL050333	Homo	dJ93K22.1 (novel protein	2439	100
1301	AL030333	sapiens	(contains DKFZP564B116))		
3500	AF179896	Homo sapiens	TALE homeobox protein Meis2b	1140	100
1502		Homo sapiens	TALE homeobox protein Meis2a	1177	100
1503	AF178948	-	Human secreted protein clone	1442	99
1504	Y53005	Homo sapiens	pm749_8 protein sequence SEQ		
		1			
	1		ID NO:16.	3580	99
1505	X82494	Homo sapiens	fibulin-2		- 10
1506	X98296	Homo sapiens	ubiquitin hydrolase	783	42
1507	AL034548	Homo sapiens	dJ1103G7.6 (novel protein)	1098	100
1508	Y76144	Homo sapiens		1736	100
	1		encoded by gene 21.	1	
1500	AF220182	Homo sapiens	uncharacterized hypothalamus	1181	98
1509	AF ZZULOZ	Homo saprems	protein HT008	1	[
	1,,,,,,,,	Go		415	58
1510	U64601	Caenorhabdit			
		is elegans	next cosmid	196	29
1511	AL356192	Neurospora	related to MDM1 protein	196	1 2 3
	1	crassa		1000	100
1512	D17629	Homo	N-acetylgalactosamine 6-	1829	100
		sapiens	sulfate sulfatase (GALNS)		
1513	AF168717	Homo sapiens	x 009 protein	694	99
1514	AJ243531	Homo sapiens		735	100
		Arabidopsis	putative C3HC4-type RING zinc	407	30
1515	AC003672	-	finger protein	1	1
		thaliana		1374	90
1516	AF115435	Rattus	syntaxin 17	13.4	1
	Í _	norvegicus			
1517	AF003140	Caenorhabdit	C44E4.5 gene product	274	31
	1	is elegans			
1518	AB002584	Rattus	beta-alanine-pyruvate	2238	82
		norvegicus	aminotransferase	I	
			yeast atp12 protein precursor	270	30

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		romyces	homolog		
1520	AF255910	Homo sapiens	vascular endothelial junction-associated molecule	547	100
1521	D31764	Homo sapiens	KIAA0064	170	27
1522	Y66634	Homo sapiens	Membrane-bound protein PRO190.	985	100
1523	Y94450	Homo sapiens	Human inflammation associated protein	250	43
1524	AC000107	Arabidopsis thaliana	F17F8.22	277	37
1525	AF109377	Mus musculus	ldlBp	1277	83
1526	AL031427	Homo sapiens	dJ167A19.4 (novel protein)	1432	99
1527	Y08135	Mus musculus	acid sphingomyelinase-like phosphodiesterase	1496	79
1528	AK024423	Homo sapiens	FLJ00012 protein	611	100
1529	AF154502	Homo sapiens	quiescent cell proline dipeptidase	679	100
1530	AF205598	Homo sapiens	transposase-like protein	1368	100
1531	AF251039	Homo sapiens	putative zinc finger protein	1420	50
1532	W74805	Homo sapiens	Human secreted protein encoded by gene 77 clone HOEAS24.	493	
1533	AF039023	Homo sapiens	Ran-GTP binding protein; RanBP6	5707	99
1534	AC007190	Arabidopsis thaliana	F23N19.9	374	37
1535	AB027564	Homo sapiens	DINB1	4482	100
1536	Y36178	Homo sapiens	Human secreted protein	377	87
1537	Y50907	Homo sapiens	Human fetal brain cDNA clone vb3_1 derived protein.	3693	99
1538	AF017368	Mus musculus	faciogenital dysplasia protein 2	177	47
1539	AF266756	Homo sapiens	sphingosine kinase	2011	99
1540	Z48804	Homo sapiens	OA1	2238	100
1541	AF000195	Caenorhabdit is elegans	Contains similarity to Pfam domain: PF00169 (PH), Score=20.6, E-value=1.9e-05, N=1	379	42
1542	¥71159	Homo sapiens	Human phosphodiesterase interacting protein, myomegalin.	9415	99
1543	X76092	Homo sapiens	DNA binding protein RFX3	3327	100
1544	AB015330	Homo sapiens	HRIHFB2007	631	50
1545	AF198487	Homo sapiens	transcription factor LBP-1b	2822	100
1546	AF016417	Caenorhabdit is elegans	Similar to BZIP transcription factor	518	42
1547	X55885	Homo sapiens	KDEL receptor	1106	100
1548	AB035495	Carassius auratus	ubiquitin-activating enzyme E1	836	42
1549	AL021707	Homo sapiens	dJ508I15.4 (KIAA0668)	3688	100
1550	AJ223978	Bacillus subtilis	YvqK protein	292	42
1551	AF145615	Drosophila melanogaster	BcDNA.GH03377	822	44
1552	AL157734	Schizosaccha romyces pombe	putative mannosyltransferase involved in N-glycosylation	435	37
1553	AF079527	Mus musculus	IER5	691	63
1554	AB026291	Rattus norvegicus	acetoacetyl-CoA synthetase	1099	88
1555	Y44722	Homo sapiens	Human immune system molecule, ISMO-3.	1780	99
1556	AF116553	Drosophila melanogaster	antennal-specific short-chain dehydrogenase/reductase	277	32
1557	Y71056	Homo sapiens	Human membrane transport	1975	99

SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
	·	SCORE	_
	protein, MTRP-1.		
Homo sapiens	Human membrane transport	1975	99
<u>r</u>	protein, MTRP-1.		
Homo sapiens	Human membrane transport	1894	97
	protein, MTRP-1.		Į.
	beta-1,3-N-	262	44
Mus muscurus	acetylglucosaminyltransferase		
Homo sapiens	dJ309K20.2 (acrosomal protein	1607	97
Homo sapiens	ACR55 (similar to rat sperm		1
	antigen 4 (SPAG4)))		
	DNA polymerase lambda	3002	100
Homo sapiens	dA22D12.1 (novel protein	3015	100
Homo sapiens	similar to Drosophila Kelch	3025	
			1
	proteins)	2790	100
Homo sapiens	Gene product with similarity	2790	1 100
İ	to Ubiquitin binding enzyme		82
Homo sapiens	R27216_1	919	
Caenorhabdit	Contains similarity to Pfam	550	45
is elegans	domain: PF00169 (PH),	1	
_	Score=20.6, E-value=1.9e-05,		
	N=1		
Ното	F-box and WD-repeats protein	2879	100
sapiens	beta-TRCP2 isoform C		·
Mus musculus	truncated form of Sox17	1047	78
Homo sapiens	unnamed protein product	210	91
	protein kinase C mu	4797	99
Homo sapiens	SCHIP-1	2388	100
Homo sapiens	CG18445 gene product	180	31
Drosophila	CG18445 gene product	100	
melanogaster		205	38
Streptomyces	NonF	203	150
griseus		Į.	
subsp.			1
griseus		144	27
Caenorhabdit	F22D3.3 gene product	144	2'
is elegans		1000	68
Homo sapiens	transcription factor ICBP90	287	100
Homo sapiens	oxytocin receptor	2002	
Drosophila	Diablo	421	54
melanogaster			
Homo sapiens	Human secreted protein, SEQ	480	100
	ID NO: 5056.		
Cryptosporid	thrombospondin-related	123	33
ium parvum	adhesive protein		
Homo sapiens		663	100
MONIO Sapiens	(translation of cDNA		1
·	Em:AK000219))	ļ	Į.
Homo sapiens	kinesin family member protein	345	33
nomo sapiens	KIF3A		1
		1198	100
Homo sapiens	glycerate kinase, putative	349	34
Thermotoga	grycerate kinase, putative	1	1
maritima		3973	100
Homo sapiens	Kelch-like 1 protein	3494	99
Homo	leucine-rich repeat	3434	1 -
sapiens	transmembrane protein FLRT1	-	97
Homo sapiens	DNb-5	2628	
Homo sapiens	NADP+-dependent malic enzyme	3167	99
Homo sapiens	ZYG homologue	3966	99
Homo sapiens	flavohemoprotein b5+b5R	2563	100
Homo sapiens		181	47
"TO" BUPTERS	cb98 4.		
Homo sapiens		7567	99
Homo sapiens			
I	B much protein /AA 1-7001	3678	99
			27
			54
	hypothetical protein	233	1 -
	Homo sapiens	hnup153 Homo sapiens B-myb protein (AA 1-700) Homo sapiens mucin Schizosaccha hypothetical protein	Homo sapiens B-myb protein (AA 1-700) 3678 Homo sapiens mucin 242 Schizosaccha hypothetical protein 235

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	8
ID	NUMBER		İ	WATERMAN	IDENTITY
NO:				SCORE	
		pombe			
1595	W78324	Homo sapiens	Fragment of human secreted	1318	98
			protein encoded by gene 81.		<u> </u>
1596	Y94906	Homo sapiens	Human secreted protein clone	2236	98
	1		rb649_3 protein sequence SEQ		
	1		ID NO:18.		
1597	AF174605	Homo sapiens	F-box protein Fbx25	1408	99
1598	AB032254	Homo	bromodomain adjacent to zinc	9676	98
1500	V02414	sapiens	finger domain 2A		
1599 1600	X73114	Homo sapiens	slow MyBP-C	5568	95
1601	X82200 Y00876	Homo sapiens	gpStaf50 Human LAPH-1 protein	2305	100
1001	100876			1149	98
1602	AJ223351	sapiens Homo sapiens	sequence. HIRA-interacting protein 3	2821	99
1603	AJ222801	Homo sapiens		2268	99
1604	AJ222801	Homo sapiens	neutral sphingomyelinase neutral sphingomyelinase	1601	99
1605	AF185576	Mus musculus	POZ/zinc finger transcription	3435	99
.1002	AF 1055 /6	Mus musculus	factor ODA-8	3435	97
1606	AF093744	Homo sapiens	unknown	131	100
1607	A12142	synthetic	UNKNOWN IFN-pseudo-omega 2	800	98
1,007	216746	construct	Tri-pseudo-omega z	300	30
1608	Y57949	Homo sapiens	Human transmembrane protein	1868	100
1000	13/343	nono sapiens	HTMPN-73.	1000	100
1609	AF151044	Homo sapiens	HSPC210	681	97
1610	X15218	Homo sapiens	ski protein (AA 1 - 728)	3765	100
1611	Y08200	Homo sapiens	rab geranylgeranyl	2976	100
****	100200	nomo saprems	transferase	2376	100
1612	AF220560	Homo sapiens	B/K protein	2486	99
1613	AC004481	Arabidopsis	nodulin-like protein	371	26
1013	110001101	thaliana	noddin like procein	371	20
1614	Y09501	Homo sapiens	NADH-cytochrome-b5 reductase	1607	100
1615	Y15521	Homo sapiens	start position 1	3150	97
1616	AJ010750	Rattus	Castration induced prostatic	890	62
		norvegicus	apoptosis related protein-1,	"	
			(CIPAR-1)		
1617	X58079	Homo sapiens	S100 alpha protein	481	100
1618	Y66678	Homo	Membrane-bound protein	967	100
		sapiens	PRO1009.		
1619	AJ242973	Homo sapiens	peptide methionine sulfoxide	929	100
			reductase		
1620	AF150733	Homo sapiens	AD-014 protein	288	100
1621	AJ007509	Homo sapiens	E1B-55kDa-associated protein	4646	98
1622	X64177	Homo sapiens	metallothionein	380	100
1623	AE001045	Archaeoglobu	A. fulgidus predicted coding	240	36
		s fulgidus	region AF0859		
1624	AL355013	Schizosaccha	mitochondrial carrier protein	403	34
	[romyces)	ĺ
1000	1100000	pombe			
1625	Y66746	Homo	Membrane-bound protein	1184	100
1606	D00053	sapiens	PRO1198.		
1626	D90053	Sus scrofa	destrin	863	100
1627	Y35954	Homo sapiens	Extended human secreted	756	100
			protein sequence, SEQ ID NO.		
1600	21031335	******	203.		1
1628 1629	AL031775 AF132484	Homo sapiens Mus musculus	dJ30M3.2 (novel protein)	470	100
1630			unknown	286	68
T020	AF017096	Drosophila	similar to C. elegans	493	61
		melanogaster	R10H10.6 and S. cerevisiae YD8419.03c		İ
1631	X03077	Homo sapiens		1704	100
1632	AF151084		lactate dehydrogenase-A HSPC250	1704	
1633	AJ101874	Homo sapiens	orf	763	100 97
1634	AC012187	Homo sapiens Arabidopsis		255	
7034	~~v+4+8/	Arabidopsis thaliana	Contains weak similarity to	143	38
		cnarrana	GATA-6 DNA-binding protein gb H36135, gb Z26200 come		
Į	ı		animoras, animagoson come		Ī
	ļ		from this gene.		

185

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	8
ID	NUMBER			WATERMAN SCORE	IDENTITY
NO:	2005045	Tii ono	HERV-E integrase	411	90
1635	AF026246 Y50943	Homo sapiens	Human adult brain cDNA clone	1126	95
1636	150943		ve8 1 derived protein.	0060	100
1637	AF134593	Homo sapiens	L-pipecolic acid oxidase	2068	99
1638	AJ238247	Mus musculus	putative phosphatase subunit	1948	100
1639	Y94942	Homo sapiens	Human secreted protein clone yk251_1 protein sequence SEQ ID NO:90.		
1640	AF235030	Homo sapiens	BM88 antigen	766	99
1641	AF233288	Drosophila melanogaster	WDS	358	26
1642	М19351	Mus musculus	immunoglobulin heavy chain binding protein	145	34
1643	Y70452	Homo sapiens	Human membrane channel protein-2 (MECHP-2).	1352	100
1644	AF176520	Mus musculus	WD repeat-containing F-box protein FBW5	2676	88
1645	W67816	Homo sapiens	Human secreted protein encoded by gene 10 clone HCEMU42.	1156	100
1646	X67155	Homo sapiens	mitotic kinase-like protein-l	4456	99
1647	M63180	Homo sapiens	threonyl-tRNA synthetase	1040	61
1648	Y87342	Homo sapiens	Human signal peptide containing protein HSPP-119 SEQ ID NO:119.	1566	93
1649	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).	4137	100
1650	AC007136	Homo sapiens	Putative map kinase interacting kinase	856	99
1651	AB015346	Homo sapiens	Eps15R	4464	99
1652	AL161576	Arabidopsis thaliana	putative protein	1341	48
1653	AC005313	Arabidopsis thaliana	putative calmodulin	288	28
1654	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1655	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1656	AB017910	Dictyosteliu m discoideum	туом	297	32
1657	Y28919	Homo sapiens	Human regulatory protein HRGP-5.	2251	99
1658	AF056191	Homo sapiens	TPA inducible protein	2744	98
1659	U76846	Arabidopsis thaliana	ubiquitin-specific protease	137	35
1660	AL078627	Schizosaccha romyces pombe	actin-like protein; (2 actin domains)	320	34
1662	X52022	Homo sapiens	collagen type VI, alpha 3	16274	99
1663	AF300648	Homo sapiens	guanine nucleotide binding protein beta subunit 4	1811	100
1664	AF214736	Homo sapiens	EH domain containing protein	2774	100
1665	Z48613	Saccharomyce s cerevisiae	unknown	138	26
1666	AF177385	Homo sapiens	cytochrome c oxidase assembly protein isoform 2	1395	99
1667	AC007842	Homo sapiens	BC331191 1	1581	47
1668	S67513	Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate,	p40	397	43

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID	NUMBER		2200	WATERMAN	IDENTITY
NO:				SCORE	120001111
		aa			
1669	Z99753	Schizosaccha	putative NOL1-NOP2-sun family	569	47
		romyces	nucleolar protein		
		pombe			
1670	G03130	Homo sapiens	Human secreted protein, SEQ	427	97
			ID NO: 7211.		
1671	M96625	Gallus	cardiac muscle tensin	1185	54
1672	AF174482	gallus Homo sapiens			
1673	Y51846	Homo sapiens	polycomb 3 Human 18.1 homolog protein	2005	99
10/3	131040 .	nomo sapiens	fragment.	233	29
1674	AF255334	Homo sapiens	EXP35	152	29
1675	Y94867	Homo	Human protein clone HP10563.	109	30
		sapiens	Mamair processi esone in 10303.	1 103	30
1676	Y25712	Homo sapiens	Human secreted protein	3043	99
			encoded from gene 2.		
1677	Y25712	Homo sapiens	Human secreted protein	1580	91
			encoded from gene 2.	İ	
1678	AF163151	Homo sapiens	dentin sialophosphoprotein	170	17
			precursor		
1679	AF163151	Homo sapiens	dentin sialophosphoprotein	170	17
			precursor		
1680	AK024453	Homo sapiens	FLJ00045 protein	1349	100
1681	AF019236	Dictyosteliu	TipD	613	34
1682	AJ243459	m discoideum			
1052	AU243459	Leishmania major	proteophosphoglycan	153	26
1683	Z69369	Schizosaccha	putative GTP-binding protein	560	46
1003	203303	romyces	paracive Gir-pinding procein	360	46
		pombe			
1684	X94910	Homo sapiens	ERp28	1334	100
1685	AF286475	Takifuqu	retinitis pigmentosa GTPase	196	19
		rubripes	regulator-like protein		
1686	AF191298	Homo sapiens	vacuolar sorting protein 35	4087	100
1687	AJ275986	Homo sapiens	transcription factor	2958	100
1688	AJ275986	Homo sapiens	transcription factor	1886	88
1689	X07311	Drosophila	heat shock protein	138	43
1690	35040455	melanogaster			
1990	AF240463	Rattus norvegicus	LIS1-interacting protein	1383	83
1691	AJ272078	Homo sapiens	APOBEC-1 stimulating protein	1256	
1692	AJ272079	Homo sapiens	APOBEC-1 stimulating protein	1336	68 60
1693	AF177942	Xenopus	katanin p60	1664	66
		laevis	katanin poo	1004	00
1694	AF263539	Homo sapiens	arginine N-methyltransferase	1774	100
1695	AF222689	Homo	protein arginine N-	1182	81
	1	sapiens	methyltransferase 1-variant 2		'
1696	AK000193	Homo sapiens	unnamed protein product	1060	100
1697	AB041035	Homo sapiens	kidney superoxide-producing	3122	100
			NADPH oxidase	L]
1698	AB041035	Homo sapiens	kidney superoxide-producing	2181	100
1000	\		NADPH oxidase		l
1699	AF025772	Homo sapiens	C2H2 zinc finger protein	488	54
1700	Y44676	Homo sapiens	Human ARF-Related Protein-1	938	97
1701	AV022422	Ytoma	(HARP-1).		
1701	AK022407 AB024574	Homo sapiens	unnamed protein product	315	98
1702	AF055078	Homo sapiens	GTP-binding like protein 2	1172	100
1704	AF198092	Homo sapiens Mus musculus	zinc finger protein 42 RP42	421	52
1705	AE003573	Drosophila	CG12474 gene product	1057	77
	10003373	melanogaster	COLZ4/4 Gene product	161	33
1706	AB036345	Drosophila	aquaporin	164	24
		melanogaster	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	103	~3
1707	Y55927	Homo sapiens	Human STLK2 protein.	2146	100
1708	U27121	Danio rerio	G12	212	47
1709	AL391710	Arabidopsis	putative protein	505	50
	•		 		

SEQ	ACCESSION	SPECIES	DESCRIPTION .	SMITH-	8
ID	NUMBER	SEECIED		WATERMAN	IDENTITY
NO:	NOMBER			SCORE	
NO:		thaliana			
	201012	Homo sapiens	Human PRO241 polypeptide.	1649	97
1710	B01311		formin binding protein 30	4561	85
1711	U40750	Mus musculus	skeletal muscle and cardiac	1490	89
1712	AJ011118	Mus musculus	protein		
1713	AF255303	Homo sapiens	membrane-associated nucleic acid binding protein	4416	99
1714	AF255303	Homo sapiens	membrane-associated nucleic acid binding protein	2960	100
1715	U08227	Rattus	Ras-related protein	511	51
1716	AF168795	norvegicus Rattus	schlafen-4	1129	44
		norvegicus	SUMO-1-specific protease	5804	99
1717	AF196304	Homo sapiens	HMG20A	1782	100
1718	AL355737	Homo sapiens	HrPET-1	1069	46
1719	AB029333	Halocynthia roretzi			
1720	AF071317	Mus musculus	COP9 complex subunit 7b	1297	97
1721	AJ272215	Homo sapiens	HEYL protein	1681	99
1722	G01982	Homo sapiens	Human secreted protein, SEQ ID NO: 6063.	718	100
1723	AL032643	Caenorhabdit is elegans	similar to Uncharacterized protein family UPF0034,	825	41
1724	G01972	Homo sapiens	Human secreted protein, SEQ	586	92
1725	Y94441	Homo sapiens	Human Adipose Specific Protein 1.	1231	100
1726	AP255443	Homo sapiens	CGI-201 protein	4397	99
		Homo sapiens	HT004 protein	1810	99
1727	AF183426	Bos taurus	neurocalcin	1002	99
1728	D10884		tensin	1411	84
1729	Z18529	Gallus gallus			
1730	273423	Caenorhabdit is elegans	cDNA EST EMBL: Z14908 comes from this gene-cDNA EST this gene	233	41
1732	AF090891	Homo sapiens	PRO0105	470	30
1733	AJ277724	Homo sapiens	histone deacetylase 8	2015	100
1734	G04050	Homo sapiens	Human secreted protein, SEQ ID NO: 8131.	503	95
		Mus musculus	leucine-rich-repeat protein	3531	94
1735	D45913	*****	failed axon connections	276	32
1736	AF096709	Drosophila virilis	protein		
1737	AF195120	Homo sapiens	dynactin p62 subunit	2417	99
1738	L15314	Caenorhabdit is elegans	family PF01772 N=1	206	37
1739	X54618	Listeria monocytogene s	phosphadidylinositol specific phospholipase C	134	27
1740	AL031658	Homo sapiens	dJ310013.4 (novel protein similar to predicted C. elegans an C. intestinalis proteins)	123	31
1741	Y35924	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 173.	1013	99
1742	AC013354	Arabidopsis thaliana	F15H18.15	202	32
1743	W75771	Homo sapiens	Human GTP binding protein APD08.	1932	59
1744	W75771	Homo sapiens	Human GTP binding protein APD08.	1854	61
1745	AF221098	Homo sapiens	Ral guanine nucleotide exchange factor RalGPS1A	1224	70
1746	¥99372	Homo sapiens	Human PRO1430 (UNQ736) amino acid sequence SEQ ID NO:116.	1332	99
1747	Y94294	Homo sapiens	Human coenzyme A-utilising	842	100

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	<u> </u>
ID	NUMBER			WATERMAN	IDENTITY
NO:			•	SCORE	
			enzyme CoAEN-2.		
1748	AK024436	Homo sapiens	FLJ00026 protein	1619	100
1749	AE000877	Methanobacte	conserved protein	231	36
		rium		232	
		thermoautotr			
		ophicum			
1750	AF101361	Drosophila	Abnormal X segregation	193	33
		melanogaster			
1751	Y15067	Homo sapiens	ZNF232	889	100
1752	AF251038	Homo sapiens	GAP-like protein	822	100
1753	AC003093	Homo sapiens	OXYSTEROL-BINDING PROTEIN;	352	57
		•	45% similarity to P22059] "
			(PID:g129308)		i
1754	X69089	Homo sapiens	165kD protein	5703	99
1755	AL049795	Homo sapiens	dJ622L5.3 (novel protein)	1039	100
1756	AL031393	Homo sapiens	dJ733D15.1 (Zinc-finger	2765	100
	ļ	_	protein)	1	
1757	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N-	2020	99
		1	acetylgalactosaminyltransfera	1	
		<u></u>	se	1	1
1758	AL022238	Homo sapiens	dJ1042K10.4 (novel protein)	776	43
1759	AF117653	Homo sapiens	double homeobox protein	375	54
1760	Y12065	Homo sapiens	hNop56	2959	99
1761	AL049712	Homo sapiens	dJ686C3.2 (nucleolar protein	2595	99
			hNop56)		
1762	AC002394	Homo	Gene product with similarity	1542	51 .
		sapiens	to dynein beta subunit	i	
1763	AF169017	Homo sapiens	formiminotransferase	877	100
			cyclodeaminase		
1764	U91541	Homo sapiens	human formiminotransferase	596	100
			cyclodeaminase (ftcd)protein,		, .
			carboxy-terminal end		
1765	AB013365	Bacillus	YlqF	350	34
1000	112.04.01	halodurans			
1766	Y38421	Homo sapiens	Human secreted protein	145	71
1767	AC009176		encoded by gene No. 36.		
1/0/	ACUU9176	Arabidopsis thaliana	putative ribulose-1,5- bisphosphate	216	27
		Liiallalia	carboxylase/oxygenase small		
			subunit N-methyltransferase I		
1768	AK000647	Homo sapiens	unnamed protein product	737	
1769	AJ238982	Homo sapiens	VNN3 protein	2665	99
1770	U73522	Homo sapiens	AMSH	1214	56
1771	U89435	Mus musculus	unknown	829	
1772	S70011	Rattus sp.	tricarboxylate carrier		86
1773	AL035086	Homo sapiens	dJ44A20.2 (novel protein)	1604 2036	95 100
1774	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino	1057	99
•		omo bapiens	acid sequence SEQ ID NO:308.	1,037	<i>33</i>
1775	AF110330	Homo sapiens	glutaminase	3146	100
1776	AJ269529	Homo sapiens	glycerol 3-phosphate permease	2787	100
1777	Z81579	Caenorhabdit	cDNA EST yk76f1.5 comes from	232	31
·		is elegans	this gene		2.1
				L	
1778	AY007239	Homo sapiens	monooxygenase X	11875	44 .
1778 1779	AY007239 AL109608	Homo sapiens Schizosaccha	monooxygenase X oxysterol-binding protein	1875	99 38
		Schizosaccha	oxysterol-binding protein	1875 644	38
		Schizosaccha romyces pombe	oxysterol-binding protein family	644	38
1779	AL109608	Schizosaccha romyces	oxysterol-binding protein family	1729	100
1779	AL109608 AF254260	Schizosaccha romyces pombe Homo sapiens	oxysterol-binding protein family tuftelin 1 guanine nucleotide	644	38
1779	AL109608 AF254260	Schizosaccha romyces pombe Homo sapiens	oxysterol-binding protein family tuftelin 1 guanine nucleotide dissociation stimulator	1729 247	100
1779 1780 1781 1782	AL109608 AF254260 L07924	Schizosaccha romyces pombe Homo sapiens Mus musculus	oxysterol-binding protein family tuftelin 1 guanine nucleotide	1729	100
1779 1780 1781 1782 1783	AL109608 AF254260 L07924	Schizosaccha romyces pombe Homo sapiens Mus musculus Homo	oxysterol-binding protein family tuftelin 1 guanine nucleotide dissociation stimulator ral guanine nucleotide dissociation stimulator	1729 247	100
1779 1780 1781 1782	AF254260 L07924 AF295773 AK024475 AK024475	Schizosaccha romyces pombe Homo sapiens Mus musculus Homo sapiens	oxysterol-binding protein family tuftelin 1 guanine nucleotide dissociation stimulator ral guanine nucleotide	1729 247 142	100 50 49.
1779 1780 1781 1782 1783	AF254260 L07924 AF295773 AK024475	Schizosaccha romyces pombe Homo sapiens Mus musculus Homo sapiens Homo sapiens	oxysterol-binding protein family tuftelin 1 guanine nucleotide dissociation stimulator ral guanine nucleotide dissociation stimulator FLJ00068 protein FLJ00068 protein	1729 247 142	100 50 49.
1779 1780 1781 1782 1783 1784	AF254260 L07924 AF295773 AK024475 AK024475	Schizosaccha romyces pombe Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens	oxysterol-binding protein family tuftelin 1 guanine nucleotide dissociation stimulator ral guanine nucleotide dissociation stimulator FLJ00068 protein	1729 247 142 4333 3996	100 50 49. 100 93

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	% IDENTITY
NO:			glucuronidase exon 11 homolog		

TRADOCS:1416280.1(%CT4011.DOC)

TABLE 3

SEQ ID NO	NO.	DESCRIPTION	RESULTS*
2	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 8.250e- 12 157-181
3	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 8.085e- 13 358-381
4	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.400e- 10 1129-1146 BL00028 16.07 1.257e-09 820- 837
5	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
6	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
7	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
8	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
9	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.119e- 09 863-917
10	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464D 17.40 6.182e- 12 294-312 PR00464G 12.41 4.231e-11 377- 393
11	PR00734	GLYCOSYL HYDROLASE FAMILY 7 SIGNATURE	PR00734I 11.46 4.296e- 09 502-520
12	PF00023	Ank repeat proteins.	PF00023B 14.20 6.500e- 10 89-99 PF00023B 14.20 2.636e-09 56-66
14	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 3.848e-
15	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208A 12.59 9.868e- 10 517-535 PR00208A 12.59 2.233e-09 520- 538
17	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e- 14 282-295 PD00066 13.92 9.400e-14 477- 490 PD00066 13.92 6.500e-13 505-518 PD00066 13.92 9.500e- 13 254-267 PD00066 13.92 1.429e-12 393- 406 PD00066 13.92 6.571e-12 421-434
18	BL00845	CAP-Gly domain proteins.	BL00845 16.43 2.200e- 25 55-80
20	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e- 26 154-199 BL00487F 18.79 8.984e-22 235- 276 BL00487G 26.82 4.082e-12 287-329
21	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e- 26 154-199 BL00487F 18.79 8.984e-22 235- 276 BL00487G 26.82 4.082e-12 348-390
22	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 3.250e- 26 302-333

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
23	BL00107	Protein kinases ATP-	BL00107A 18.39 3.250e- 26 302-333
A.F.	- Dr. 00115	binding region proteins. Eukaryotic RNA	BL00115T 8.45 7.273e-
25	BL00115	polymerase II	29 1208-1242 BL001150
	į	heptapeptide repeat	18.08 2.776e-21 953-
	1	proteins.	983 BL00115Y 11.86
		_	8.000e-17 1604-1650
			BL00115M 19.19 8.130e-
			16 731-774 BL00115H 14.34 9.392e-16 463-
			496 BL00115A 15.44
			7.414e-15 43-82
		ļ	BL00115R 6.50 6.128e-
			14 983-1010 BL00115J
		·	16.71 9.289e-14 591-
		·	617 BL00115I 8.33 4.336e-13 535-590
		İ	BL00115L 12.25 5.939e-
			13 662-694 BL00115G
			11.65 6.011e-13 435-
			463 BL00115K 15.03
			3.417e-10 617-659
			BL001150 16.76 5.805e- 10 863-913 BL00115P
			11.54 7.538e-10 913-
			953 BL00115S 18.24
			7.968e-10 1010-1052
			BL00115U 10.34 4.475e-
			09 1242-1265 BL00420A 20.42 4.109e-
26	BL00420	Speract receptor repeat proteins domain	11 81-110 BL00420A
		proteins domain	20.42 8.820e-10 84-113
27	BL00050	Ribosomal protein L23	BL00050A 23.71 9.250e-
		proteins.	27 94-127 BL00050B
1	Ì		14.81 8.125e-12 133-
			PR00925B 3.73 3.089e-
28	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY	10 41-54
		SIGNATURE	
29	PF00756	Putative esterase.	PF00756C 14.12 1.108e-
			09 486-516
32	BL00557	FMN-dependent alpha-	BL00557D 17.76 5.065e- 37 274-316 BL00557A
		hydroxy acid dehydrogenases proteins.	35.08 8.909e-29 24-73
		denydrogenases proceins.	BL00557C 15.59 1.000e-
			28 227-257 BL00557B
			21.27 8.898e-22 130-
			PR00629E 9.90 5.886e-
34	PR00629	SHC PHOSPHOTYROSINE INTERACTION DOMAIN	35 299-328 PR00629F
		SIGNATURE	10.95 8.364e-32 334-
			361 PR00629B 13.66
1		1	3.786e-27 224-247
			PR00629A 13.45 8.364e-
			21 206-222 PR00629C 3.80 4.000e-12 249-261
	ĺ		PR00629D 12.45 3.739e-
1		1	11 276-286
35	PD01270	RECEPTOR FC	PD01270A 17.22 1.000e-
		IMMUNOGLOBULIN AFFIN.	40 39-79 PD01270B
1		· ·	22.18 2.875e-38 94-131
1		1	PD01270D 24.66 3.700e-
			34 171-207 PD01270C 19.54 3.455e-30 137-
			166
L		PHOTEOTO TO	PD01270A 17.22 1.000e-
36	PD01270	I RECEPTOR FC	PD012/0A 17.22 1.0000
36	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	40 39-79 PD01270B 22.18 2.875e-38 94-131

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	† · · · · · · · · · · · · · · · · · · ·		PD01270D 24.66 3.700e-
			34 171-207 PD01270C
		·	19.54 3.455e-30 137-
37	BL00412	Neuromodulin (GAP-43)	BL00412C 10.28 9.241e-
		proteins.	10 264-298
38	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e- 10 264-298
39	BL00412	Neuromodulin (GAP-43)	BL00412C 10.28 9.241e-
33	2200122	proteins.	10 264-298
40	PR00380	KINESIN HEAVY CHAIN	PR00380B 12.64 7.366e-
	1	SIGNATURE	14 342-360 PR00380C 13.18 6.927e-13 375-
			394 PR00380D 9.93
			2.180e-12 429-451
			PR00380A 14.18 5.154e-
44	BL00345	Ets-domain proteins.	12 143-165 BL00345B 21.28 1.000e-
77	BB00345	Beb-domain processes.	40 239-290 BL00345A
			13.96 2.452e-14 204-
	Dr. 003.15	De de de de de de de de de de de de de de	223
45	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e-
			13.96 2.452e-14 180-
			199
46	DM01551	kw OSTEOINDUCTIVE YOPM	DM01551A 15.63 3.538e-
		MEMBRANE OUTER.	26 172-202 DM01551C 14.62 3.571e-17 232-
		,	252 DM01551B 8.84
			4.750e-11 214-226
47	PR00876	NEMATODE METALLOTHIONEIN	PR00876B 7.66 9.328e-
48	PD01066	SIGNATURE PROTEIN ZINC FINGER	11 246-260 PD01066 19.43 4.231e-
10	1202000	ZINC-FINGER METAL-	33 6-45
		BINDING NU.	
50	BL00972	Ubiquitin carboxyl- terminal hydrolases	BL00972D 22.55 7.750e- 19 994-1019 BL00972A
		family 2 proteins.	11.93 7.120e-18 216-
			234 BL00972E 20.72
_			9.471e-14 1020-1042
·	1		BL00972C 16.48 7.000e- 13 360-375 BL00972B
		·	9.45 8.269e-10 302-312
51	BL00972	Ubiquitin carboxyl-	BL00972D 22.55 7.750e-
		terminal hydrolases	19 990-1015 BL00972A
		family 2 proteins.	11.93 7.120e-18 216- 234 BL00972E 20.72
			9.471e-14 1016-1038
			BL00972C 16.48 7.000e-
			13 360-375 BL00972B 9.45 8.269e-10 302-312
52	BL01115	GTP-binding nuclear	BL01115A 10.22 3.063e-
		protein ran proteins.	14 10-54
53	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 8.500e-
		j	17 20-38 PR00988F 12.23 7.828e-15 196-
			210 PR00988C 13.64
		1	6.108e-14 104-120
	}		PR00988E 8.27 3.872e-
		1	11 174-186 PR00988D 5.95 6.878e-10 160-171
		1	PR00988B 11.60 2.915e-
			09 57-69
55	PR00762	CHLORIDE CHANNEL	PR00762C 9.29 4.682e-
		SIGNATURE	21 294-314 PR00762D
	I	į.	11.29 4.103e-19 509-
			530 PR00762A 14.22

÷.

źz.

193

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		PR00762F 15.12 3.100e-
			16 563-583 PR00762B
			12.12 6.063e-16 230-
	1		250 PR00762E 12.07
			2.286e-15 545-562
	j		PR00762G 14.13 6.276e-
			13 601-616
56	BL00216	Sugar transport	BL00216B 27.64 B.800e-
		proteins.	10 153-203
58	PF00791	Domain present in ZO-1	PF00791B 28.49 2.049e-
		and Unc5-like netrin	10 1080-1135
		receptors.	PF00791B 28.49 2.049e-
59	PF00791	Domain present in ZO-1	10 1062-1117
		and Unc5-like netrin	10 1002-1117
	5701000	receptors. KINASE TYPE RESISTANCE	PD01929E 10.75 9.018e-
61	PD01929	ANTIBIOTIC TRANSFERASE	09 206-221
	1	AM.	
68	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-
66	PROUDUO	01 00111111	09 680-693
69	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-
0,5			09 670-683
70	PF00651	BTB (also known as BR-	PF00651 15.00 8.714e-
• •	•	C/Ttk) domain proteins.	10 51-64
72	DM00179	w KINASE ALPHA ADHESION	DM00179 13.97 5.304e-
		T-CELL.	09 108-118
73	BL00239	Receptor tyrosine kinase	BL00239B 25.15 7.075e-
		class II proteins.	12 118-166
74	BL00790	Receptor tyrosine kinase	BL00790N 13.25 6.116e-
_		class V proteins.	10 93-120 DM00471A 11.73 9.357e-
76	DM00471	0 PROKARYOTIC DNA	13 53-66 DM00471B
		TOPOISOMERASE I.	8.45 4.857e-12 70-81
	7700075	DECARBOXYLASE	PD02876C 8.80 2.723e-
80	PD02876	PHOSPHATIDYLSERINE.	13 223-236 PD02876D
		PROSPRATIDIESERINE.	12.13 2.588e-12 334-
		İ	351
81	PD02876	DECARBOXYLASE	PD02876C 8.80 2.723e-
01	1 2020,0	PHOSPHATIDYLSERINE.	13 282-295 PD02876D
			12.13 2.588e-12 393-
			410
83	BL00708	Prolyl endopeptidase	BL00708B 24.91 7.197e-
		family serine proteins.	12 570-601
84	PR00014	FIBRONECTIN TYPE III	PR00014C 15.44 8.043e-
		REPEAT SIGNATURE	09 985-1004
86	PR00678	PI3 KINASE P85	PR00678H 9.13 1.379e-
		REGULATORY SUBUNIT	09 246-269
		SIGNATURE	PR00320C 13.01 8.200e-
89	PR00320	G-PROTEIN BETA WD-40	09 264-279 PR00320B
	1	REPEAT SIGNATURE	12.19 8.650e-09 264-
			279
		Date of the Date o	BL00455 13.31 2.588e-
93	BL00455	Putative AMP-binding domain proteins.	14 316-332
	12500207	Protein kinases ATP-	BL00107A 18.39 4.000e-
95	BL00107	binding region proteins.	
	DT 00107	Protein kinases ATP-	BL00107A 18.39 4.000e-
96	BL00107	binding region proteins.	10 212-243
	DD00003	GLUCOSE/RIBITOL	PR00081B 10.38 6.318e-
97	PR00081	DEHYDROGENASE FAMILY	13 134-146 PR00081A
		SIGNATURE	10.53 2.500e-12 54-72
00	DD00390	KINESIN HEAVY CHAIN	PR00380A 14.18 5.500e-
98	PR00380	SIGNATURE	24 401-423 PR00380D
		STORMIONE	9.93 7.188e-20 613-635
		(PR00380B 12.64 7.517e-
			16 529-547 PR00380C
			13.18 2.756e-13 560-
	1	i	579

SEQ ID NO	ACCESSION NO.	DESCRIPTION	RESULTS*
102	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 7.545e- 14 289-308
104	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.786e- 18 298-314 BL00479A 19.86 4.913e-16 155- 178 BL00479A 19.86 4.300e-13 272-295 BL00479B 12.57 6.294e- 12 181-197
106	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 8.013e- 12 43-83
107	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 5.000e- 16 403-416
108	BL00191	Cytochrome b5 family, heme-binding domain proteins.	BL00191K 17.38 4.951e- 27 238-282 BL00191J 11.37 6.447e-17 182- 204
109	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.938e- 37 8-47
110	BL01138	Scorpion short toxins proteins.	BL01138A 10.96 8.297e- 10 38-50
113	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 5.800e- 23 156-187 BL00107B 13.31 9.100e-14 225- 241
117	BL00214	Cytosolic fatty-acid binding proteins.	BL00214B 26.51 1.000e- 17 46-91 BL00214A 21.17 7.052e-11 5-31
118	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 8.560e- 13 36-67
119	PR00529	GONADOTROPHIN RELEASING HORMONE RECEPTOR SIGNATURE	PR00529C 11.03 7.506e- 10 158-177
120	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 9.400e- 09 80-95
121	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 9.400e- 09 80-95
127	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 7.158e- 13 216-241
128	BL01032	Protein phosphatase 2C proteins.	BL01032C 6.14 3.195e- 12 147-157 BL01032H 11.25 5.680e-11 318- 331 BL01032G 8.33 8.932e-11 282-296 BL01032I 10.42 8.902e- 09 379-389
129	BL01310	ATP1G1 / PLM / MAT8 family proteins.	BL01310 14.74 6.694e- 26 28-64
130	PR00990	RIBOKINASE SIGNATURE	PR00990B 12.32 9.534e- 15 47-67 PR00990A 16.23 5.500e-14 20-42 PR00990C 12.62 2.412e- 09 119-133
133	BL00880	Acyl-CoA-binding protein.	BL00880 17.52 5.576e- 26 72-122
134	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 9.308e- 14 18-37
135	PR00215	NEUROMODULIN SIGNATURE	PR00215C 13.98 6.779e- 10 475-496
136	BL01310	ATP1G1 / PLM / MAT8 family proteins.	BL01310 14.74 2.432e- 29 71-107
140	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.882e- 14 214-231 BL00028 16.07 9.471e-14 102- 119 BL00028 16.07 2.800e-13 18-35

EQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		BL00028 16.07 5.500e-
		1	13 74-91 BL00028
		1	
		1	16.07 9.100e-13 186-
		1	203 BL00028 16.07
			8.043e-12 46-63
		1	BL00028 16.07 8.435e-
	1		12 130-147 BL00028
			16.07 9.217e-12 270-
			287 BL00028 16.07
	ì		6.192e-11 242-259
	İ	1	BL00028 16.07 4.000e-
		ļ .	10 158-175
	<u> </u>		BL00501D 16.69 9.538e-
41	BL00501	Signal peptidases I	
		serine proteins.	14 113-133 BL00501C
			9.61 8.688e-10 89-101
43	BL01020	SAR1 family proteins.	BL01020C 15.35 7.722e-
.43	БДОТОЕО	Dimin Tummer, P	20 79-130
		THE BINCER	PD01066 19.43 6.400e-
46	PD01066	PROTEIN ZINC FINGER	
		ZINC-FINGER METAL-	25 335-374
	1	BINDING NU.	
49	BL00126	3'5'-cyclic nucleotide	BL00126C 22.07 1.450e-
.27	1 2500120	phosphodiesterases	25 509-550 BL00126E
	1	proteins.	35.22 3.951e-16 654-
	i	proceins.	709 BL00126D 25.50
			1.360e-15 565-604
	ļ		BL00126B 15.20 8.200e-
			11 483-495 BL00126A
			27.56 8.269e-11 442-
			479
			BL00632 23.79 5.271e-
151	BL00632	Ribosomal protein S4	1
	1	proteins.	20 106-149
154	BL00559	Eukaryotic molybdopterin	BL00559I 13.63 5.304e-
174	1 2200000	oxidoreductases	19 29-58 BL00559K
		proteins.	13.17 2.957e-18 172-
		procerns.	199 BL00559J 19.63
			8.385e-13 99-151
			BL00559L 13.60 5.814e-
			12 241-259
155	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.692e-
100	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	RAS SIGNATURE	13 13-35
	D7 00406	Actins proteins.	BL00406D 12.58 2.547e-
157	BL00406	ACCINS Processes.	18 275-330 BL00406A
			9.95 5.776e-16 15-50
		1	
	1		BL00406B 5.47 7.429e-
		1	12 69-124 BL00406C
	1		6.75 9.682e-12 128-183
	-	Zinc carboxypeptidases,	BL00132A 26.07 7.000e-
160	BL00132	zinc-binding region 1	14 22-63 BL00132C
			21.35 3.466e-12 104-
	1	proteins.	1
		.	145
165	PR00109	TYROSINE KINASE	PR00109B 12.27 9.043e-
		CATALYTIC DOMAIN	13 139-158
		SIGNATURE	1
			BL00362 24.67 9.700e-
168	BL00362	Ribosomal protein S15	15 129-172
		proteins.	BL00039D 21.67 1.000e-
169	BL00039	DEAD-box subfamily ATP-	
	1	dependent helicases	35 640-686 BL00039A
		proteins.	18.44 1.964e-13 212-
	1	[251 BL00039B 19.19
	1		4.553e-13 378-404
	1		BL00039C 15.63 8.773e
	1		•
	[12 465-489
175	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 3.721e
1/3	1200333	RAS SIGNATURE	12 14-36
			BL01310 14.74 2.432e-
178	BL01310	ATPIG1 / PLM / MAT8	29 133-169
		family proteins.	PD01066 19.43 9.455e-
	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 9.455e-
179	1	ZINC-FINGER METAL-	

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.	DIOCKIFIION	KESOBIS.
	 	BINDING NU.	
180	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007B 14.16 7.429e- 20 160-180 PR00007A 19.33 4.938e-19 133- 160 PR00007C 15.60 1.225e-15 206-228 PR00007D 9.64 6.885e-
			11 238-249
181	BL00027	'Homeobox' domain	BL00027 26.43 9.526e-
		proteins.	24 280-323
182	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e- 24 263-306
183	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e- 24 280-323
184	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e- 24 263-306
188	PR00929	AT-HOOK-LIKE DOMAIN	PR00929C 5.26 3.328e-
		SIGNATURE	09 460-471
189	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	PR00929C 5.26 3.328e- 09 440-451
190 191 193 194	PR00450 PF00564 PR00503	Tyrosine specific protein phosphatases proteins. RECOVERIN FAMILY SIGNATURE Octicosapeptide repeat proteins. BROMODOMAIN SIGNATURE	BL00383F 15.51 7.188e- 17 666-682 BL00383A 13.34 8.714e-17 162- 177 BL00383E 10.35 1.000e-14 333-344 BL00383E 10.35 7.300e- 14 628-639 BL00383F 15.51 1.720e-13 371- 387 BL00383C 10.10 3.000e-13 217-228 BL00383D 11.92 7.000e- 13 295-308 BL00383B 7.61 1.692e-11 187-196 BL00383C 10.10 1.750e- 09 509-520 BL00383D 11.92 4.000e-09 589- 602 BL00383B 7.61 8.000e-09 479-488 PR00450C 12.22 7.911e- 15 83-105 PR00450C 12.22 6.286e-13 47-69 PF00564B 24.74 6.164e- 16 227-278 PR00503D 20.81 9.156e- 15 204-224 PR00503B 9.96 9.571e-13 170-187 BL00901C 20.63 3.429e-
197	BL00636	synthase/cystathionine beta-synthase P- phosphate att. Nt-dnaJ domain proteins.	18 67-117 BL00636A 8.07 6.211e-
171	9.00016	Nt-anau domain proteins.	17 40-57 BL00636B 15.11 2.000e-13 67-88
198	PR00690	ADHESIN FAMILY SIGNATURE	PR00690A 10.86 9.866e- 09 463-482
199	BL01131	Ribosomal RNA adenine dimethylases proteins.	BL01131A 26.62 2.343e- 12 84-130
201	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.352e- 12 509-522
203	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.286e- 10 39-72
206	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE	PR00261A 11.02 4.462e- 19 65-87 PR00261C 11.37 9.308e-19 65-87 PR00261D 12.47 2.667e- 18 65-87 PR00261B 14.12 4.000e-18 143- 165 PR00261A 11.02

SEO ID NO:	ACCESSION	DESCRIPTION	RESULTS*
SEQ ID NO:	NO.	DESCRIPTION	
	1.0.		4.833e-18 143-165
			PR00261D 12.47 7.500e-
	ļ		18 143-165 PR00261B
		•	14.12 5.065e-16 65-87
	Ì		PR00261C 11.37 8.967e-
	Ì		16 143-165 PR00261F
		1	11.57 4.938e-13 143-
			165 PR00261E 11.08
			7.188e-13 65-87
			PR00261F 11.57 7.188e-
			13 65-87 PR00261E
			11.08 1.643e-11 143-
			165
209	PF00791	Domain present in ZO-1	PF00791B 28.49 6.143e-
209	2200752	and Unc5-like netrin	13 118-173 PF00791C
		receptors.	20.98 7.680e-10 132-
		100cpto15.	171
	PR00007	COMPLEMENT C1Q DOMAIN	PR00007A 19.33 5.781e-
211	PROGOGY	SIGNATURE	19 131-158 PR00007B
		SIGNATORD	14.16 4.115e-18 158-
			178 PR00007C 15.60
		. 1	1.675e-15 201-223
		1	PR00007D 9.64 7.231e-
!	1	,	11 233-244
	77.001.03	Ubiquitin-conjugating	BL00183 28.97 1.545e-
212	BL00183	enzymes proteins.	30 43-91
		Ubiquitin-conjugating	BL00183 28.97 1.545e-
213	BL00183	enzymes proteins.	30 43-91
	57.0000	DEAD-box subfamily ATP-	BL00039D 21.67 1.900e-
215	BL00039		29 568-614 BL00039A
	1	dependent helicases	18.44 1.871e-23 21-60
	1	proteins.	BL00039C 15.63 1.720e-
]		11 364-388 BL00039B
	••		19.19 4.064e-11 277-
	•		1 '
			303 BL00100D 17.22 8.484e-
217	BL00100	Chloramphenicol	
İ		acetyltransferase	09 68-106
		proteins.	PR00213C 15.94 3.969e-
219	PR00213	MYELIN PO PROTEIN	11 199-227
		SIGNATURE	BL00678 9.67 1.947e-09
222	BL00678	Trp-Asp (WD) repeat	•
1		proteins proteins.	144-155
224	PR00875	MOLLUSC METALLOTHIONEIN	PR00875A 5.83 1.000e-
ł		SIGNATURE	09 901-913
225	BL00636	Nt-dnaJ domain proteins.	BL00636B 15.11 8.200e-
1			19 18-39
226	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 1.000e-
		1	21 21-38 BL00636B
i			15.11 8.200e-19 45-66
229	PR00301	70 KD HEAT SHOCK PROTEIN	PR00301F 13.98 7.563e-
1		SIGNATURE .	13 329-346 PR00301G
		1	13.78 4.300e-12 361-
	1		382
230	BL00460	Glutathione peroxidases	BL00460A 28.67 8.773e-
		selenocysteine proteins.	20 35-70 BL00460B
			9.73 7.429e-16 78-96
	- !	1	BL00460C 14.35 2.831e-
			12 111-134 BL00460D
			16.89 8.773e-11 140-
			160
231	PR00647	SENR ORPHAN RECEPTOR	PR00647B 10.19 8.522e-
231	EK00047	SIGNATURE	09 273-287
233	BL00292	Cyclins proteins.	BL00292B 20.31 7.429e-
233	PH00232	Cyclina processes.	27 244-275 BL00292A
1			22.87 7.750e-27 201-
1			235
224	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 6.308e-
234	EKOO##3	RAS SIGNATURE	13 7-29 PR00449C
1	i	I VUO OTGIVUTOVO	

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			17.27 4.462e-11 47-70 PR00449D 10.79 7.120e-
	-		11 109-123
235	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e- 10 251-265 PR00019B 11.36 5.320e-09 119- 133 PR00019B 11.36
			1.000e-08 229-243
236	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e- 10 245-259 PR00019B 11.36 5.320e-09 113- 127 PR00019B 11.36 1.000e-08 223-237
237	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYNA.	PD00289 9.97 8.448e-09 67-81
240	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e- 10 616-635
241	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e-
244	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 8.941e- 12 54-64
245	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 8.043e-
248	BL00246	Wnt-1 family proteins.	BL00246D 23.97 1.000e- 40 186-239 BL00246E 20.32 1.000e-40 305- 351 BL00246B 13.69 4.176e-36 105-140 BL00246A 15.75 2.286e- 24 70-90 BL00246C 15.56 4.857e-22 150- 175
250	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927E 14.93 5.114e- 10 253-275
254	BL00674	AAA-protein family proteins.	BL00674B 4.46 1.000e- 09 223-245
255	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 6.045e-
256	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 2.800e- 10 421-435
258	PR00094	ADENYLATE KINASE SIGNATURE	PR00094C 12.94 2.200e- 18 87-104 PR00094D 12.52 2.731e-14 161- 177 PR00094A 10.31 5.500e-14 11-25 PR00094B 11.01 4.115e- 13 39-54 PR00094E 11.25 7.333e-13 178- 193
259	BL00892	HIT family proteins.	BL00892A 18.17 5.500e- 13 60-91
262	BL00388 ·	Proteasome A-type subunits proteins.	BL00388A 23.14 1.000e- 40 8-54 BL00388B 31.38 3.864e-33 66-108 BL00388D 20.71 1.000e- 21 153-184 BL00388C 18.79 8.147e-16 126- 148
264	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 5.821e- 09 91-101
		Protein kinases ATP-	BL00107B 13.31 1.529e-
267	BL00107	binding region proteins.	09 241-257

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	 		23.86 8.043e-35 196-
	1		244 BL00226C 13.23
	İ		7.000e-20 261-292
			BL00226A 12.77 6.143e-
		ĺ	15 96-111
271	PD02952	KINASE TRANSFERASE	PD02952C 15.76 9.731e-
211	120235	CHOLINE PROTEIN	16 235-265 PD02952B
		MULTIGENE FAMI.	15.57 5.625e-09 215-
			229
272	PD02929	ADHESION GLYCOPROTEIN	PD02929A 28.27 1.000e-
212	1202323	PRECURSOR I.	40 106-160 PD02929B
	1		18.36 8.800e-17 179-
			199
004	BL01027	Glycosyl hydrolases	BL01027B 15.34 3.486e-
274	BLUIUZI	family 39 proteins.	09 213-250
	7700424	ADENOSINE RECEPTOR	PR00424D 14.32 6.451e-
275	PR00424	SIGNATURE	11 39-59
		Ribosomal protein S7	BL00052A 27.85 6.000e-
277	BL00052		13 137-184 BL00052B
		proteins.	15.17 5.143e-12 208-
	1		235
			BL00790N 13.25 5.659e-
279	BL00790	Receptor tyrosine kinase	13 267-294
		class V proteins.	PR00319D 11.64 6.625e-
280	PR00319	BETA G-PROTEIN	PR00319D 11.64 6.625e- 23 107-125 PR00319C
		(TRANSDUCIN) SIGNATURE	
		1	13.41 1.000e-21 89-105
			PR00319A 15.27 8.364e-
			21 51-68 PR00319B
			11.47 8.200e-19 70-85
281	PR00319	BETA G-PROTEIN	PR00319D 11.64 6.625e-
201		(TRANSDUCIN) SIGNATURE	23 94-112 PR00319C
		·	13.41 1.000e-21 76-92
			PR00319A 15.27 8.364e-
		1	21 38-55 PR00319B
			11.47 8.200e-19 57-72
287	PF00929	Exonuclease.	PF00929D 16.17 7.366e-
287	PEUUJZJ	2.10	09 149-163
	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e-
291	BD00326	110pomyobana padadasa	09 93-127
	7.00326	Tropomyosins proteins.	BL00326A 14.01 2.360e-
292	BL00326	Tropomyosins processes.	09 93-127
		PROTEIN ZINC-FINGER	PD00066 13.92 8.714e-
294	PD00066		12 203-216
		METAL-BINDI	BL00028 16:07 5.500e-
295	BL00028	Zinc finger, C2H2 type,	15 322-339 BL00028
	1	domain proteins.	16.07 9.471e-14 433-
	·		450 BL00028 16.07
			4.600e-13 648-665
			BL00028 16.07 5.500e-
			13 760-777 BL00028
	1	1	16.07 9.550e-13 788-
			805 BL00028 16.07
			3.348e-12 704-721
			BL00028 16.07 6.478e-
[12 461-478 BL00028
ļ			16.07 8.435e-12 844-
ļ			861 BL00028 16.07
1			1.692e-11 593-610
1			BL00028 16.07 2.038e-
}	1		11 211-228 BL00028
1	1		16.07 5.154e-11 732-
			749 BL00028 16.07
	1		5.846e-11 377-394
1			BL00028 16.07 6.885e-
		· ·	11 816-833 BL00028
1		i	16.07 7.231e-11 676-
	}	1	693 BL00028 16.07 9.654e-11 564-581
T C			

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			BL00028 16.07 4.086e- 09 517-534 BL00028 16.07 7.429e-09 489- 506
296	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 8.333e- 16 111-136 BL00215A 15.82 2.723e-11 10-35 BL00215B 10.44 9.526e- 11 152-165 BL00215B 10.44 7.375e-10 59-72 BL00215A 15.82 9.824e-
302	PF00953	Glycosyl transferase.	10 205-230 PF00953C 19.70 8.773e- 34 236-269 PF00953A 19.68 5.000e-25 102- 129 PF00953B 6.17
304	PF00152	tRNA synthetases class	1.000e-13 182-194 PF00152D 21.30 8.364e- 28 422-461 PF00152C 28.03 9.250e-21 220- 257 PF00152B 15.67 2.658e-13 159-184 PF00152A 19.68 5.714e- 11 44-67
305	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 8.250e- 35 37-76
305	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 5.840e- 09 92-135
307	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e- 09 1167-1186
308	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237E 13.03 5.091e- 13 188-212 PR00237G 19.63 7.207e-13 268- 295 PR00237A 11.48
:			4.375e-11 24-49 PR00237C 15.69 3.057e- 10 101-124 PR00237D 8.94 4.750e-10 137-159 PR00237F 13.57 5.364e- 10 230-255 PR00237B 13.50 9.438e-10 57-79
309	BL00522	DNA polymerase family X proteins.	BL00522C 11.90 7.577e- 24 315-339 BL00522F 14.90 1.310e-15 470- 494 BL00522A 25.52 1.265e-14 179-226 BL00522E-19.63 8.615e- 14 430-460 BL00522B 27.30 9.625e-12 267- 313
310	BL00326	Tropomyosins proteins.	BL00326D 8.76 5.235e- 10 856-897
312	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.706e- 14 151-174 BL00290B 13.17 9.000e-12 211- 229
313	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e- 40 34-85 BL00345A 13.96 9.217e-16 1-20
315	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 5.091e- 15 63-76
317	BL01020	SAR1 family proteins.	BL01020C 15.35 3.198e- 17 79-130
318	BL00216	Sugar transport proteins.	BL00216B 27.64 4.696e- 11 164-214
320	PR00109	TYROSINE KINASE CATALYTIC DOMAIN	PR00109B 12.27 4.814e- 10 216-235

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	
321	BL00027	'Homeobox' domain	BL00027 26.43 5.688e-
J21		proteins.	10 329-372
322	PR00109	TYROSINE KINASE	PR00109B 12.27 8.765e-
		CATALYTIC DOMAIN SIGNATURE	12 558-577
324	BL01241	Link domain proteins.	BL01241 35.81 8.313e-
			30 183-236 BL01241
			35.81 3.222e-13 282- 335
326	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 4.000e-
		proteins.	12 515-566 BL00412D
			16.54 5.705e-11 516-
			567 BL00412D 16.54
			7.848e-10 518-569 BL00412D 16.54 1.827e-
			09 514-565 BL00412D
		,	16.54 1.918e-09 513-
			564 BL00412D 16.54
			2.102e-09 520-571
220	BL00232	Cadherins extracellular	BL00232B 32.79 9.557e-
328	220022	repeat proteins domain	20 151-199 BL00232B
		proteins.	32.79 2.246e-18 41-89
		ļ ⁻	BL00232B 32.79 5.985e-
	ļ		18 370-418 BL00232B
			32.79 5.500e-16 258-
	1		306 BL00232B 32.79
			9.384e-15 475-523 BL00232C 10.65 2.537e-
			12 256-274 BL00232C
	1		10.65 4.326e-11 368-
			386 BL00232C 10.65
			7.261e-11 473-491
	1		BL00232C 10.65 7.457e-
			11 39-57
330	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e-
			09 1167-1186
331	BL00598	Chromo domain proteins.	BL00598 14.45 8.393e-
		Glycoprotease family	BL01016C 22.84 3.925e~
333	BL01016	proteins.	32 70-115 BL01016E
		proceins.	14.88 5.286e-19 149-
			177 BL01016H 13.71
			7.577e-13 291-301
			BL01016D 8.86 3.298e-
			11 127-140 BL01016G
			7.14 5.622e-10 261-271
			BL01016A 5.65 7.167e- 10 4-19 BL01016F
		1	13.34 1.563e-09 200-
		1	212 BL01016B 8.93
		1	8.855e-09 38-50
339	BL01115	GTP-binding nuclear	BL01115A 10.22 5.500e-
337		protein ran proteins.	11 17-61
340	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 1.231e-
		ZINC-FINGER METAL-	33 10-49
	ļ.	BINDING NU.	
341	BL01160	Kinesin light chain	BL01160B 19.54 5.042e-
		repeat proteins.	09 55-109
342	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 2.400e-
1		ZINC-FINGER METAL-	30 16-55
		BINDING NU.	DM00031A 16.80 1.000e-
343	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e-
<u> </u>			PR00109B 12.27 4.764e-
346	PR00109	TYROSINE KINASE	11 135-154
	1	CATALYTIC DOMAIN	TT 100 100
		SIGNATURE	1

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		CATALYTIC DOMAIN SIGNATURE	11 135-154
351	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 1.783e- 13 100-116 BL01187B 12.04 8.435e-13 276- 292 BL01187B 12.04 8.800e-11 13-29 BL01187B 12.04 7.429e- 10 54-70 BL01187B 12.04 5.725e-09 231- 247 BL01187A 9.98 7.000e-09 255-267
352	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e- 10 366-379 PD00078B 13.14 4.522e-09 168- 181
354	BL00380	Rhodanese proteins.	BL00380F 9.76 6.694e-
355	PF00628	PHD-finger.	PF00628 15.84 1.000e- 11 116-131
356	PR00587	SOMATOSTATIN RECEPTOR TYPE 1 SIGNATURE	PR00587A 8.06 9.700e- 09 17-37
359	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e- 15 261-274 PD00066 13.92 6.500e-13 233- 246 PD00066 13.92 4.300e-09 289-302
361	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 9.604e- 13 54-109 PF00791B 28.49 1.095e-12 21-76 PF00791A 27.85 1.432e- 09 71-126 PF00791B 28.49 7.440e-09 184- 239
362	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.273e- 11 279-334
363	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 5.080e- 10 73-95 PR00450C 12.22 3.278e-09 109- 131
364	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
365	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
366	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e- 09 1038-1092
367	PR.00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e- 09 229-243 PR00019B 11.36 6.040e-09 91-105 PR00019A 11.19 8.667e- 09 370-384
368	PR00011	TYPE III EGF-LIKE SIGNATURE	PRO0011D 14.03 9.000e- 15 30-49 PRO0011A 14.06 9.830e-15 30-49 PRO0011B 13.08 4.500e- 14 30-49 PRO0011C 24.25 5.143e-09 6-35
369	BL01032	Protein phosphatase 2C proteins.	BL01032H 11.25 4.150e- 09 417-430
372	BL00478	LIM domain proteins.	BL00478B 14.79 7.750e- 12 410-425
373	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.757e- 34 26-65
376	PR00170	SODIUM CHANNEL SIGNATURE	PR00170E 6.48 2.739e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		10 88-118
	DY 001 07	Protein kinases ATP-	BL00107A 18.39 1.000e-
380	BL00107	binding region proteins.	23 276-307 BL00107B
		binding region protession	13.31 1.692e-12 342-
			358
201	BL00455	Putative AMP-binding	BL00455 13.31 5.714e-
381	BL00455	domain proteins.	12 50-66
	PR00624	HISTONE H5 SIGNATURE	PR00624G 4.08 4.900e-
382	PR00624	HISTONE AS SIGNATORS	09 524-544
	PD00078	REPEAT PROTEIN ANK	PD00078B 13.14 5.950e-
384	PD00078	NUCLEAR ANKYR.	10 366-379 PD00078B
	l .	NOCHIMIC MINING	13.14 4.522e-09 168-
			181
	PR00511	TEKTIN SIGNATURE	PR00511D 7.11 5.371e-
385	PRUUSII	IBRITA BIOMITORE	09 67-80
205	PD02870	RECEPTOR INTERLEUKIN-1	PD02870B 18.83 6.000e-
386	PD02870	PRECURSOR.	10 97-130
	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 5.000e-
388	PD00066	METAL-BINDI.	13 516-529
	Dr 00000	Immunoglobulins and	BL00290A 20.89 7.667e-
389	BL00290	major histocompatibility	09 151-174
		complex proteins.	
300	BL00215	Mitochondrial energy	BL00215A 15.82 5.200e-
390	PPOOSTS	transfer proteins.	15 221-246 BL00215A
		crambter processis:	15.82 7.618e-14 20-45
			BL00215A 15.82 8.851e-
	1		11 123-148 BL00215B
			10.44 9.526e-11 69-82
		1	BL00215B 10.44 7.300e-
			09 272-285 BL00215B
			10.44 8.500e-09 165-
			178
394	BL00674	AAA-protein family	BL00674B 4.46 2.723e-
374	2200074	proteins.	16 299-321
397	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 8.579e-
391	1.00040	SIGNATURE	11 141-155
398	PR00761	BINDIN PRECURSOR	PR00761B 9.93 6.764e-
320		SIGNATURE	09 55-74
399	BL00240	Receptor tyrosine kinase	BL00240B 24.70 7.907e-
		class III proteins.	10 118-142
401	PF00676	Dehydrogenase E1	PF00676B 24.71 8.071e-
101		component.	18 331-369 PF00676D
		_	14.40 3.854e-15 486-
,		,	506 PF00676C 16.88
			9.182e-14 454-478
402	BL00514	Fibrinogen beta and	BL00514C 17.41 4.673e-
		gamma chains C-terminal	28 4432-4469 BL00514G
		domain proteins.	15.98 6.092e-14 4555-
		j	4585 BL00514D 15.35
1			2.532e-12 4473-4486
		1	BL00514F 11.65 4.288e-
		,	10 4519-4534 BL00514H
	ł	1	14.95 4.955e-10 4584-
ļ.			4609
403	PF00992	Troponin.	PF00992A 16.67 5.974e-
1			09 105-140
404	PR00019	LEUCINE-RICH REPEAT	PR00019B 11.36 1.450e-
l .	1	SIGNATURE	10 73-87 PR00019A
			11.19 8.043e-10 76-90
1			PR00019B 11.36 1.000e-
			09 50-64 PR00019B
	ļ		11.36 1.000e-09 96-110
405	BL00232	Cadherins extracellular	BL00232B 32.79 9.557e-
		repeat proteins domain	20 139-187 BL00232B
		proteins.	32.79 2.246e-18 29-77
1		\ -	BL00232B 32.79 5.985e-
			18 358-406 BL00232B
1	1	i	32.79 5.500e-16 246-

000 70 500	T 2 000000 - 000	LDECONTRACM	DEGIT MC+
SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	1.0.		294 BL00232B 32.79
			9.384e-15 463-511
			BL00232C 10.65 2.537e- 12 244-262 BL00232C
			10.65 4.326e-11 356-
			374 BL00232C 10.65
			7.261e-11 461-479
		1	BL00232C 10.65 7.457e-
405	D700406	Other Contidents VD4	11 27-45 PF00426S 15.67 5.634e-
407	PF00426	Outer Capsid protein VP4 (Hemagglutinin).	09 902-940
409	BL01160	Kinesin light chain	BL01160B 19.54 9.695e-
		repeat proteins.	09 126-180
410	BL00741	Guanine-nucleotide	BL00741B 14.27 2.731e-
		dissociation stimulators CDC24 family sign.	09 252-275
411	PF00646	F-box domain proteins.	PF00646A 14.37 6.344e-
		·	09 86-100
412	BL00603	Thymidine kinase	BL00603B 11.39 8.500e-
415	PLOOSE	cellular-type proteins. Carbamoyl-phosphate	09 542-557 BL00866B 36.29 3.571e-
415	BL00866	carbamoyi-phosphate synthase subdomain	31 245-291 BL00866C
	[proteins.	23.26 9.000e-25 331-
		<u> </u>	366
418	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239E 1.58 6.114e-
421	PF00791	TERMINAL TAIL SIGNATURE Domain present in ZO-1	PF00791B 28.49 7.955e-
321	F F 00 / 9 1	and Unc5-like netrin	14 23-78 PF00791B
		receptors.	28.49 3.653e-12 273-
	i		328 PF00791B 28.49
			4.273e-11 156-211 PF00791B 28.49 7.818e-
			11 89-144 PF00791B
			28.49 1.524e-10 56-111
			PF00791C 20.98 3.559e-
			09 37-76 PF00791C
			20.98 5.235e-09 170- 209 PF00791C 20.98
-			5.235e-09 381-420
			PF00791B 28.49 6.202e-
:			09 189-244 PF00791B 28.49 7.028e-09 435-
•	ł		490 PF00791B 28.49
1			8.679e-09 367-422
424	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 7.207e-
425	DD00100	COURSE VILVA OR	28 1645-1679
425	PR00109	TYROSINE KINASE CATALYTIC DOMAIN	PR00109D 17.04 5.881e-
		SIGNATURE	
429	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 4.600e-
		(RING finger), proteins.	11 31-40
431	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 1.844e- 34 490-536 BL00039A
		dependent helicases proteins.	18.44 5.615e-19 205-
	1		244 BL00039B 19.19
			8.920e-16 251-277
			BL00039C 15.63 5.781e-
432	PR00452	SH3 DOMAIN SIGNATURE	15 333-357 PR00452B 11.65 7.652e-
4 44	FR00452	SILS DOWNIN SIGNATURE	12 169-185
433	PR00828	FORMIN SIGNATURE	PR00828B 5.23 8.218e-
<u></u>		<u> </u>	10 382-405
436	BL00415	Synapsins proteins.	BL00415N 4.29 8.643e-
			11 195-239 BL00415N 4.29 3.036e-09 809-853
443	PR00834	HTRA/DEGO PROTEASE	PR00834F 10.91 6.040e-
	-3.00003	FAMILY SIGNATURE	11 221-234
446	PF01140	Matrix protein (MA),	PF01140D 15.54 9.663e-
			

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		p15.	10 183-218 PF01140D 15.54 3.093e-09 246- 281
449	PR00568	DOPAMINE D3 RECEPTOR SIGNATURE	PR00568G 13.95 5.551e- 09 39-53
451	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 3.813e- 10 47-59
452	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.821e- 09 618-649
456	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 1.000e- 25 77-99 PR00380D 9.93 1.000e-21 281-303 PR00380C 13.18 8.286e- 17 230-249 PR00380B 12.64 4.724e-16 194- 212
457	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 9.143e- 24 246-267 PR00253B 13.47 2.000e-23 272- 294 PR00253C 13.85 7.000e-23 306-328 PR00253D 16.68 5.950e- 21 452-473
467	PR00849	GLYCOSYL HYDROLASE FAMILY 58 SIGNATURE	PR00849D 9.77 9.236e- 09 910-937 BL00678 9.67 8.200e-12
471	BL00678	Trp-Asp (WD) repeat proteins proteins.	33-44 BL00226B 23.86 3.721e-
472	BL00226	Intermediate filaments proteins.	09 282-330 BL00344 17.99 7.000e-
473	BL00344	GATA-type zinc finger domain proteins.	12 814-852 BL00481E 13.07 8.909e-
474	BL00481	Thiol-activated cytolysins proteins. BETA G-PROTEIN	09 173-199 PR00319B 11.47 2.571e-
479	PR00319	(TRANSDUCIN) SIGNATURE	09 393-408 PD01066 19.43 1.900e-
480	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	38 8-47
481	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405C 19.41 1.000e- 19 451-473 PR00405B 11.83 4.333e-18 430- 448 PR00405A 17.71 4.971e-18 411-431
482	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.286e- 10 959-974 PR00049D 0.00 9.857e-10 958-973 PR00049D 0.00 1.305e- 09 937-952 PR00049D 0.00 8.322e-09 939-954
486	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007B 14.16 8.615e- 23 653-673 PR00007A 19.33 6.192e-22 626- 653 PR00007C 15.60 5.846e-19 698-720 PR00007D 9.64 3.647e- 13 732-743
487	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567B 18.23 2.853e- 09 200-214
488	PR00988	URIDINE KINASE SIGNATURE	12 3-21
489	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 4.882e- 27 30-69 PD01066 19.43 3.430e-10 71-110
490	PR00049	BINDING NU. WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.864e- 09 663-678
492	BL01128	Shikimate kinase proteins.	BL01128A 18.84 6.464e- 17 58-92
497	PF00429	ENV polyprotein (coat	PF00429 31.08 7.171e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		polyprotein).	15 21-71
498	BL00120	Lipases, serine proteins.	BL00120B 11.37 7.923e- 09 185-200
500	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.353e- 11 299-318
501	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 8.579e- 12 131-146
505	BL00021	Kringle domain proteins.	BL00021B 13.33 3.739e- 17 492-510
508	PR00120	H+TRANSPORTING ATPASE (PROTON PUMP) SIGNATURE	PR00120C 9.90 5.800e-
509	DM01417	6 kw INDUCING XPMC2 MUSHROOM SPAC22G7.04.	DM01417E 20.62 2.938e- 16 362-395 DM01417D 11.08 3.800e-13 322- 338
510	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e-
511	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e- 09 293-317
512	PF00534	Glycosyl transferases	PF00534B 14.47 6.625e-
513	PD01841	group 1. PHOSPHORYLASE KINASE ALPHA MUSCL.	09 366-390 PD01841A 21.71 1.000e-40 110-160 PD01841B 14.35 1.000e-40 181-222 PD01841D 17.87 1.000e-40 243-295 PD01841F 13.36 1.000e-40 333-382 PD01841G 24.26 1.000e-40 386-40 PD01841L 18.42 1.000e-40 968-1010 PD01841I 23.00 4.545e-37 762-804 PD01841E 18.60 3.750e-36 295-333 PD01841J 14.94 6.023e-35 851-888 PD01841H 21.30 2.909e-33 490-527 PD01841K 14.81 7.088e-33 924-954 PD01841C 13.78 9.386e-23 222-243 PD01841M 10.82 8.594e-21 1054-1073 PD01841I 23.00 2.667e-13 549-591
514	PR00153	CYCLOPHILIN PEPTIDYL- PROLYL CIS-TRANS ISOMERASE SIGNATURE	PR00153C 11.01 7.188e- 13 95-111 PR00153E
515	BL00740	MAM domain proteins.	9.10 4.150e-12 122-138 BL00740A 13.87 7.188e- 12 410-423
516	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 6.087e-
517	BL00242	Integrins alpha chain proteins.	BL00242C 16.86 8.320e- 09 12-42
523	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e- 39 20-68 DM00031B 15.41 1.000e-25 84-118
525	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 8.375e- 10 61-95
526	PF00789	Domain present in ubiquitin-regulatory proteins.	PF00789B 19.70 3.308e- 12 322-343 PF00789C 20.98 5.269e-09 367- 392
528	BL01162	Quinone oxidoreductase / zeta-crystallin proteins.	BL01162C 22.80 1.500e- 16 120-164

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
529	PR00910	LUTEOVIRUS ORF6 PROTEIN	PR00910A 2.51 3.893e-
323	-1100520	SIGNATURE	09 60-73
532	BL00215	Mitochondrial energy	BL00215A 15.82 4.000e-
		transfer proteins.	17 11-36 BL00215A
			15.82 8.660e-11 123-
	BL00215	Mitochondrial energy	BL00215A 15.82 4.000e-
533	BT00512	transfer proteins.	17 11-36 BL00215A
		Crambrez process.	15.82 8.660e-11 97-122
534	BL00098	Thiolases acyl-enzyme	BL00098C 21.65 2.800e-
		intermediate proteins.	38 181-227 BL00098B
			32.59 5.345e-38 86-141
			BL00098D 26.30 8.364e- 35 245-288 BL00098E
			22.12 1.000e-34 314-
			352 BL00098F 10.18
	ļ		4.971e-22 365-386
			BL00098A 10.60 6.455e-
			11 38-50 PR00370E 11.96 7.429e-
535	PR00370	FLAVIN-CONTAINING	PR00370E 11.96 7.429E-
		MONOOXYGENASE (FMO) SIGNATURE	16.33 6.143e-21 185-
		D L DIVILLE DILLE	204 PR00370F 17.75
	1		6.559e-21 376-396
			PR00370B 10.91 9.591e-
			21 27-46 PR00370C 12.72 3.500e-20 140-
			157 PR00370A 3.35
			6.442e-17 4-20
536	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.429e-
		domain proteins.	16 285-302 BL00028
	•		16.07 6.294e-14 341- 358 BL00028 16.07
ļ			1.346e-11 369-386
			BL00028 16.07 1.692e-
			11 397-414 BL00028
			16.07 4.462e-11 453-
			470 BL00028 16.07 7.231e-11 425-442
			BL00028 16.07 4.300e-
	•		10 313-330
537	BL00762	WHEP-TRS domain	BL00762A 23.43 9.419e-
		proteins.	15 844-881
538	BL00762	WHEP-TRS domain	BL00762A 23.43 9.419e-
	1	proteins.	15 819-856 BL00762A 23.43 9.419e-
539	BL00762	WHEP-TRS domain . proteins.	15 822-859
540	PR00985	LEUCYL-TRNA SYNTHETASE	PR00985A 12.10 9.000e-
		SIGNATURE	10 357-375
541	PD02102	SUBUNIT E V-ATPASE	PD02102A 16.74 1.000e-
1		VACUOLAR ATP SYNTHASE	40 3-47 PD02102B
		HYDROL.	18.28 4.375e-34 57-100 PD02102D 21.69 1.923e-
			30 179-218 PD02102C
			26.34 8.929e-26 100-
			146
543	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 1.000e-
		domain proteins.	10 48-65 BL00028
			16.07 6.400e-10 193- 210 BL00028 16.07
}			1.000e-09 343-360
			BL00028 16.07 6.914e-
			09 78-95
545	BL00250	TGF-beta family	BL00250A 21.24 8.000e-
		proteins.	31 293-329 BL00250B
			27.37 5.286e-24 354- 390
547	PR00319	BETA G-PROTEIN	PR00319B 11.47 2.714e-
1	1		

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		(TRANSDUCIN) SIGNATURE	09 186-201 PR00319A 15.27 7.344e-09 210-
548	ВЬ01204	NF-kappa-B/Rel/dorsal domain proteins.	BL01204A 17.74 1.000e- 40 8-56 BL01204D 16.42 1.000e-40 177- 221 BL01204E 13.83 7.652e-30 225-250 BL01204C 13.93 8.714e- 22 141-160 BL01204B 15.41 4.333e-16 102- 116
549	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.364e-
551	PF00632	HECT-domain (ubiquitin- transferase).	PF00632C 20.66 3.302e- 23 1569-1601 PF00632B 18.45 3.700e-21 1515- 1543
554	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 1.600e- 14 187-205 BL00290A 20.89 2.059e-14 130- 153
557	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.339e- 09 846-879
559	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111L 11.93 3.762e- 09 7-35
562	PF00658	Poly-adenylate binding protein, unique domain proteins.	PF00658C 16.33 9.455e- 32 118-155
564	BL00141	Bukaryotic and viral aspartyl proteases proteins.	BL00141A 12.10 4.150e- 10 472-488
566	PF00855	PWWP domain proteins.	PF00855 13.75 5.667e- 15 272-289
567	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.977e- 13 229-268
569	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183- 199
570	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183- 199
572	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e- 34 454-483 PR00193C 12.60 2.636e-31 223- 251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 508- 537
573	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e-34 470-499 PR00193C 12.60 2.636e-31 239-267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e-22 115-135 PR00193E 19.47 6.559e-19 524-553
575 576	BL00752 BL00030	XPA protein. Eukaryotic RNA-binding	BL00752B 19.17 9.703e- 10 885-929 BL00030A 14.39 7.000e-
		region RNP-1 proteins.	09 276-295
577	BL00116	DNA polymerase family B	BL00116A 12.81 5.737e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins.	13 864-877 BL00116B 11.82 1.529e-12 952- 965
578	BL00195	Glutaredoxin proteins.	BL00195B 15.31 7.158e- 09 121-141
579	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PRO0019B 11.36 9.000e- 11 217-231 PR00019B 11.36 1.360e-09 386- 400 PR00019A 11.19 3.333e-09 389-403 PR00019B 11.36 8.920e- 09 363-377
580	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 2.125e- 25 275-296 PR00253B 13.47 7.923e-24 301- 323 PR00253D 16.68 5.846e-23 444-465 PR00253C 13.85 2.241e- 20 335-357
583	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 2.286e- 11 1233-1252 PR00343C 16.85 5.500e-11 333- 352 PR00343C 16.85 5.500e-11 783-802 PR00343C 16.85 4.246e- 10 1491-1510 PR00343C 16.85 8.230e-10 1686- 1705
584	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 1.878e- 37 79-126 DM01537B 21.63 9.491e-30 916- 963 DM01537A 15.14 3.186e-11 784-804
586	PF00013	KH domain proteins family of RNA binding proteins.	PF00013 5.78 1.450e-09 124-136
587	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 4.409e- 13 262-296
589	BL00478	LIM domain proteins.	BL00478B 14.79 1.643e- 13 261-276 BL00478B 14.79 7.709e-09 321- 336
590	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 931-948
591	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 1062-1079
593	PF00628	PHD-finger.	PF00628 15.84 3.455e- 12 424-439
594	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 2.241e- 16 558-576 PR00205A 14.73 9.308e-13 542- 558 PR00205C 13.65 5.304e-12 594-609 PR00205B 11.39 4.273e- 10 336-354
596	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 4.789e- 18 307-338
598	PD01675	GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3.	PD01675C 19.89 2.330e- 10 55-89
600	BL00242	Integrins alpha chain proteins.	BL00242E 9.03 9.591e- 27 985-1014 BL00242C 16.86 4.115e-26 286- 316 BL00242D 13.57 4.150e-25 357-382 BL00242B 8.13 7.353e- 12 189-199 BL00242D 13.57 3.455e-11 421- 446 BL00242A 13.80

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.		5.000e-11 61-73 BL00242D 13.57 4.986e-
601	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	10 291-316 PR00320A 16.74 5.610e- 09 198-213
602	PR00278	PANCREATIC HORMONE SIGNATURE	PR00278A 12.43 4.569e- 10 331-348
603	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479C 12.01 3.250e- 12 170-183
604	BL00315	Dehydrins proteins.	BL00315A 9.35 1.672e- 09 424-452
605	BL00415	Synapsins proteins.	BL00415N 4.29 9.794e- 10 295-339
606	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 1.000e- 13 335-358
608	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e- 15 265-282
609	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e- 15 211-228
612	DM01206	CORONAVIRUS NUCLEOCAPSID . PROTEIN .	DM01206B 10.69 7.411e- 10 877-897 DM01206B 10.69 8.027e-10 861- 881 DM01206B 10.69 9.137e-10 873-893 DM01206B 10:69 1.456e- 09 859-879 DM01206B 10.69 1.797e-09 879- 899 DM01206B 10.69 4.076e-09 865-885 DM01206B 10.69 7.038e- 09 898-918 DM01206B 10.69 7.949e-09 871- 891 DM01206B 10.69 8.291e-09 767-787
615	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699A 8.91 2.023e- 28 129-158 PD02699C 24.84 1.000e-27 317- 364 PD02699B 18.28 1.000e-17 158-182
616	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455
617	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455
618	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535- 555
621	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 3.160e- 21 561-582
622	BL00239	Receptor tyrosine kinase class II proteins.	BL00239F 28.15 3.222e- 10 647-692 BL00239C 18.75 8.304e-10 543- 566
623	PR00407	EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	PR00407K 9.94 8.448e- 09 326-339
624	BL00641	Respiratory-chain NADH	BL00641C 21.10 1.000e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		subunit proteins.	24.37 1.000e-40 255- 308 BL00641F 33.12 1.000e-40 571-623 BL00641A 17.15 1.818e- 37 48-80 BL00641B 12.62 5.846e-34 113- 139 BL00641D 13.23 9.308e-29 216-240
627	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE	PR00103E 17.80 2.500e- 18 367-380 PR00103B 13.39 2.080e-14 297- 312 PR00103A 9.59 2.957e-14 282-297 PR00103D 10.83 3.077e- 12 346-358 PR00103C 15.68 1.000e-11 334- 344 PR00103B 13.39 1.450e-11 175-190 PR00103A 9.59 1.720e- 10 160-175
630	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081A 10.53 6.211e- 16 4-22
631	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 8.500e- 14 37-50
632	DM01205	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 2.233e- 10 1324-1344 DM01206B 10.69 4.822e-10 1276- 1296 DM01206B 10.69 7.658e-10 1328-1348 DM01206B 10.69 8.274e- 10 1280-1300 DM01206B 10.69 4.532e-09 1320- 1340 DM01206B 10.69 7.266e-09 1326-1346
635	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.600e- 23 145-176 BL00107B 13.31 2.636e-13 211- 227
636	BL00657	Fork head domain proteins.	BL00657A 19.39 1.545e- 30 101-143 BL00657B 22.27 7.750e-26 149- 192
637	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 10 607-623
643	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 4.913e-09 199-212
647	PF00628	PHD-finger.	PF00628 15.84 2.350e- 13 385-400 PF00628 15.84 3.455e-12 464- 479
648	BL01129	Hypothetical yabO/yceC/sfhB family proteins.	BL01129E 13.25 4.000e- 25 332-357 BL01129C 25.56 8.200e-23 236- 279 BL01129B 12.51 6.118e-13 191-212
649	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 3.908e- 10 455-480
650	BL00027	'Homeobox' domain proteins.	BL00027 26.43 6.684e- 13 771-814
651	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 1.750e- 12 1026-1045
653	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 4.000e- 24 253-274 PR00253C 13.85 8.800e-24 313- 335 PR00253B 13.47 3.143e-22 279-301 PR00253D 16.68 7.652e-

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
			20 422-443
654	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 4.452e- 11 969-997 PD01719A 12.89 3.961e-10 128- 156 PD01719A 12.89 7.395e-10 1276-1304 PD01719A 12.89 1.222e- 09 1220-1248
657	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 8.397e- 09 563-578
658	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 8.397e- 09 580-595
659	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.174e- 13 539-572 DM00215 19.43 4.750e-12 549- 582 DM00215 19.43 9.824e-11 551-584 DM00215 19.43 2.929e- 10 548-581 DM00215 19.43 4.054e-10 550- 583 DM00215 19.43 5.339e-10 552-585 DM00215 19.43 7.107e- 10 544-577
660	PR00688	XYLOSE ISOMERASE SIGNATURE	PR00688I 13.78 9.518e- 09 224-236
661	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.950e- 23 249-292
662	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
663	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
664	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
666	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 8.988e-
667	BL50040	Elongation factor 1 gamma chain profile.	BL50040C 22.62 2.143e- 16 135-178
668	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e- 09 139-153 PR00019A 11.19 1.667e-09 94-108 PR00019B 11.36 4.600e- 09 163-177
670	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 3.250e-10 681-694 BL00018 7.41 6.400e-10 717-730
672	PD00131	ATP-BINDING TRANSPORT TRANSMEMBR.	PD00131B 34.97 1.000e- 34 356-410 PD00131C 19.59 1.346e-26 504- 542
673	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	PR00667G 15.33 7.557e- 10 106-123
674	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 593-608 PR00320B 12.19 4.115e-12 635- 650 PR00320C 13.01 8.435e-11 717-732 PR00320C 13.01 2.800e- 10 635-650 PR00320C 13.01 6.400e-10 593- 608 PR00320B 12.19 3.250e-09 593-608
675	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 572-587 PR00320B 12.19 4.115e-12 614-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	-		629 PR00320C 13.01
			8.435e-11 696-711
			PR00320C 13.01 2.800e-
	1		10 614-629 PR00320C
	1		13.01 6.400e-10 572-
			587 PR00320B 12.19
			3.250e-09 572-587
676	PR00019	LEUCINE-RICH REPEAT	PR00019A 11.19 9.667e-
		SIGNATURE	09 249-263
679	PF00642	Zinc finger C-x8-C-x5-C-	PF00642 11.59 3.700e-
		x3-H type (and similar).	16 225-236 PF00642
	<u> </u>		11.59 7.900e-12 187-
			198 PR00308C 3.83 8.754e-
680	PR00308	TYPE I ANTIFREEZE	10 286-296
		PROTEIN SIGNATURE	BL00019D 15.33 4.200e-
681	BL00019	Actinin-type actin-	BL00019D 15.33 4.200e- 19 227-257
		binding domain proteins.	PR00700D 12.47 4.000e-
682	PR00700	PROTEIN TYROSINE	09 99-118
		PHOSPHATASE SIGNATURE	PR00049D 0.00 8.500e-
687	PR00049	WILM'S TUMOUR PROTEIN	10 538-553
		SIGNATURE	BL01024A 10.26 1.000e-
689	BL01024	Protein phosphatase 2A	40 22-69 BL01024B
		regulatory subunit PR55	8.91 1.000e-40 86-127
		proteins.	BL01024C 7.80 1.000e-
			40 146-185 BL01024D
			13.22 1.000e-40 185-
			222 BL01024E 11.96
			1.000e-40 222-266
			BL01024F 9.42 1.000e-
			40 266-317 BL01024G
			11.09 1.000e-40 317-
			349 BL01024H 13.88
	1		1.000e-40 389-442
601	BL00027	'Homeobox' domain	BL00027 26.43 8.071e-
691	BE00027	proteins.	31 152-195
692	BL00211	ABC transporters family	BL00211A 12.23 5.050e-
032	PHOOFIE	proteins.	09 45-57
693	BL00211	ABC transporters family	BL00211A 12.23 5.050e-
	2200222	proteins.	09 45-57
694	BL00211	ABC transporters family	BL00211A 12.23 5.050e-
051		proteins.	09 58-70
696	BL00680	Methionine	BL00680 14.37 5.304e-
	' '	aminopeptidase subfamily	17 173-195
		1 proteins.	
697	BL00741	Guanine-nucleotide	BL00741B 14.27 3.418e-
~~ .		dissociation stimulators	11 242-265
1		CDC24 family sign.	
698	DM01930	2 kw FINGER SMCX SMCY	DM01930E 15.41 1.367e-
1		YDR096W.	37 170-215 DM01930F
1			14.16 8.232e-28 267-
			303 DM01930B 19.86
1			9.163e-10 37-71
700	PR00869	DNA-POLYMERASE FAMILY X	PR00869A 12.80 1.281e-
		SIGNATURE	16 245-263
701	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 2.174e-
		SIGNATURE	10 77-91 PR00048A
	,		10.52 6.870e-10 133- 147 PR00048A 10.52
		l l	8.826e-10 105-119
			PR00048A 10.52 5.320e-
1			09 161-175
702	BL00523	Sulfatases proteins.	BL00523E 19.27 2.565e- 25 326-356 BL00523A
		1	25 326-356 BH00523A
			13.36 5.050e-16 38-55 BL00523B 8.64 5.909e-
Ì		1	15 86-98 BL00523C
			15 86-98 BL00323C 12.64 5.500e-13 137-
1	1	ī	1 12.64 3.5006-13 13/-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
-			148 BL00523D 9.89 1.844e-11 290-302 BL00523G 9.46 5.500e- 10 513-523 BL00523F 10.85 6.351e-09 413- 424
703	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.412e- 12 376-390 PR00048B 6.02 1.000e-10 334-344 PR00048B 6.02 1.474e-
707	PD00787	SYNTHASE BIOSYNTHESIS TRANSFERASE.	09 364-374 PD00787A 14.84 8.941e- 14 66-82
708	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761E 14.32 8.500e- 10 822-841
712	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354Y 10.69 4.977e- 38 425-465 DM01354X 13.86 7.300e-34 376- 415 DM01354V 12.97 4.923e-17 311-358 DM01354W 12.64 5.596e- 10 356-376
713	BF00035	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 7.545e- 27 450-496 BL00039A 18.44 2.537e-18 147- 186 BL00039C 15.63 2.216e-14 280-304 BL00039B 19.19 1.947e- 13 194-220
715	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383E 10.35 4.981e- 10 150-161
717	PF00777	Sialyltransferase family.	PF00777C 18.60 4.035e- 21 106-161
718	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e- 39 20-68 DM00031B 15.41 2.688e-28 84-118 DM00031C 12.79 1.300e- 12 131-142
719	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243B 17.54 1.000e- 40 131-172 BL00243C 16.42 1.000e-40 172- 208 BL00243D 24.07 1.000e-40 222-274 BL00243F 22.63 1.000e- 40 314-358 BL00243I 31.77 6.571e-39 607- 650 BL00243E 16.70 3.077e-35 274-304 BL00243G 21.38 3.625e- 34 358-400 BL00243H 17.53 5.235e-29 567- 593 BL00243A 17.61 3.250e-21 63-84 BL00243H 17.53 7.167e- 16 477-503 BL00243H 17.53 2.304e-11 524- 550 BL00243H 17.53 5.304e-11 606-632 BL00243I 31.77 1.380e- 09 610-653
720	PR00217	43 KD POSTSYNAPTIC	PR00217C 10.91 8.022e-
722	PR00704	PROTEIN SIGNATURE CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE	09 20-36 PR00704D 11.05 5.909e- 34 135-161 PR00704F 13.61 7.000e-26 190- 218 PR00704E 12.55 8.071e-26 165-189

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.		PR00704B 17.94 2.241e-
		1	23 75-98 PR00704A
		ł	14.68 4.094e-19 30-54
			PR00704C 11.88 1.871e-
			18 99-116
725	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e-
			09 169-187 PR00194A 7.86 7.652e-
726	PR00194	TROPOMYOSIN SIGNATURE	09 169-187
		TO THE PROPERTY OF THE ACC	PR00320C 13.01 2.125e-
727	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	13 277-292 PR00320A
		REPEAT SIGNATURE	16.74 1.310e-11 277-
			292 PR00320C 13.01
		•	4.522e-11 323-338
			PR00320A 16.74 6.586e-
			11 323-338 PR00320B
			12.19 4.343e-10 323-
			33B PR00320B 12.19
			6.914e-10 277-292
731	PR00195	DYNAMIN SIGNATURE	PRO0195A 11.94 8.627e- 16 288-307 PR00195E
			9.82 3.912e-11 457-474
		Zinc finger C-x8-C-x5-C-	PF00642 11.59 9.082e-
733	PF00642	x3-H type (and similar).	10 787-798
	77.00020	DEAD-box subfamily ATP-	BL00039A 18.44 2.565e-
738	BL00039	dependent helicases	28 26-65 BL00039D
		proteins.	21.67 2.105e-20 338-
		processes.	384 BL00039C 15.63
			9.100e-13 160-184
			BL00039B 19.19 9.617e-
			11 73-99
739	BL01289	TSC-22 / dip / bun	BL01289A 12.18 8.909e-
	1	family proteins.	31 326-353 BL01289B
			10.45 9.571e-17 353-
			383
742	BL01019	ADP-ribosylation factors	BL01019A 13.20 7.078e- 12 41-81
		family proteins. Phosphomannose isomerase	BL00965C 23.78 1.000e-
743	BL00965	type I proteins.	40 256-305 BL00965B
		cype i proceina.	17.77 1.600e-25 126-
		· ·	153 BL00965A 10.57
			6.400e-19 94-113
747	BL00021	Kringle domain proteins.	BL00021D 24.56 4.563e-
, . ,			25 231-273 BL00021B
			13.33 5.345e-21 60-78
748	BL00612	Osteonectin domain	BL00612B 11.35 2.034e-
		proteins.	11 93-126
749	PR00450	RECOVERIN FAMILY	PR00450C 12.22 6.880e-
		SIGNATURE	10 135-157 BL00795C 17.06 6.000e-
752	BL00795	Involucrin proteins.	11 384-429 BL00795C
		i	17.06 9.444e-11 370-
			415
	DT 00053	Ribosomal protein L39e	BL00051 20.92 1.935e-
754	BL00051	proteins.	16 4-50
	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 7.723e-
755	DMOTATO	ENDOSOMAL III.	09 171-184
760	BL01020	SAR1 family proteins.	BL01020C 15.35 9.020e-
760	5501020	Drait tomitty processio.	12 99-150
762	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e-
102	12200040	The production of the producti	40 33-88
763	PD02411	PROTEIN TRANSCRIPTION	PD02411 21.89 9.137e-
, 03		REGULATION NUCLEAR.	10 206-240
764	BL00027	'Homeobox' domain	BL00027 26.43 8.800e-
	1	proteins.	29 417-460
767	BL01208	VWFC domain proteins.	BL01208B 15.83 6.063e-
j		-	10 309-324 BL01208B 15.83 8.031e-10 165-
		•	1 1 5 02 0 0210 10 165-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	1.0.		180 BL01208B 15.83
			4.162e-09 85-100
770	BL00031	Nuclear hormones	BL00031A 19.55 9.571e-
		receptors DNA-binding	32 -208-241 BL00031B
1	1	region proteins.	22.25 5.500e-27 242-
	<u>l</u>		274
772	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.450e-
		RAS SIGNATURE	18 4-26 PR00449E
}			13.50 3.520e-14 142-
ł	1	1	165 PR00449C 17.27
	İ		3.032e-13 44-67
	f		PR00449D 10.79 8.579e-
			13 107-121 PR00449B
773	BL00523	0.76	14.34 3.455e-11 27-44
173	BE00223	Sulfatases proteins.	BL00523E 19.27 9.333e-
			23 299-329 BL00523A 13.36 2.200e-13 47-64
	ì		BL00523B 8.64 2.607e-
			13 91-103 BL00523D
			9.89 7.923e-12 224-236
]	1	BL00523C 12.64 4.512e-
			10 141-152 BL00523F
			10.85 5.821e-10 373-
			384
775	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
		domain proteins.	09 568-585
776	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
		domain proteins.	09 621-638
777	ВL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
880		domain proteins.	09 595-612
778	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 8.412e-
		region RNP-1 proteins.	11 322-341 BL00030A
	ì	i	14.39 7.000e-10 220- 239
779	PR00079	GLUCOSE-6-PHOSPHATE	PR00079B 12.98 2.929e-
	- Autoria	DEHYDROGENASE SIGNATURE	26 193-222 PR00079E
			16.65 4.150e-23 348-
		1	375 PR00079C 8.68
			6.351e-16 246-264
	;		PR00079D 13.51 7.070e-
:			16 264-281 PR00079A
;		•	16.12 6.769e-13 169-
			183
781	BL00215	Mitochondrial energy	BL00215A 15.82 9.250e-
:		transfer proteins.	17 10-35 BL00215A
•.			15.82 6.000e-16 221-
:	1		246 BL00215A 15.82
			7.857e-12 108-133 BL00215B 10.44 9.526e-
•			11 168-181
783	PD00289	PROTEIN SH3 DOMAIN	PD00289 9.97 6.276e-09
		REPEAT PRESYNA.	159-173
785	BL00690	DEAH-box subfamily ATP-	BL00690B 13.38 1.000e-
		dependent helicases	12 147-165 BL00690A
		proteins.	6.87 5.320e-10 114-124
]	BL00690C 7.51 3.189e-
			09 218-228
786	PR00449	TRANSFORMING PROTEIN P21	PR00449C 17.27 8.500e-
	1	RAS SIGNATURE	16 50-73 PR00449A
			13.20 5.235e-14 8-30
			PR00449E 13.50 2.853e-
			11 150-173 PR00449D
			10.79 1.545e-09 111-
788	DM01206	CODONAUTDIR MICH POCARCE	125 DM0120CD 10 60 0 7675
, 30	20101200	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 8.767e-
790	BL00915	Phosphatidylinositol 3-	BL00915C 22.43 9.182e-
		and 4-kinases proteins.	39 725-764 BL00915B
		processes.	785 704 55005455

EQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.		22.78 5.050e-33 633- 671 BL00915D 27.02
			1.529e-21 795-831
		İ	BL00915A 10.09 1.000e-
			13 395-407
91	PR00208	GLIADIN AND LMW GLUTENIN	PR00208A 12.59 6.294e-
9 1	1.00200	SUPERFAMILY SIGNATURE	10 120-138 PR00208A
	}		12.59 6.294e-10 121-
		j '	139 PR00208A 12.59
			6.294e-10 122-140 PR00208A 12.59 6.294e-
		· [10 123-141 PR00208A
			12.59 6.294e-10 124-
			142 PR00208A 12.59
			6.294e-10 125-143
			PR00208A 12.59 6.294e-
		i	10 126-144 PR00208A
			12.59 6.294e-10 127-
			145 PR00208A 12.59 6.294e-10 128-146
			PR00208A 12.59 6.294e-
			10 129-147 PR00208A
			12.59 7.411e-09 130-
	/	\ •	148 PR00208A 12.59
			7.658e-09 131-149
			PR00208A 12.59 7.904e-
			09 132-150 PR00208A
			12.59 8.274e-09 118-
			136 PR00208A 12.59 8.274e-09 119-137
		TARVER THE GEOMETRIES	PR00205B 11.39 5.034e-
795	PR00205	CADHERIN SIGNATURE	16 302-320 PR00205A
			14.73 1.257e-11 284-
	}	1	300 PR00205C 13.65
			1.333e-11 337-352
796	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 4.000e-
.,,,		proteins.	12 196-247 BL00412D
		\	16.54 5.705e-11 197- 248 BL00412D 16.54
			7.848e-10 199-250
			BL00412D 16.54 1.827e-
	ļ	•	09 195-246 BL00412D
			16.54 1.918e-09 194-
	1		245 BL00412D 16.54
		<u></u>	2.102e-09 201-252
797	BL00021	Kringle domain proteins.	BL00021B 13.33 6.339e-
			13 40-58 BL01052C 18.51 1.000e-
799	BL01052	Calponin family repeat	BL01052C 18.51 1.000e-
		proteins.	16.12 1.529e-32 3-35
			BL01052B 15.31 1.257e-
			25 52-78 BL01052D
	<u> </u>		10.26 5.737e-25 174-
			194
800	BL00348	p53 tumor antigen	BL00348F 23.19 3.714e-
		proteins.	09 197-240
801	BL00309	Vertebrate galactoside-	BL00309C 18.65 1.621e-
		binding lectin proteins.	09 62-87 PR00245D 10.47 5.224e-
802	PR00245	OLFACTORY RECEPTOR	09 187-199
		SIGNATURE	PF00774A 16.47 8.457e-
804	PF00774	Dihydropyridine sensitive L-type calcium	l .
	1	channel (Beta subuni.	
908	PR00667	RETINAL PIGMENT	PR00667C 11.71 9.875e-
808	**************************************	EPITHELIUM-RETINAL GPCR	09 12-28
	- 1	SIGNATURE	i
810	PD02346	PHOTOSYSTEM II PROTEIN	PD02346F 12.89 4.340e-
	1	PRECURSOR	09 317-354

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
811	77.00505	PHOTOSYNTHESIS.	
811	BL00685	CBF-A/NF-YB subunit proteins.	BL00685B 14.41 6.779e- 14 54-95 BL00685A
		proceins.	11.22 4.798e-13 5-54
812	PR00080	ALCOHOL DEHYDROGENASE	PR00080A 9.32 9.419e-
		SUPERFAMILY SIGNATURE	10 93-105
813	BL00357	Histone H2B proteins.	BL00357 7.74 1.988e-17
		_ .	22-65
815	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 7.923e-
		METAL-BINDI.	15 158-171 PD00066
			13.92 5.200e-14 46-59 PD00066 13.92 7.000e-
			·14 18-31 PD00066
			13.92 7.000e-13 130-
			143 PD00066 13.92
			7.500e-13 214-227
			PD00066 13.92 9.000e- 13 102-115 PD00066
			13.92 4.429e-12 186-
			199 PD00066 13.92
			1.783e-11 74-87
816	BL01195	Peptidyl-tRNA hydrolase	BL01195C 20.12 3.348e-
820	PT-00530	proteins.	20 100-139
	BL00520	Interleukin-10 family proteins.	BL00520A 6.21 6.471e-
822	BL00972	Ubiquitin carboxyl-	BL00972A 11.93 8.113e-
		terminal hydrolases	09 224-242
		family 2 proteins.	
825	PR00876	NEMATODE METALLOTHIONEIN	PR00876B 7.66 2.268e-
000	2000055	SIGNATURE	10 101-115
829	PD02855	FLAVOPROTEIN PROTEIN DNA/PANTOTHEN.	PD02855A 18.37 4.732e- 28 88-124 PD02855B
		DIA, FANTOINEN.	8.36 6.478e-09 132-142
830	PR00405	HIV REV INTERACTING	PR00405B 11.83 7.000e-
		PROTEIN SIGNATURE	21 44-62 PR00405C
			19.41 1.000e-13 65-87
		[PR00405A 17.71 7.283e-
831	PR00019	LEUCINE-RICH REPEAT	13 25-45 PR00019A 11.19 1.000e-
		SIGNATURE	09 47-61 PR00019B
:		,	11.36 1.720e-09 136-
•			150 PR00019B 11.36
832	PR00011	TYPE III EGF-LIKE	3.880e-09 44-58
632	PROUDIT	SIGNATURE	PR00011B 13.08 3.438e- 16 164-183 PR00011D
		DIGITATIONS	14.03 6.850e-16 164-
•	1		183 PRO0011A 14.06
	l .	i i	0 264- 24 264 202
			8.364e-14 164-183
			PR00011C 24.25 5.415e-
			PR00011C 24.25 5.415e- 12 231-260 PR00011D
			PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212-
834	PD00306	PROTEIN GLYCOPROTEIN	PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231
· .	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212-
834	PD00306	PRECURSOR RE. PROTEIN GLYCOPROTEIN	PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231 PD00306A 10.26 7.000e- 12 232-246 PD00306A 10.26 4.000e-
835	PD00306	PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE.	PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231 PD00306A 10.26 7.000e- 12 232-246 PD00306A 10.26 4.000e- 10 290-304
· .		PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE. PROTEIN GLYCOPROTEIN	PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231 PD00306A 10.26 7.000e- 12 232-246 PD00306A 10.26 4.000e- 10 290-304 PD00306A 10.26 7.000e-
835	PD00306	PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE.	PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231 PD00306A 10.26 7.000e- 12 232-246 PD00306A 10.26 4.000e- 10 290-304 PD00306A 10.26 7.000e- 12 216-230
835	PD00306	PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE. PROTEIN GLYCOPROTEIN	PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231 PD00306A 10.26 7.000e- 12 232-246 PD00306A 10.26 4.000e- 10 290-304 PD00306A 10.26 7.000e- 12 216-230 DM00215 19.43 3.898e-
835	PD00306	PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE.	PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231 PD00306A 10.26 7.000e- 12 232-246 PD00306A 10.26 4.000e- 10 290-304 PD00306A 10.26 7.000e- 12 216-230
835 836 837	PD00306 PD00306 DM00215	PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE. PROLINE-RICH PROTEIN 3.	PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231 PD00306A 10.26 7.000e- 12 232-246 PD00306A 10.26 4.000e- 10 290-304 PD00306A 10.26 7.000e- 12 216-230 DM00215 19.43 3.898e- 09 78-111
835 836 837	PD00306 PD00306 DM00215	PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE. PROLINE-RICH PROTEIN 3. PROTEIN NUCLEAR	PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231 PD00306A 10.26 7.000e- 12 232-246 PD00306A 10.26 4.000e- 10 290-304 PD00306A 10.26 7.000e- 12 216-230 DM00215 19.43 3.898e- 09 78-111 PD02784B 26.46 8.302e-
835 836 837 839	PD00306 PD00306 DM00215 PD02784	PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE. PROLINE-RICH PROTEIN 3. PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231 PD00306A 10.26 7.000e- 12 232-246 PD00306A 10.26 4.000e- 10 290-304 PD00306A 10.26 7.000e- 12 216-230 DM00215 19.43 3.898e- 09 78-111 PD02784B 26.46 8.302e- 09 73-116 PR00700B 16.80 5.091e- 22 369-390 PR00700D
835 836 837 839	PD00306 PD00306 DM00215 PD02784	PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE. PROLINE-RICH PROTEIN 3. PROTEIN NUCLEAR RIBONUCLEOPROTEIN. PROTEIN TYROSINE	PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231 PD00306A 10.26 7.000e- 12 232-246 PD00306A 10.26 4.000e- 10 290-304 PD00306A 10.26 7.000e- 12 216-230 DM00215 19.43 3.898e- 09 78-111 PD02784B 26.46 8.302e- 09 73-116 PR00700B 16.80 5.091e- 22 369-390 PR00700D 12.47 5.765e-21 491-
835 836 837 839	PD00306 PD00306 DM00215 PD02784	PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE. PROTEIN GLYCOPROTEIN PRECURSOR RE. PROLINE-RICH PROTEIN 3. PROTEIN NUCLEAR RIBONUCLEOPROTEIN. PROTEIN TYROSINE	PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231 PD00306A 10.26 7.000e- 12 232-246 PD00306A 10.26 4.000e- 10 290-304 PD00306A 10.26 7.000e- 12 216-230 DM00215 19.43 3.898e- 09 78-111 PD02784B 26.46 8.302e- 09 73-116 PR00700B 16.80 5.091e- 22 369-390 PR00700D

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	140.		11 538-549 PR00700E
			17.57 3.100e-10 522-
			538
		TYROSINE KINASE	PR00109B 12.27 5.404e-
341 .	PR00109	CATALYTIC DOMAIN	13 134-153
			13 131 130
		SIGNATURE	PD02785B 14.43 1.000e-
844	PD02785	PROTEIN RIBOSOMAL 60S	40 58-112 PD02785A
		L22 RNA-BINDING HEP.	1 -
•	1		15.23 1.915e-28 8-57
845	BL00826	MARCKS family proteins.	BL00826C 7.63 6.738e-
			09 203-230
846	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 4.429e-
0.10		(RING finger), proteins.	10 15-24
849	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 1.000e-
043	BECOSEO	(RING finger), proteins.	08 340-349
	5000300	TYPE I ANTIFREEZE	PR00308A 5.90 6.506e-
850	PR00308	PROTEIN SIGNATURE	09 12-27
		PROTEIN TRANSCRIPTION	PD02411 21.89 7.000e-
851	PD02411		16 246-280
		REGULATION NUCLEAR.	BL00420B 22.67 1.000e-
852	BL00420	Speract receptor repeat	
		proteins domain	40 723-778 BL00420B
		proteins.	22.67 1.321e-38 933-
			988 BL00420B 22.67
			8.457e-28 482-537
			BL00420B 22.67 4.500e-
		Į.	27 587-642 BL00420B
			22.67 9.625e-27 270-
			325 BL00420B 22.67
	1		4.205e-26 163-218
			BL00420B 22.67 5.731e-
			23 55-110 BL00420B
		•	22.67 5.464e-20 377-
	Ì		432 BL00420B 22.67
			1
			2.800e-15 830-885
			BL00420C 11.90 1.900e-
	1		13 355-366 BL00420C
			11.90 1.900e-12 808-
	ļ		819 BL00420C 11.90
	}		3.550e-12 248-259
•		÷+-	BL00420C 11.90 2.831e-
			11 141-152 BL00420C
	İ	l'	11.90 5.119e-11 1018-
			1029 BL00420C 11.90
	· f	1	7.955e-10 567-578
			BL00420B 22.67 1.000e-
853	BL00420	Speract receptor repeat	40 756-811 BL00420B
		proteins domain	
	Ī	proteins.	22.67 1.321e-38 966-
		ļ	1021 BL00420B 22.67
			8.457e-28 482-537
	İ		BL00420B 22.67 4.500e-
			27 620-675 BL00420B
			22.67 9.625e-27 270-
	ŀ		325 BL00420B 22.67
ţ		1	4.205e-26 163-218
			BL00420B 22.67 5.731e-
			23 55-110 BL00420B
i	İ		22.67 6.464e-20 377-
l .			
1			432 BL00420B 22.67
	1		2.800e-15 863-918
Į.			BL00420C 11.90 1.900e-
1	1	1	13 355-366 BL00420C
Į.	1		11.90 1.900e-12 841-
		1	852 BL00420C 11.90
	1		3.550e-12 248-259
			BL00420C 11.90 2.831e
			11 141-152 BL00420C
1	1	j	11 141-152 Bh00420C
1	\	!	11.90 5.119e-11 1051- 1062 BL00420C 11.90
•			

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
·			7.955e-10 567-578
857	PR00388	3',5'-CYCLIC NUCLEOTIDE	PR00388A 10.45 2.778e-
		CLASS II	09 64-83
		PHOSPHODIESTERASE	
	Į.	SIGNATURE	
859	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 2.929e-
		region RNP-1 proteins.	13 37-56 BL00030B
•			7.03 1.900e-11 167-177
			BL00030A 14.39 2.000e-
:		L	10 128-147
861	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.250e-
			17 23-41 PR00988C
			13.64 8.714e-16 107-
			123 PR00988F 12.23
			7.828e-15 198-212
)	PR00988E 8.27 9.769e-
			5.95 8.250e-11 163-174
			PR00988B 11.60 4.512e-
			10 60-72
863	BL00215	Mitochondrial energy	BL00215B 10.44 8.071e-
		transfer proteins.	12 41-54
864	PR00775	90 KD HEAT SHOCK PROTEIN	PR00775E 8.06 1.000e-
• `		SIGNATURE	24 198-221 PR00775B
			3.52 1.837e-23 107-130
		1	PR00775D 8.91 4.484e-
			17 171-189 PR00775A
		 	9.90 8.342e-17 86-107
			PR00775C 10.68 9.379e-
	ł		17 153-171 PR00775G
:	,		10.64 6.850e-15 267- 286 PR00775F 12.76
		ļ ·	6.769e-14 249-267
866	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 9.460e-
		1011 10 1111111	09 89-121
867	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 5.596e-
	, i	ZINC-FINGER METAL-	29 14-53
	<u> </u>	BINDING NU.	•
868	BL01287	RNA 3'-terminal	BL01287A 17.95 2.688e-
		phosphate cyclase	26 16-48
869	DM00215	proteins. PROLINE-RICH PROTEIN 3.	200005 10 10 5 151
. 608	DM:00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.464e-
872	BL00046	Histone H2A proteins.	10 304-337 BL00046 12.95 1.000e-
	PT00040	Histone HZA proteins.	40 30-85
874	BL00188	Biotin-requiring enzymes	BL00188 30.29 9.036e-
		attachment site	32 665-711
		proteins.	· ·
876	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
	İ	domain proteins.	09 298-315
	L		
877	PD02102	SUBUNIT E V-ATPASE	PD02102A 16.74 4.176e-
877	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE	PD02102A 16.74 4.176e- 10 97-141
		SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	10 97-141
877	PD02102 BL01189	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. Ribosomal protein S12e	10 97-141 BL01189A 14.27 1.000e-
		SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	10 97-141 BL01189A 14.27 1.000e- 40 35-71 BL01189B
879	BL01189	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. Ribosomal protein S12e proteins.	10 97-141 BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125
		SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. Ribosomal protein S12e	BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125 BL00284C 28.56 6.400e-
879	BL01189	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. Ribosomal protein S12e proteins.	BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125 BL00284C 28.56 6.400e- 25 62-104 BL00284B
879 882	BL01189 BL00284	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. Ribosomal protein S12e proteins. Serpins proteins.	BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125 BL00284C 28.56 6.400e- 25 62-104 BL00284B 17.99 6.182e-12 35-56
879	BL01189	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. Ribosomal protein S12e proteins. Serpins proteins.	BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125 BL00284C 28.56 6.400e- 25 62-104 BL00284B 17.99 6.182e-12 35-56 BL00216B 27.64 4.375e-
879 882 889	BL00189 BL00284 BL00216	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. Ribosomal protein S12e proteins. Serpins proteins. Sugar transport proteins.	10 97-141 BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125 BL00284C 28.56 6.400e- 25 62-104 BL00284B 17.99 6.182e-12 35-56 BL00216B 27.64 4.375e- 21 35-85
879 882	BL01189 BL00284	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. Ribosomal protein S12e proteins. Serpins proteins. Sugar transport proteins. PHOSPHATIDYLINOSITOL	BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125 BL00284C 28.56 6.400e- 25 62-104 BL00284B 17.99 6.182e-12 35-56 BL00216B 27.64 4.375e- 21 35-85 FR00391E 12.50 7.785e-
879 882 889	BL00189 BL00284 BL00216	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. Ribosomal protein S12e proteins. Serpins proteins. Sugar transport proteins. PHOSPHATIDYLINOSITOL TRANSFER PROTEIN	10 97-141 BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125 BL00284C 28.56 6.400e- 25 62-104 BL00284B 17.99 6.182e-12 35-56 BL00216B 27.64 4.375e- 21 35-85 PR00391E 12.50 7.785e- 15 211-231 PR00391B
879 882 889	BL00189 BL00284 BL00216	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. Ribosomal protein S12e proteins. Serpins proteins. Sugar transport proteins. PHOSPHATIDYLINOSITOL	BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125 BL00284C 28.56 6.400e- 25 62-104 BL00284B 17.99 6.182e-12 35-56 BL00216B 27.64 4.375e- 21 35-85 FR00391E 12.50 7.785e-
879 882 889	BL00189 BL00284 BL00216	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. Ribosomal protein S12e proteins. Serpins proteins. Sugar transport proteins. PHOSPHATIDYLINOSITOL TRANSFER PROTEIN	10 97-141 BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125 BL00284C 28.56 6.400e- 25 62-104 BL00284B 17.99 6.182e-12 35-56 BL00216B 27.64 4.375e- 21 35-85 PR00391E 12.50 7.785e- 15 211-231 PR00391B 8.39 1.000e-13 83-104
879 882 889	BL00189 BL00284 BL00216	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL. Ribosomal protein S12e proteins. Serpins proteins. Sugar transport proteins. PHOSPHATIDYLINOSITOL TRANSFER PROTEIN	BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125 BL00284C 28.56 6.400e- 25 62-104 BL00284B 17.99 6.182e-12 35-56 BL00216B 27.64 4.375e- 21 35-85 PR00391E 12.50 7.785e- 15 211-231 PR00391B 8.39 1.000e-13 83-104 PR00391D 12.21 9.328e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	09 313-328
898	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 7.800e-
		dependent helicases	26 386-432 BL00039A
	1	proteins.	18.44 6.674e-16 113-
	1	_	152 BL00039B 19.19
			1.947e-13 153-179
	1		BL00039C 15.63 9.460e-
			11 236-260
901	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 8.200e-
-		METAL-BINDI.	16 254-267 PD00066
			13.92 8.200e-16 282-
		\	295 PD00066 13.92
			8.200e-16 310-323
			PD00066 13.92 8.200e-
·			16 366-379 PD00066
		1	13.92 8.200e-16 394-
			407 PD00066 13.92
	1	l	8.200e-14 338-351
	DT 02115	GTP-binding nuclear	BL01115A 10.22 9.321e-
902	BL01115	protein ran proteins.	11 6-50
	1 550000		PR00806B 4.28 9.160e-
903	PR00806	VINCULIN SIGNATURE	09 97-111
			PR00381E 8.75 6.586e-
904	PR00381	KINESIN LIGHT CHAIN	25 335-356 PR00381B
	1	SIGNATURE	18.17 2.667e-24 204-
			1
			224 PR00381A 9.55
			2.800e-24 107-125
			PR00381C 12.48 4.522e-
			24 226-245 PR00381D
			13.94 1.084e-22 291-
			309 PR00381F 9.13
			3.288e-22 370-392
			PR00381F 9.13 7.181e-
	ļ		13 286-308 PR00381E
	1		8.75 4.066e-11 251-272
			PR00381E 8.75 7.033e-
			11 293-314 PR00381E
	1		8.75 8.364e-10 377-398
			PR00381D 13.94 5.230e-
		•	09 333-351 PR00381C
			12.48 7.120e-09 310-
			329
906	PR00345	STATHMIN FAMILY	PR00345C 4.54 8.557e-
300	1100343	SIGNATURE	09 525-549
907	PR00345	. STATHMIN FAMILY	PR00345C 4.54 8.557e-
907	PR00345	SIGNATURE	09 513-537
	DT 00670	Trp-Asp (WD) repeat	BL00678 9.67 9.308e-11
908	BL00678	proteins proteins.	144-155
010	DD03.055	PROTEIN ZINC FINGER	PD01066 19.43 2.800e-
910	PD01066		30 48-87
		ZINC-FINGER METAL-	30 40-07
		BINDING NU.	BL01104C 15.14 6.000e-
912	BL01104	Ribosomal protein L13e	
		proteins.	09 364-392
922	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 3.842e-09
		proteins proteins.	500-511
923	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 2.500e-
		REPEAT SIGNATURE	09 323-338 PR00320C
	1		13.01 5.500e-09 187-
	1		202
924	PD02181	PROTOCHLOROPHYLLIDE	PD02181D 12.85 8.609e-
724		REDUCTASE PHOTOSYNT.	09 36-64
026	PI OCOTO	Actinin-type actin-	BL00019C 14.66 7.453e-
926	BL00019	binding domain proteins.	
l	l l	binding domain proceins.	13.34 6.510e-11 61-84
1			BL00019D 15.33 9.338e-
			1
1		1	11 205-235 BL00019A
			12.56 2.373e-10 34-45 BL00678 9.67 9.308e-11
	BL00678	Trp-Asp (WD) repeat	

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.	nyotoina nyotoina	272 224 224 24
		proteins proteins.	273-284 BL00678 9.67 1.600e-10 314-325
		,	BL00678 9.67 7.600e-10
			360-371 BL00678 9.67
			8.579e-09 206-217
929	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 1.857e-
		(RING finger), proteins.	10 137-146
930	BL01085	Ribulose-phosphate 3-	BL01085D 16.55 4.600e-
,	}	epimerase family	24 134-165 BL01085B
		proteins.	10.15 5.680e-22 30-52
			BL01085E 18.87 8.676e- 20 172-202 BL01085C
	}		21.81 2.038e-14 66-97
931	BL01085	Ribulose-phosphate 3-	BL01085D 16.55 4.600e-
		epimerase family	24 152-183 BL01085B
	1	proteins.	10.15 5.680e-22 30-52
			BL01085E 18.87 8.676e-
			20 190-220 BL01085C
633	PD00301		21.81 2.038e-14 66-97
933	FDOOTOT	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 6.400e- 09 160-171
936	PF00168	C2 domain proteins.	PF00168C 27.49 4.000e-
		Ja domain processis.	12 336-362
937	BL00415	Synapsins proteins.	BL00415N 4.29 9.519e-
	1		10 5-49
940	PR00862	PROLYL OLIGOPEPTIDASE	PR00862D 16.17 4.086e-
		SERINE PROTEASE (S9A)	09 63-84
945	D7 01030	SIGNATURE	
345	BL01230	RNA methyltransferase trmA family proteins.	BL01230B 11.62 2.373e- 09 407-420
948	BL00479	Phorbol esters /	BL004798 12.57 7.429e-
	22001.7	diacylglycerol binding	18 52-68 BL00479A
	•	domain proteins.	19.86 2.200e-13 26-49
949	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 1.474e-09
		proteins proteins.	100-111
954	PD01311	PROTEIN OXIDOREDUCTASE	PD01311A 30.23 5.909e-
955	PF00651	NAD INTERGENIC RE. BTB (also known as BR-	10 66-111 PF00651 15.00 3.250e-
,	FFUUBSI	C/Ttk) domain proteins.	12 47-60
956	PF00651	BTB (also known as BR-	PF00651 15.00 3.250e-
•		C/Ttk) domain proteins.	12 47-60
957	BL00379	CDP-alcohol	BL00379 24.64 1.610e-
•		phosphatidyltransferases	15 111-148
		proteins.	
959	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 1.884e-
960	BL01115	GTP-binding nuclear	10 31-75 BL01115A 10.22 3.438e~
- -		protein ran proteins.	14 110-154
962	BL00061	Short-chain	BL00061B 25.79 6.586e-
	1	dehydrogenases/reductase	13 198-236
		s family proteins.	<u> </u>
963	PR00502	MUTT DOMAIN SIGNATURE	PR00502A 15.06 8.200e-
966	DD003.00	MVNT T NIMTON	11 210-225
700	PR00308	TYPE I ANTIFREEZE	PR00308A 5.90 7.035e-
967	DM01206	PROTEIN SIGNATURE CORONAVIRUS NUCLEOCAPSID	09 55-70 DM01206B 10.69 1.286e-
		PROTEIN.	12 104-124 DM01206B
			10.69 5.299e-11 23-43
			DM01206B 10.69 8.274e-
			10 73-93 DM01206B
			10.69 3.962e-09 108-
		1	128 DM01206B 10.69
060	DE01000		5.671e-09 38-58
969	PF01008	Initiation factor 2 subunit.	PF01008B 25.59 4.724e-
i		Swullt.	31 417-460 PF01008C 12.25 5.333e-18 506-
			526 PF01008A 20.14
		1	5.875e-15 369-390
	L		

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
70	BL01277	Ribonuclease PH	BL01277C 10.18 7.648e- 10 112-143 BL01277A
		proteins.	17.39 9.806e-10 40-78
75	BL01159	WW/rsp5/WWP domain	BL01159 13.85 3.605e-
		proteins.	12 130-145 BL01159 13.85 4.122e-10 171-
			186
977	PF00791	Domain present in ZO-1	PF00791C 20.98 2.235e-
		and Unc5-like netrin	09 55-94
	20000	receptors. Ribosomal protein L17	BL01167B 20.66 8.258e-
978	BL01167	proteins.	19 88-127
979	BL00478	LIM domain proteins.	BL00478B 14.79 9.357e-
			13 33-48 BL00478B 14.79 7.250e-12 98-113
	PR00312	CALSEQUESTRIN SIGNATURE	PR00312E 8.32 3.423e-
980	PRUUSIZ	Camping of the campin	36 169-199 PR00312I
			15.78 5.286e-35 332- 361 PR00312F 15.06
			5.865e-35 199-229
			PR00312H 13.31 8.313e-
			35 263-291 PR00312J
			13.73 5.688e-34 363- 392 PR00312D 9.43
			2.636e-33 128-158
			PR00312C 15.14 8.839e-
			33 92-122 PR00312B 15.08 8.941e-33 62-92
			PR00312G 11.11 6.657e-
			32 230-258 PR00312A
			11.70 6.914e-27 35-59
981	PF00992	Troponin.	PF00992A 16.67 8.816e- 09 414-449
000	PR00299	ALPHA CRYSTALLIN	PR00299F 13.20 2.367e-
982	PR00299	SIGNATURE	09 127-149
983	BL01150	Respiratory-chain NADH	BL01150B 17.16 1.000e- 40 156-202 BL01150A
		dehydrogenase 20 Kd subunit proteins.	14.10 8.200e-39 100-
	ŀ	subunic process.	138
986	BL00795	Involucrin proteins.	BL00795C 17.06 7.211e-
		:	14 4-49 BL00795C 17.06 1.778e-11 1-46
		1	BL00795C 17.06 3.407e-
		ļ	10 14-59 BL00795C
	l i		17.06 7.802e-10 2-47 BL00795C 17.06 8.640e-
			10 19-64 BL00795C
	· ·		17.06 7.400e-09 11-56
		Į.	BL00795C 17.06 7.800e-
		Ribosomal protein Lle	09 3-48 BL00939F 17.27 5.393e-
987	BL00939	proteins.	09 810-840
988	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e-
			11 525-541 PR00452B 11.65 6.538e-
989	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e-
994	BL00027	'Homeobox' domain	BL00027 26.43 2.500e-
JJ4	5200027	proteins.	25 146-189
997	BL01304	ubiH/COQ6 monooxygenase	BL01304A 8.05 3.893e-
		family proteins.	11 65-79 DM01767B 10.07 7.868e-
998	DM01767	5 TRANSMITTER DOMAIN.	09 22-39
1000	PR00926	MITOCHONDRIAL CARRIER	PR00926C 16.07 1.750e-
		PROTEIN SIGNATURE	24 73-94 PR00926D
			10.53 3.250e-23 126- 145 PR00926F 17.75
			6.211e-23 217-240
	1	1	PR00926E 11.70 6.625e-

No.	SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
16.07 2.125e-18 24-39 PRO025A 10.41 1.000e-15 11-25 PR0025EF 17.75 5.55e-09 120-143 1005 BL00406	DDQ ID NO.		DESCRIPTION	RESULTS"
PRO0926A 10.41 1.000e-15 11-25 PRO0926F 17.75 5.55se-09 120-143 133				20 174-193 PR00926B
15 11-25 PRO0926F 17.75 5.55e-09 120-143 17.75 5.55e-09 120-143 17.75 5.55e-09 120-143 18.004066 17.75 5.55e-09 120-143 18.004066 17.75 5.55e-09 120-143 18.004066 17.75 5.55e-09 120-143 18.004066 17.75 5.55e-09 120-143 18.004066 17.75 5.55e-09 120-143 18.004066 17.75 5.55e-09 120-143 18.004066 17.75 5.55e-09 120-143 18.004066 17.75 5.55e-140-147-202 18.004068 18.00406				16.07 2.125e-18 24-39
17.75 5.555e-09 120-143				PR00926A 10.41 1.000e-
143				15 11-25 PR00926F
December December				17.75 5.565e-09 120-
1006 BL00406 Actins proteins BL00406E 8.44 7.375e-38 3.770e-40 270-325 BL00406B 8.44 7.375e-38 3.27-377 BL00406B 9.95 3.348e-29 11.46 BL00406B 9.45 3.348e-29 11.46 BL00406B 9.44 1.00e-40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406B 9.44 1.00e-35 248-298 BL00406C 8.75 1.000e-40 147-202 BL00406B 9.44 1.00e-35 248-298 BL00406C 8.75 1.000e-40 147-202 BL00406B 9.45 1.000e-40 147-202 BL00406B 9.45 1.000e-40 147-202 BL00406B 9.45 1.000e-40 147-202 BL00406B 9.45 1.000e-40 147-202 BL00406B 9.45 1.000e-40 147-202 BL00406B 9.45 1.000e-40 147-202 BL00406B 9.45 1.000e-40 147-202 BL00406B 9.45 1.000e-40 147-202 BL00406B 9.45 1.000e-40 147-202 BL00406B 9.45 1.000e-40 11.000e-4				<u> </u>
BL00406 BL00406 Actins proteins. BL00406B 2.5 a 3.7006-40 270-325 BL00406B 8. 44 7.375-38 327-37 BL00406B 9.95 3.348e-39 11-46 BL00406B 5.47 1.000e-40 49.89-134 BL00406C 6.75 1.000e-40 49.89-134 BL00406C 8.44 1.000e-35 249-298 BL00406A 9.95 3.348e-29 11-46 PRO0006	1005	BL00406	Actins proteins.	
BL00406D 12.58 3.700e-40 270-325 BL00406B 8.44 7.375e-38 327-377 BL00406B 9.95 3.348e-29 11.46 8.41 BL00406B 5.47 1.000e-40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406B 8.44 1.000e-35 248-298 BL00406C 6.75 1.000e-40 147-202 BL00406B 8.44 1.000e-35 248-298 BL00406C 6.75 1.000e-40 147-202 BL00406B 8.44 1.000e-35 248-298 BL00406C 6.75 1.000e-40 147-202 BL00406B 8.44 1.000e-35 248-298 BL00406C 8.75 1.000e-40 147-202 BL00406B 8.40 1.000e-35 248-298 BL00406C 8.75 1.000e-40 147-202 BL00406B 8.40 1.000e-35 248-298 BL00406B 8.40 1.000e-35 248-298 BL00406B 8.40 1.000e-35 248-298 BL00406B 8.59 4.667e-20 98-118 PRO0304B 11.00 4.714e-19 19 68-87 PRO0304B 11.00 4.714e-19 19 68-87 PRO0304B 11.00 4.714e-19 19 68-87 PRO0304B 11.00 4.714e-19 19 19 19 19 19 19 19 19 19 19 19 19 1				
Actins proteins				
R.44 7.375s-38 327-377				
BL00406 BL00406 Actins proteins BL004068 9.95 3.348e- 29 11-46				
29 11-46				
December December				1
A0 88-143 BL00406C	1006	BL00406	Actins proteins.	1
1007 PR00304 TAILLESS COMPLEX PR00304D 1.4 1.000e-35 248-298 EL00406A 3.5 3.488-29 11.46 3.55 3.488-29 11.46 3.55 3.488-29 11.46 3.55 3.488-29 11.46 3.55 3.488-29 11.46 3.55 3.488-29 11.46 3.55 3.488-29 11.46 3.55 3.488-29 11.46 3.55 3.488-29 11.46 3.55 3.488-29 11.46 3.55 3.488-29 3.148-20 3.55 3.488-29 3.148-20 3.55 3.488-29 3.148-20 3.55 3.488-29 3.148-20 3.55 3.488-29 3.148-20 3.55 3.488-29 3.148-20 3.55 3.488-29 3.148-20 3.55 3.488-29 3.148-20 3.25			Parameter Parameter	
1007 PR00304 TAILLESS COMPLEX PR00304D 11.04 8.714e- PR00304D 11.04 8.714e- PR00304D 11.04 8.714e- PR00304D 11.04 8.714e- PR00304D 11.04 8.714e- PR00304D 11.04 8.714e- PR00304D 11.04 8.714e- PR00304D 11.04 8.714e- PR00304D 11.06 7.577e- 19.68-87 PR00304B 11.60 7.577e- 19.68-87 PR00306B 11.43 2.929e- 29.68-87 PR0036B 11.43 2.929e- 29.68-87 PR0036B 11.43 2.929e- 29.68-87 PR0036B 11.43 2.929e- 29.68-87 PR0036B 11.43 2.929e- 20.68-87 PR00				
1007 PR00304 TAILLESS COMPLEX PR00304D 11.04 8.714e-POLYPEPTIDE 1 22 384-407 PR00304C (CHAPERONE) SIGNATURE PR00304B 11.06 8.7577e-19 68-87 PR00304B PR00304B 0.7.577e-19 68-87 PR00304B PR00304B 0.7.577e-19 68-87 PR00304B PR00304B 0.7.577e-19 68-87 PR00304B PR00304B 0.7.577e-19 68-87 PR00304B PR00304B 0.7.577e-19 68-87 PR00304B PR00304B 0.7.577e-19 68-87 PR00304B PR00304B 0.7.577e-19 68-87 PR00304B 0.7.577e-19 68-87 PR00304B PR00304B 0.7.577e-19 68-87 PR00304B 0.7.577e-19 68-87 PR00304B 0.7.577e-19 68-87 PR00304B 0.7.577e-19 68-87 PR00304B 0.7.577e-19 68-87 PR00304B 0.7.577e-19 68-87 PR00304B 0.7.577e-19 68-87 PR00304B 0.7.577e-19 68-87 PR00304B 0.7.577e-19 68-87 PR00304B 0.7.577e-19 68-87 PR00304B 0.7.577e-19 68-87 PR00306B 0.7.577e-19 68-87 PR00306B 0.7.577e-19 68-87 PR00308				BL00406E 8.44 1.000e-
TAILLESS COMPLEX				35 248-298 BL00406A
POLYPEPTIDE 1				
CHAPERONE SIGNATURE	1007	PR00304	,	
PRO0304B 11.60 7.577e-19 68-87 PRO0304A 9.20 3.382e-16 46-63 PRO0304E 7.79 6.870e-13 418-431			I	
19 68-87 PR00304A 9.20 3.382e-116 46-63 PR00304E 7.79 6.870e-13 418-431 1009 PD01066 PROTEIN ZINC FINGER PD01066 19.43 2.929e-2 21NC-FINGER METAL-32 9-48 BINDING NU. PROTEIN ZINC FINGER PD01066 19.43 2.929e-32 9-48 21NC-FINGER METAL-32 68-107 BINDING NU. PD01066 19.43 2.929e-32 68-107 BINDING NU. PD01066 19.43 2.929e-32 68-107 BINDING NU. PD01068 SYNTHETASE LIGASE PD01168H 12.08 1.000e-10168 SYNTHETASE LIGASE PD01168H 12.08 1.000e-11 174-194 PD00930			(CHAPERONE) SIGNATURE	i .
Protein zinc finger	•			
PRO0304E 7.79 6.870e- 13 418-431 1419-48 1419-49 141		•		
13 418-431 1009 PD01066 PROTEIN ZINC FINGER PD01066 19.43 2.929e- ZINC-FINGER METAL- BINDING NU. PROTEIN ZINC FINGER PD01066 19.43 2.929e- ZINC-FINGER METAL- BINDING NU. 2 68-107 BL00518 Zinc-FINGER METAL- BINDING NU. 2 68-107 BL00518 Zinc-FINGER METAL- BINDING NU. 10 64-73 10				ł .
PD01066				•
21NC-FINGER METAL-BINDING NU.	1009	PD01066	DDOTETN ZINC FINGER	
BINDING NU. PD01066 PROTEIN ZINC FINGER PD01066 19.43 2.929e- ZINC-FINGER METAL- 32 68-107 BINDING NU. BL00518 Zinc finger, C3HC4 type	1005		1	
PRO1066				32 3 40
ZINC-FINGER METAL-BINDING NU. 32 68-107	1011	PD01066		PD01066 19.43 2.929e-
Display				
RING finger), proteins. 10 64-73 1016 PD01168 SYNTHETASE LIGASE PD01168H 12.08 1.000e-PROTEIN ALANYL. 11 174-194 1018 PD00930 PROTEIN GTPASE DOMAIN PD00930E 33.72 1.391e-ACTIVATION. 32 261-302 PD00930A 25.62 9.550e-22 157-183 1022 BL00175 Phosphoglycerate mutase BL00175A 15.42 5.179e-family phosphohistidine 22 6-26 BL00175C Proteins. 23.75 8.062e-10 79-111 1025 PR00305 14-3-3 PROTEIN ZETA PR00305D 16.34 1.439e-SIGNATURE 10 158-185 1		ĺ		
RING finger), proteins. 10 64-73 1016 PD01168 SYNTHETASE LIGASE PD01168H 12.08 1.000e-PROTEIN ALANYL. 11 174-194 1018 PD00930 PROTEIN GTPASE DOMAIN PD00930E 33.72 1.391e-ACTIVATION. 32 261-302 PD00930A 25.62 9.550e-22 157-183 1022 BL00175 Phosphoglycerate mutase BL00175A 15.42 5.179e-family phosphohistidine 22 6-26 BL00175C Proteins. 23.75 8.062e-10 79-111 1025 PR00305 14-3-3 PROTEIN ZETA PR00305D 16.34 1.439e-SIGNATURE 10 158-185 1	1012	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 6.143e-
PROTEIN ALANYL. 11 174-194 1018 PD00930 PROTEIN GTPASE DOMAIN 22 661-302 PD00930A ACTIVATION. 32 261-302 PD00930A 25.62 9.550e-22 157-183 1022 BL00175 Phosphoglycerate mutase family phosphohistidine proteins. 23.75 8.062e-10 79-111 1025 PR00305 14-3-3 PROTEIN ZETA PR00305D 16.34 1.439e-SIGNATURE 10 158-185 1026 BL00353 HMG1/2 proteins. BL00353B 11.47 2.436e-18 238-288 BL00353C 14.83 8.844e-11 288-335 1028 BL00183 Ubiquitin-conjugating BL00183 28.97 1.310e-enzymes proteins. 33 43-91 1033 PF00580 UvrD/REP helicase. PF00580A 13.37 4.720e-09 111-133 1034 PR00413 HALOACID PR00413E 15.78 3.429e-09 154-171 1037 PD01066 PROTEIN ZINC FINGER PD01066 19.43 9.657e-ZINC-FINGER METAL-BINDING NU. 1038 PD01796 PROTEIN TRANSMEMBRANE PD01796 15.01 4.259e-COBALT ZINC CADMIU. 11 55-82 1039 BL00299 Ubiquitin domain BL00299 28.84 9.036e-proteins. 09 17-69 1040 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-			(RING finger), proteins.	10 64-73
PD00930	1016	PD01168	SYNTHETASE LIGASE	PD01168H 12.08 1.000e-
ACTIVATION. 32 261-302 PD00930A 25.62 9.550e-22 157- 183 1022 BL00175 Phosphoglycerate mutase family phosphohistidine proteins. PR00305 14-3-3 PROTEIN ZETA PR00305D 16.34 1.439e- SIGNATURE 10 158-185 1026 BL00353 HMG1/2 proteins. BL00353B 11.47 2.436e- 18 238-288 BL00353C 14.83 8.844e-11 288- 335 1028 BL00183 Ubiquitin-conjugating enzymes proteins. 1033 PF00580 UvrD/REP helicase. PF00580A 13.37 4.720e- 09 111-133 1034 PR00413 HALOACID PR00413E 15.78 3.429e- DEHALOGENASE/EPOXIDE HYDROLASE FAMILY SIGNATURE 1037 PD01066 PROTEIN ZINC FINGER PD01066 19.43 9.657e- ZINC-FINGER METAL- BINDING NU. 1038 PD01796 PROTEIN TRANSMEMBRANE PD01796 15.01 4.259e- COBALT ZINC CADMIU. 1039 BL00299 Ubiquitin domain BL00299 28.84 9.036e- proteins. 1040 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-			. 1	
25.62 9.550e-22 157- 183	1018	PD00930		
183	·.	· ·	ACTIVATION.	,
BL00175			·	1
family phosphohistidine proteins. 12 6-26 BL00175C 23.75 8.062e-10 79-111 1025 PR00305 14-3-3 PROTEIN ZETA PR00305D 16.34 1.439e-10 158-185 1026 BL00353 HMG1/2 proteins. BL00353B 11.47 2.436e-18 238-288 BL00353C 14.83 8.844e-11 288-335 HMG1/2 proteins. BL00183 28.97 1.310e-18 28.97 1.310e-18 28.97 1.310e-18 28.97 1.310e-18 28.97 1.310e-18 28.97 1.310e-19	1022	DI AA175	Dhogahaali gaarata mita aa	
Proteins. 23.75 8.062e-10 79-111	1022	PT001/2		
1025 PR00305 14-3-3 PROTEIN ZETA PR00305D 16.34 1.439e- 10 158-185 10 1		· ·	proteins	
SIGNATURE 10 158-185	1025	PR00305		1
BL00353			I .	
18 238-288 BL00353C 14.83 8.844e-11 288-335 1028 BL00183 Ubiquitin-conjugating enzymes proteins. 33 43-91 33 43-91 1033 PF00580 UvrD/REP helicase. PF00580A 13.37 4.720e-09 111-133 1034 PR00413 HALOACID PR00413E 15.78 3.429e-09 154-171 HYDROLASE FAMILY SIGNATURE PD01066 19.43 9.657e-2INC-FINGER METAL-BINDING NU. PROTEIN TRANSMEMBRANE PD01796 15.01 4.259e-COBALT ZINC CADMIU. 11 55-82 1039 BL00299 Ubiquitin domain BL00299 28.84 9.036e-09 17-69 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-	1026	BL00353		1
14.83 8.844e-11 288-335 1028 BL00183 Ubiquitin-conjugating enzymes proteins. 33 43-91 1033 PF00580 UvrD/REP helicase. PF00580A 13.37 4.720e-09 111-133 1034 PR00413 HALOACID PR00413E 15.78 3.429e-09 154-171 HYDROLASE FAMILY SIGNATURE PD01066 19.43 9.657e-2INC-FINGER METAL-BINDING NU. P001796 PROTEIN TRANSMEMBRANE PD01796 15.01 4.259e-COBALT ZINC CADMIU. 11 55-82 1039 BL00299 Ubiquitin domain BL00299 28.84 9.036e-09 17-69 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-		-	1	
335 335 336 336 336 337 337 338 3391 339 3391 339 3391 339				1
enzymes proteins. 33 43-91 1033 PF00580 UvrD/REP helicase. PF00580A 13.37 4.720e- 09 111-133 1034 PR00413 HALOACID PR00413E 15.78 3.429e- DEHALOGENASE/EPOXIDE 09 154-171 HYDROLASE FAMILY SIGNATURE 1037 PD01066 PROTEIN ZINC FINGER PD01066 19.43 9.657e- ZINC-FINGER METAL- BINDING NU. 1038 PD01796 PROTEIN TRANSMEMBRANE PD01796 15.01 4.259e- COBALT ZINC CADMIU. 11 55-82 1039 BL00299 Ubiquitin domain BL00299 28.84 9.036e- proteins. 09 17-69 1040 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-			1	1
1033 PF00580 UvrD/REP helicase. PF00580A 13.37 4.720e- 09 111-133 1034 PR00413 HALOACID PR00413E 15.78 3.429e- DEHALOGENASE/EPOXIDE 09 154-171 HYDROLASE FAMILY SIGNATURE 1037 PD01066 PROTEIN ZINC FINGER PD01066 19.43 9.657e- ZINC-FINGER METAL- BINDING NU. 1038 PD01796 PROTEIN TRANSMEMBRANE PD01796 15.01 4.259e- COBALT ZINC CADMIU. 11 55-82 1039 BL00299 Ubiquitin domain BL00299 28.84 9.036e- proteins. 09 17-69 1040 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-	1028	BL00183	Ubiquitin-conjugating	BL00183 28.97 1.310e-
1034 PR00413 HALOACID PR00413E 15.78 3.429e- DEHALOGENASE/EPOXIDE O9 154-171 HYDROLASE FAMILY SIGNATURE 1037 PD01066 PROTEIN ZINC FINGER PD01066 19.43 9.657e- ZINC-FINGER METAL- O9 5-44 BINDING NU. 1038 PD01796 PROTEIN TRANSMEMBRANE PD01796 15.01 4.259e- COBALT ZINC CADMIU. 11 55-82 1039 BL00299 Ubiquitin domain BL00299 28.84 9.036e- Proteins. O9 17-69 1040 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-			enzymes proteins.	1
1034 PR00413 HALOACID PR00413E 15.78 3.429e- DEHALOGENASE/EPOXIDE 09 154-171 HYDROLASE FAMILY SIGNATURE 1037 PD01066 PROTEIN ZINC FINGER PD01066 19.43 9.657e- ZINC-FINGER METAL- BINDING NU. 1038 PD01796 PROTEIN TRANSMEMBRANE PD01796 15.01 4.259e- COBALT ZINC CADMIU. 11 55-82 1039 BL00299 Ubiquitin domain BL00299 28.84 9.036e- proteins. 09 17-69 1040 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-	1033	PF00580	UvrD/REP helicase.	PF00580A 13.37 4.720e-
DEHALOGENASE/EPOXIDE HYDROLASE FAMILY SIGNATURE 1037 PD01066 PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU. 1038 PD01796 PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU. 11 55-82 1039 BL00299 Ubiquitin domain Proteins. PRO0970 PRO0970 PRO0970 PRO0970 PRO0970 PRO0970 DEFAULT OF TRANSMEMBRANE OP 17-69 PRO0970A 17.73 6.143e-				09 111-133
HYDROLASE FAMILY SIGNATURE 1037 PD01066 PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU. 1038 PD01796 PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU. 11 55-82 1039 BL00299 Ubiquitin domain Proteins. D9 17-69 1040 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-	1034	PR00413		,
SIGNATURE SIGNATURE			· •	09 154-171
PD01066]
ZINC-FINGER METAL- BINDING NU. 1038 PD01796 PROTEIN TRANSMEMBRANE PD01796 15.01 4.259e- COBALT ZINC CADMIU. 11 55-82 1039 BL00299 Ubiquitin domain BL00299 28.84 9.036e- proteins. 09 17-69 1040 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-				
BINDING NU. 1038 PD01796 PROTEIN TRANSMEMBRANE PD01796 15.01 4.259e- COBALT ZINC CADMIU. 11 55-82 1039 BL00299 Ubiquitin domain BL00299 28.84 9.036e- proteins. 09 17-69 1040 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-	1037	PD01066	1	
1038 PD01796 PROTEIN TRANSMEMBRANE PD01796 15.01 4.259e- COBALT ZINC CADMIU. 11 55-82 1039 BL00299 Ubiquitin domain BL00299 28.84 9.036e- proteins. 09 17-69 1040 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-				09 5-44
COBALT ZINC CADMIU. 11 55-82 1039 BL00299 Ubiquitin domain BL00299 28.84 9.036e- proteins. 09 17-69 1040 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-				
1039 BL00299 Ubiquitin domain BL00299 28.84 9.036e- proteins. 09 17-69 1040 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-	1038	PD01796		1
proteins. 09 17-69 1040 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-	1030	77.0000		<u> </u>
1040 PR00970 ARGININE ADP- PR00970A 17.73 6.143e-	1039	BT00533	, -	
1110211111 1111 1111 1111 1111 1111 111	3040	777777		
RIBUSILIRANSFERASE 20 56-78 PR00970D	1040	PR009/0		l i
			KIBOSILIKANSPEKASE	20 20-18 PK003/0D

EQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.	SIGNATURE	9.96 2.154e-18 154-171
	İ		PR00970F 12.30 1.000e-
			16 224-241 PR00970G
			9.97 9.229e-15 242-258
			PR00970B 16.37 1.290e-
			13 86-105 PR00970C
		i	11.05 1.643e-11 115-
	1	1	130 PR00970E 11.23
			9.820e-11 202-218
			BL00678 9.67 2.200e-10
1042	BL00678	Trp-Asp (WD) repeat	
		proteins proteins.	243-254
1043	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 6.786e-
	•	SIGNATURE	13 114-128 PR00048A
			10.52 1.000e-09 172-
	1		186
	BL00615	C-type lectin domain	BL00615A 16.68 1.720e-
1045	PD00913	proteins.	11 218-236 BL00615B
	1	process.	12.25 1.857e-10 317-
	\		331
			BL01092N 13.54 8.924e-
1046	BL01092	Adenylate cyclases	10 3-40
		class-I proteins.	BL01216D 21.75 4.316e-
1047	BL01216	ATP-citrate lyase /	28 314-344 BL01216A
		succinyl-CoA ligases	13.91 1.000e-10 97-112
		family proteins.	13.91 1.000e-10 97-112
1049	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 7.618e-
1047		Ì	12 102-136
1050	BL01073	Ribosomal protein L24e	BL01073 24.30 1.000e-
1050	Впотока	proteins.	40 12-62
	BL00571	Amidases proteins.	BL00571 25.69 5.875e-
1054	B700217	Amidabes protection	31 160-212
		Eukaryotic RNA-binding	BL00030A 14.39 5.235e-
1055	BL00030	Eukaryotic kin-binding	11 98-117 BL00030B
	Ĭ	region RNP-1 proteins.	7.03 4.316e-09 137-147
	}		BL00223C 24.79 8.754e-
1058	BL00223	Annexins repeat proteins	BL00223C 24.79 8.754e-
	ļ	domain proteins.	23 262-317 BL00223A
			15.59 9.478e-14 46-80
	1		BL00223A 15.59 5.557e~
			11 118-152
2060	BL00027	'Homeobox' domain	BL00027 26.43 3.455e-
1060	B100027	proteins.	35 158-201
		Putative AMP-binding	BL00455 13.31 6.211e-
1064	BL00455		13 280-296
		domain proteins.	PR00019A 11.19 2.000e-
1065	PR00019 .	LEUCINE-RICH REPEAT	09 115-129 PR00019B
Į		SIGNATURE	11.36 3.880e-09 87-101
			11.30 3.0000-03 67-101
1066	PR00326	GTP1/OBG GTP-BINDING	PRO0326A 8.75 4.600e-
1		PROTEIN FAMILY SIGNATURE	16 151-172 PR00326C
1			9.79 1.290e-14 200-216
1			PR00326B 16.74 8.548e-
	1		14 172-191 PR00326D
			19.09 1.257e-13 217-
			236
·		RECEPTOR INTERLEUKIN-1	PD02870B 18.83 8.518e-
1071	PD02870		11 164-197
1		PRECURSOR.	PF00856A 26.14 5.976e-
1072	PF00856	SET domain proteins.	
j			09 350-387
1075	BL01009	Extracellular proteins	BL01009D 14.19 4.300e-
		SCP/Tpx-1/Ag5/PR-1/Sc7	20 127-148 BL01009A
I	1	proteins.	13.75 6.586e-13 57-75
	1		BL01009E 13.50 1.439e-
	1	1	11 159-175
		CARBOXYPEPTIDASE C	PR00724A 10.91 1.000e
1077	PR00724	CARBOXYPEPTIDASE C	08 366-379
		SERINE PROTEASE (S10)	00 300-379
		FAMILY SIGNATURE	
1078	BL00215	Mitochondrial energy	BL00215A 15.82 1.000e
		transfer proteins.	12 170-195 BL00215A
1	}	· ·	15.82 7.529e-10 79-10 BL00678 9.67 4.316e-0

SEQ ID NO	: ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins proteins.	298-309
1081	BL00326	Tropomyosins proteins.	BL00326A 14.01 7.398e- 10 23-57
1094	BL00460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 3.204e- 18 57-92 BL00460B 9.73 6.400e-13 100-118 BL00460D 16.89 9.143e- 12 162-182 BL00460C 14.35 5.500e-09 133- 156
1095	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 67-105 PD02811B 17.07 2.263e-21 118- 151 PD02811C 13.25 5.696e-13 154-167
1096	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 60-98 PD02811B 17.07 2.263e-21 111- 144 PD02811C 13.25 5.696e-13 147-160
1097	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.143e- 09 200-216
1105	PF00881	Nitroreductase family.	PF00881A 27.15 9.229e- 13 111-147
1109	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 3.077e- 10 15-37 PR00449E 13.50 1.857e-09 185- 208 PR00449D 10.79 8.364e-09 131-145
1115	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 5.737e- 20 42-60 PR00405A 17.71 2.703e-17 23-43 PR00405C 19.41 6.902e- 10 63-85
1116	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1117	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1120	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 4.857e- 10 290-306
1123	PR00412	EPOXIDE HYDROLASE SIGNATURE	PR00412F 18.76 9.526e- 12 301-324
1125	PR00186	HEMERYTHRIN SIGNATURE	PR00186A 13.62 2.800e- 09 87-101
1129	BL00170	Cyclophilin-type peptidyl-prolyl cis- trans isomerase signatur.	BL00170C 18.49 3.077e- 33 84-129 BL00170B 20.97 6.838e-25 37-77 BL00170A 17.08 3.455e- 15 10-37
1131	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80
1132	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1133	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1136	BL00990	Clathrin adaptor complexes medium chain proteins.	BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e- 27 157-187 BL00990D 16.13 5.320e-18 403- 422
1137	PR00314	CLATHRIN COAT ASSEMBLY PROTEIN SIGNATURE	PR00314B 15.68 8.000e- 34 100-128 PR00314D 9.66 3.531e-33 233-261 PR00314C 16.05 8.909e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		32 159-188 PR00314A
			14.53 1.281e-22 13-34
	<u> </u>		BL01115A 10.22 6.364e-
1139	BL01115	GTP-binding nuclear protein ran proteins.	13 13-57
		Protein kinases ATP-	BL00107A 18.39 4.000e-
1141	BL00107		19 451-482 BL00107B
		binding region proteins.	13.31 3.077e-12 519-
		·	13.31 3.077e-12 519-
			PR00685A 13.62 4.676e-
1148	PR00685	TRANSCRIPTION INITIATION	l .
		FACTOR IIB SIGNATURE	09 21-42
1155	PD01652	RECEPTOR CELL NK	PD01652B 8.50 9.396e-
	}	GLYCOPROTEIN IMMUNOGLOB.	10 522-574 PD01652B
			8.50 9.463e-10 740-792
1157	PD02894	HYDROLASE N4- PRECURSOR	PD02894A 21.96 7.873e-
	1	PROTEIN SIGNAL BE.	28 81-127 PD02894B
	1		13.93 1.188e-27 178-
			211
1159	BL00623	GMC oxidoreductases	BL00623E 15.00 3.531e-
1133		proteins.	20 391-414 BL00623C
		F	10.86 4.240e-20 155-
			176
7161	PD01937	DNA PROTEIN POLYMERASE	PD01937A 6.68 3.475e-
1161	FDOTAL	ENDONUCLEASE DNA	09 330-341
	PD01937	DNA PROTEIN POLYMERASE	PD01937A 6.68 3.475e-
1162	PD01321	ENDONUCLEASE DNA	09 221-232
	1 200 200	HISTONE H5 SIGNATURE	PR00624D 11.94 7.455e-
1163	PR00624	HISTONE HS SIGNATURE	10 214-239 PR00624D
			11.94 1.961e-09 312-
			337
			BL00226B 23.86 7.384e-
1167	BL00226	Intermediate filaments	
		proteins.	09 302-350
1177	BL01032	Protein phosphatase 2C	BL01032G 8.33 1.422e-
		proteins.	10 34-48
1178	PR00320	G-PROTEIN BETA WD-40	PR00320A 16.74 1.794e-
	•	REPEAT SIGNATURE	10 205-220 PR00320C
	1		13.01 7.840e-10 205-
			220 PR00320B 12.19 .
			8.457e-10 35-50
			PR00320A 16.74 7.146e-
		•	09 35-50 PR00320B
			12.19 9.100e-09 79-94
1180	PR00454	ETS DOMAIN SIGNATURE	PR00454D 10.89 4.150e-
1 1 1 0 0	12.00		19 765-784
1181	BL00291	Prion protein.	BL00291A 4.49 8.962e-
1 1 1 1	5200251		11 152-187
1104	BL00720	Guanine-nucleotide	BL00720B 16.57 4.103e-
1184	PT00150	dissociation stimulators	18 1089-1113
l	1	CDC25 family sign.	
	DT 00015	Mitochondrial energy	BL00215A 15.82 4.553e-
1185	BL00215		13 204-229 BL00215A
		transfer proteins.	15.82 1.429e-12 11-36
1	[1	BL00215A 15.82 9.809e-
	1		11 104-129
			BL00983C 12.69 2.761e-
1187	BL00983	Ly-6 / u-PAR domain	
	i	proteins.	10 77-93
1188	BL00878	Orn/DAP/Arg	BL00878B 10.95 6.000e-
Į.		decarboxylases family 2	16 189-204 BL00878C
	1	pyridoxal-P attachment	17.74 8.435e-15 225-
1		si.	245 BL00878F 19.67
		1	3.625e-13 379-402
			BL00878D 16.56 1.621e-
			09 270-289
1191	PD02939	PROTEIN GLUTATHIONE	PD02939B 10.10 2.723e-
1131	FD02333	SYNTHETASE SY.	12 203-220 PD02939C
1		SIMILIAND SI.	20.01 1.000e-11 224-
1	ļ		252
	i		PR00345B 7.12 2.800e-
	50000345	CONDIMENT CANTE	1 DRUG (45B / 12 2.000E
1193	PR00345	STATHMIN FAMILY SIGNATURE	28 72-101 PR00345E

SEQ ID NO: ACCESSION NO. B.54 7.652e-28 PR00345C 4.54 9 28 101-125 PR0 10.97 1.964e-24 149 PR00345A 1 5.645e-16 43-62 1194 PR00345 STATHMIN FAMILY PR00345B 7.12 2 SIGNATURE 28 108-137 PR0 8.54 7.652e-28 PR00345C 4.54 9 28 137-161 PR0 10.97 1.964e-24 10.97	149-174
PR00345C 4.54 9 28 101-125 PR0 10.97 1.964e-24 149 PR00345A 1 5.645e-16 43-62 1194 PR00345 STATHMIN FAMILY PR00345B 7.12 2 SIGNATURE 28 108-137 PR0 8.54 7.652e-28 PR00345C 4.54 9 28 137-161 PR0 10.97 1.964e-24	149-174
28 101-125 PR0 10.97 1.964e-24 149 PR00345A 1 5.645e-16 43-62 1194 PR00345 STATHMIN FAMILY PR00345B 7.12 2 SIGNATURE 28 108-137 PR0 8.54 7.652e-28 PR00345C 4.54 9 28 137-161 PR0 10.97 1.964e-24	
10.97 1.964e-24 149 PR00345A 1 5.645e-16 43-62 1194 PR00345 STATHMIN FAMILY PR00345B 7.12 2 SIGNATURE 28 108-137 PR0 8.54 7.652e-28 PR00345C 4.54 9 28 137-161 PR0 10.97 1.964e-24	
149 PR00345A 1 5.645e-16 43-62 1194 PR00345 STATHMIN FAMILY PR00345B 7.12 2 SIGNATURE 28 108-137 PR0 8.54 7.652e-28 PR00345C 4.54 9 28 137-161 PR0 10.97 1.964e-24	
1194 PR00345 STATHMIN FAMILY PR00345B 7.12 2 SIGNATURE 28 108-137 PR0 8.54 7.652e-28 PR00345C 4.54 9 28 137-161 PR0 10.97 1.964e-24	
SIGNATURE 28 108-137 PR0 8.54 7.652e-28 PR00345C 4.54 9 28 137-161 PR0 10.97 1.964e-24	
8.54 7.652e-28 PR00345C 4.54 9 28 137-161 PR0 10.97 1.964e-24	-
PR00345C 4.54 9 28 137-161 PR0 10.97 1.964e-24	
10.97 1.964e-24	
185 PR00345A 1 5.645e-16 79-98	
1195 PF00995 Sec1 family. PF00995B 17.37	
13 224-264	
BL00982 Bacterial-type phytoene BL00982A 18.41	6.738e-
dehydrogenase proteins. 11 15-47 1197 BL01298 Dihydrodipicolinate BL01298A 13.90	5.9596-
reductase proteins. 09 51-73	J. J J J C *
1203 BL00061 Short-chain BL00061B 25.79	1.000e-
dehydrogenases/reductase 14 152-190	
s family proteins. 1204 PR00118 BETA-LACTAMASE CLASS A PR00118F 16.42	0 3060-
SIGNATURE 09 213-229	
1206 BL01183 ubiE/COQ5 BL01183B 21.31	1.429e-
methyltransferase family 37 184-229 BLO	
proteins. 27.71 8.535e-27 307 BL01183A 1	
307 BB01163A 1 3.250e-23 51-73	
BL01183C 10.77	
09 246-258	
1208 BL00979 G-protein coupled BL00979L 20.63 receptors family 3 09 105-146	2.485e-
proteins.	
1209 PF00023 Ank repeat proteins. PF00023A 16.03	4.857e-
11 49-65 PF000	
14.20 1.818e-09 1212 PR00048 C2H2-TYPE ZINC FINGER PR00048A 10.52	
SIGNATURE 14 227-241 PRO	
10.52 4.316e-11	
213	
1213 PR00450 RECOVERIN FAMILY PR00450C 12.22 SIGNATURE 10 20-42 PR004	
SIGNATURE 10 20-42 PR004: 12.22 3.506e-09	
PR00450D 16.58	
09 44-64	
1216 BL00412 Neuromodulin (GAP-43) BL00412D 16.54 proteins. 10 179-230	5.598e-
1219 PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 5	.348e-
SIGNATURE 11 249-264	
1222 PD00066 PROTEIN ZINC-FINGER PD00066 13.92 7	
METAL-BINDI. 15 295-308 PD00	
13.92 7.2316-13 419 PD00066 13	
2.286e-12 378-39	91
PD00066 13.92 7	
12 434-447 PD00 13.92 3.348e-11	
363	220-
1223 BL50058 G-protein gamma subunit BL50058 27.23 1.	.000e-
profile. 40 13-61	
1226 BL00412 Neuromodulin (GAP-43) BL00412D 16.54 8	3.439e-
proteins.	1.000e-
ligand proteins. 40 49-101 BL004	
16.28 1.000e-40	114-
168 BL00437C 21	.86

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.		1.000e-40 190-239
			BL00437D 25.72 1.000e-
			40 248-301 BL00437E
			23.95 1.000e-40 327-
	1		379
	<u> </u>		BL01160B 19.54 8.297e-
1230	BL01160	Kinesin light chain	10 6-60
		repeat proteins.	PR00735A 11.19 6.857e-
1231	PR00735	GLYCOSYL HYDROLASE	
		FAMILY 8 SIGNATURE	09 391-405
1232	PR00497	NEUTROPHIL CYTOSOL	PR00497A 6.92 5.553e-
	1	FACTOR P40 SIGNATURE	10 158-176
1233	PR00497	NEUTROPHIL CYTOSOL	PR00497A 6.92 5.553e-
		FACTOR P40 SIGNATURE	10 158-176
1235	BL00866	Carbamoyl-phosphate	BL00866B 36.29 2.776e-
		synthase subdomain	09 75-121
		proteins.	
1237	BL00027	'Homeobox' domain	BL00027 26.43 1.818e-
123 /	BE00027	proteins.	21 36-79
		WW DOMAIN SIGNATURE	PR00403B 12.19 1.184e-
1243	PR00403	WW DOFFAIN BIGHATORE	11 10-25
		SYNTHETASE LIGASE	PD01168L 9.47 2.837e-
1246	PD01168	+	10 31-46 PD01168L
		PROTEIN ALANYL.	9.47 4.490e-10 174-189
		•	PD01168L 9.47 7.612e-
			1
			10 183-198
1249	BL00018	EF-hand calcium-binding	BL00018 7.41 2.800e-10
		domain proteins.	183-196
1254	BL00183	Ubiquitin-conjugating	BL00183 28.97 2.440e-
		enzymes proteins.	36 96-144
1255	BL01115	GTP-binding nuclear	BL01115A 10.22 5.670e-
1233	2201113	protein ran proteins.	11 8-52
1056	BL00373	Phosphoribosylglycinamid	BL00373C 10.35 3.348e-
1256	2000773	e formyltransferase	12 143-156
	1	proteins.	
		TYPE III EGF-LIKE	PR00011B 13.08 3.217e-
1258	PR00011	•	10 174-193
		SIGNATURE	BL00518 12.23 8.286e-
1259	BL00518	Zinc finger, C3HC4 type	10 31-40
		(RING finger), proteins.	PR00070D 11.63 1.000e-
1261	PR00070	DIHYDROFOLATE REDUCTASE	15 112-127 PR00070C
		SIGNATURE	13.09 9.500e-15 51-63
			13.09 9.5008-15 51-63
			PR00070A 12.92 5.500e-
		. <u> </u>	12 16-27
1262	BL00462	Gamma-	BL00462A 20.89 6.438e-
	1	glutamyltranspeptidase	24 140-183 BL00462B
		proteins.	17.88 5.500e-20 230-
			267 BL00462C 27.41
			2.023e-11 292-347
1000	DT 00039	Myc-type, 'helix-loop-	BL00038B 16.97 9.455e-
1263	BL00038	helix' dimerization	11 62-83
		domain proteins.	
			BL01115A 10.22 5.670e-
1264	BL01115	GTP-binding nuclear	11 17-61
		protein ran proteins.	PR00837C 17.21 2.714e-
1266	PR00837	ALLERGEN V5/TPX-1 FAMILY	
	1	SIGNATURE	18 165-182 PR00837A
İ			14.77 4.512e-12 86-105
			PR00837D 11.12 7.577e-
			12 201-215
1269	PR00449	TRANSFORMING PROTEIN P21	PR00449C 17.27 9.308e
1		RAS SIGNATURE	22 40-63 PR00449E
ŀ		1	13.50 1.000e-16 137-
	1		160 PR00449D 10.79
1			3.520e-11 102-116
1270	BL00276	Channel forming colicins	09 17~29
1		proteins.	PD02327C 15.47 9.769e
1275	PD02327	GLYCOPROTEIN ANTIGEN	r
1		PRECURSOR IMMUNOGLO.	09 228-243
	PR00412	EPOXIDE HYDROLASE	PR00412B 12.59 7.894e

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
מבע דה אה:	NO.		
		SIGNATURE	12 119-135 PR00412C
			11.30 1.857e-11 165-
			179 PR00412A 13.23
1090	DROCEEC	D. Land and a second	3.400e-11 100-119
1277	PF00756	Putative esterase.	PF00756C 14.12 9.538e- 10 127-157
1279	BL00134	Serine proteases,	BL00134A 11.96 9.325e-
		trypsin family, histidine proteins.	13 128-145
1280	BL01220	Phosphatidylethanolamine	BL01220C 14.75 9.348e-
:		-binding protein family proteins.	15 248-276
1285	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 2.286e- 10 33-42
1287	PF00791	Domain present in ZO-1	PF00791B 28.49 7.182e-
		and Unc5-like netrin receptors.	11 288-343
1292	PR00802	SERUM ALBUMIN FAMILY	PR00802B 16.51 1.610e-
		SIGNATURE	10 81-105
1297	PR00716	M-PHASE INDUCER	PR00716C 17.65 5.696e-
1200	BL00478	PHOSPHATASE SIGNATURE	09 23-44
1298	BL004/8	LIM domain proteins.	BL00478B 14.79 6.478e-
1301	BL00127	Pancreatic ribonuclease	BL00127C 31.49 3.571e-
2000		family proteins.	28 82-126 BL00127B
			26.57 8.800e-28 23-68
1302	PR00637	TYPE 3 BOMBESIN RECEPTOR	PR00637E 11.27 4.250e-
		SIGNATURE	09 290-306
1307	BL00215	Mitochondrial energy	BL00215A 15.82 5.500e-
	· ·	transfer proteins.	17 13-38 BL00215A
	f		15.82 1.000e-16 226- 251 BL00215A 15.82
			2.658e-13 107-132
1308	PR00898	VASOPRESSIN V2 RECEPTOR	PR00898H 11.34 4.682e-
	,	SIGNATURE	09 552-572
1309	PD00301	PROTEIN REPEAT MUSCLE	PD00301B 5.49 2.731e-
		CALCIUM-BI.	09 390-401
1310	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 9.654e-
•		proceins.	13 73-89 BL00983B 8.19 3.132e-09 12-22
1313	BL00194	Thioredoxin family	BL00194 12.16 1.900e-
		proteins.	11 15-28
1314	BL00594	Aromatic amino acids	BL00594A 16.75 8.969e-
		permeases proteins.	10 53-97
1316	BL00134	Serine proteases,	BL00134A 11.96 9.325e-
•		trypsin family,	13 128-145
1320	BL00783	histidine proteins. Ribosomal protein L13	BL00783C 22.43 6.559e-
1320	200763	proteins.	24 87-117 BL00783A
		F-3002	14.55 1.600e-19 8-33
			BL00783B 12.76 3.500e-
	<u> </u>		12 74-86
1327	PF00514	Armadillo/beta-catenin-	PF00514A 31.30 7.268e-
		like repeat proteins.	11 82-120
1329	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 6.294e-
		region RNP-1 proteins.	11 129-148 BL00030B 7.03 4.789e-09 168-178
1331	PR00497	NEUTROPHIL CYTOSOL	PR00497A 6.92 7.239e-
<u>_</u>		FACTOR P40 SIGNATURE	09 25-43
1332	PR00161	NICKEL-DEPENDENT	PR00161C 9.51 4.930e-
		HYDROGENASE/B-TYPE	09 317-337
		CYTOCHROME SIGNATURE	_
1333	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 6.769e-
	1	ZINC-FINGER METAL-	33 10-49
1226	7700700	BINDING NU.	DDG G G G G G G G G G G G G G G G G G G
1336	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 2.200e- 09 262-281
1337	PR00700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-
,		Troibin Livosina	- ****** T * * * * * * * * * * * * * *

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		PHOSPHATASE SIGNATURE	09 211-230
1340	PR00860	VERTEBRATE	PR00860A 5.46 5.034e-
		METALLOTHIONEIN SIGNATURE	13 5-18
1341	BL00893	mutT domain proteins.	BL00893 18.99 6.750e- 16 46-71
1343	BL01282	BIR repeat proteins.	BL01282B 30.49 5.974e- 21 383-422
1344	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 8.313e- 09 417-427
1345	BL00923	Aspartate and glutamate racemases proteins.	BL00923B 11.41 5.935e- 10 135-146
1348	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 7.231e- 13 44-57
1350	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 3.571e- 32 416-445 PR00193C 12.60 6.318e-31 179- 207 PR00193B 11.69 3.571e-24 133-159 PR00193E 19.47 9.069e- 22 470-499 PR00193A 15.41 1.783e-20 77-97
1352	PR00447	NATURAL RESISTANCE- ASSOCIATED MACROPHAGE PROTEIN SIGNATURE	PR00447E 9.73 1.554e- 15 299-319 PR00447D 13.54 3.408e-15 200- 224 PR00447A 12.73 6.357e-11 97-124 PR00447G 6.69 9.877e- 10 353-373
1353	BL00303	S-100/ICaBP type calcium binding protein.	BL00303A 21.77 6.667e- 26 45-82 BL00303B 26.15 1.000e-24 93-130
1355	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 5.950e- 29 375-421 BL00039A 18.44 7.136e-29 99-138 BL00039C 15.63 4.000e- 18 225-249 BL00039B 19.19 3.182e-14 141- 167
1357	PF00615	Regulator of G protein signalling domain proteins.	PF00615B 16.25 2.216e- 12 84-101 PF00615C 10.06 8.412e-12 162- 176
1360	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.234e- 29 10-49
1361	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925A 5.47 5.091e- 18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87
1362	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117
1363	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 113-148 BL01272C 11.68 3.314e-25 226- 251 BL01272A 6.49 1.231e-18 76-94
1364	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e- 09 167-177
1368	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.592e- 09 76-96
1370	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 1.794e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
· ·	NO.		
1371	BL00242	Integrins alpha chain	10 1-19
	5200242	proteins.	BL00242B 8.13 8.615e- 09 469-479
1372	PR00625	DNAJ PROTEIN FAMILY	PR00625B 13.48 7.353e-
		SIGNATURE	19 46-67 PR00625A
		1	12.84 1.391e-16 14-34
1373	BL00434	HSF-type DNA-binding	BL00434C 23.85 3.778e-
		domain proteins.	09 90-130
1374	PR00962	LETHAL (2) GIANT LARVAE	PR00962C 8.00 6.337e-
1375	PD02475	PROTEIN SIGNATURE MUCIN EPITHELIAL TUMOR-	09 505-526
1 -3/3	FD02475	ASSOCIATE.	PD02475A 23.18 8.552e- 10 1111-1150
1376	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 9.571e-
	1	ZINC-FINGER METAL-	32 24-63
		BINDING NU.	1 - 2 - 3 - 3
1380	BL00194	Thioredoxin family	BL00194 12.16 8.333e-
		proteins.	12 48-61
1381	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 1.458e-
1383	77.00650	ENDOSOMAL III.	15 1123-1136
1303	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 7.600e-10
1384	BL00678	proteins proteins. Trp-Asp (WD) repeat	243-254 BL00678 9.67 7.600e-10
	2200070	proteins proteins.	271-282
1385	BL00303	S-100/ICaBP type calcium	BL00303B 26.15 6.203e-
		binding protein.	10 95-132
1386	BL01160	Kinesin light chain	BL01160B 19.54 5.042e-
		repeat proteins.	09 1574~1628
1387	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 1.000e-
1389	PD01066	(RING finger), proteins.	11 52-61
1369	bD01086	PROTEIN ZINC FINGER	PD01066 19.43 3.600e-
		ZINC-FINGER METAL- BINDING NU.	30 10-49
1390	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 3.512e-
		ZINC-FINGER METAL-	31 32-71
		BINDING NU.	
1392	PR00308	TYPE I ANTIFREEZE	PR00308C 3.83 9.723e-
		PROTEIN SIGNATURE	10 127-137
1393	PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 9.625e-
		SIGNATURE	25 88-110 PR00380D
		·	9.93 2.406e-20 304-326 PR00380B 12.64 4.414e-
	İ	1	16 208-226 PR00380C
			13:18 6.538e-16 243-
			262
1394	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 3.400e-
		METAL-BINDI.	14 462-475 PD00066
•			13.92 8.800e-14 348-
			361 PD00066 13.92
			9.571e-12 405-418 · PD00066 13.92 6.087e-
			11 490-503 PD00066
		1	13.92 8.043e-11 320-
			333
1398	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 6.786e-
]	ZINC-FINGER METAL-	32 10-49
1400	DM01206	BINDING NU.	200
	21701200	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 7.038e-
1406	PD00930	PROTEIN GTPASE DOMAIN	09 270-290 PD00930A 25.62 7.324e-
		ACTIVATION.	15 363-389
1407	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 7.500e-
i		region RNP-1 proteins.	10 457-476
1408	PR00019	LEUCINE-RICH REPEAT	PR00019A 11.19 9.550e-
		SIGNATURE	11 179-193 PR00019A
			11.19 8.826e-10 228-
			242 PR00019B 11.36
			1.360e-09 199-213
	L	<u> </u>	PR00019B 11.36 4.960e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	+ ····		09 176-190
1409	PR00510	NEBULIN SIGNATURE	PR00510A 9.09 4.150e-
1409	FROUSIO	THE STORES	12 182-202 PR00510B
			12.96 8.767e-12 210-
			230 PR00510F 9.88
			8.172e-10 58-75
		İ	PR00510D 9.21 2.367e-
)	09 251-267
1410	PD00078	REPEAT PROTEIN ANK	PD00078B 13.14 5.696e-
7470	12000.0	NUCLEAR ANKYR.	09 31-44
1412	BL00358	Ribosomal protein L5	BL00358B 22.76 1.000e-
1412	DEGUSSO	proteins.	40 57-103 BL00358C
	į	P	13.75 6.087e-14 122-
			136 BL00358D 14.26
	1		5.500e-13 143-158
			BL00358A 13.06 1.931e-
			11 33-44
1414	BL00282	Kazal serine protease	BL00282 16.88 7.338e-
		inhibitors family	10 511-534
		proteins.	
1415	BL00023	Type II fibronectin	BL00023 24.31 4.300e-
		collagen-binding domain	29 40-77
		proteins.	
1417	PR00681	RIBOSOMAL PROTEIN S1	PR00681G 12.54 2.149e-
	· · · -	SIGNATURE	09 38-60
1418	DM00973	3 kw RESISTANCE BENOMYL	DM00973A 21.17 1.462e-
		YLL028W CYCLOHEXIMIDE.	09 171-208
1419	PR00319	BETA G-PROTEIN	PR00319B 11.47 1.571e-
		(TRANSDUCIN) SIGNATURE	09 428-443
1420	PD01941	TRANSMEMBRANE	PD01941A 14.81 1.000e-
		COTRANSPORTER SYMP.	40 142-196 PD01941B
			15.02 7.049e-30 400-
			447 PD01941E 15.92
			2.475e-20 817-864
ļ			PD01941C 19.96 3.118e-
1			19 488-543 PD01941D
	}	ļ	27.18 9.614e-18 641-
			690 PD01941F 28.52
			5.382e-15 1038-1093
1422	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 8.043e-
ļ			12 199-217
1423	PR00209	ALPHA/BETA GLIADIN	PR00209B 4.88 6.318e-
		FAMILY SIGNATURE	11 1009-1028
1424	BL50002	Src homology 3 (SH3)	BL50002A 14.19 8.200e-
Į.	1	domain proteins profile.	14 367-386 BL50002A
	1		14.19 9.250e-12 298-
ĺ	1	İ	317 BL50002A 14.19
1	1	1	4.462e-11 208-227
1	}		BL50002B 15.18 1.000e-
L			09 244-258 PF00628 15.84 3.045e-
1425	PF00628	PHD-finger.	
			12 330-345
1426	PF00628	PHD-finger.	PF00628 15.84 3.045e-
			12 377-392
1427	PR00405	HIV REV INTERACTING	PR00405B 11.83 5.114e- 16 281-299 PR00405A
		PROTEIN SIGNATURE	16 281-299 PR00405A
			282 BL00039D 21.67 5.219e-
1428	BL00039	DEAD-box subfamily ATP-	
1		dependent helicases	34 147-193
1		proteins.	j.
		1	77000000 12 01 0 000-
1429	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 8.920e-
		G-PROTEIN BETA WD-40 REPEAT SIGNATURE	10 577-592
1429	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE INOSITOL PHOSPHATASE	10 577-592 PR00378D 16.86 7.563e-
		G-PROTEIN BETA WD-40 REPEAT SIGNATURE	10 577-592 PR00378D 16.86 7.563e- 12 295-314 PR00378B
		G-PROTEIN BETA WD-40 REPEAT SIGNATURE INOSITOL PHOSPHATASE	10 577-592 PR00378D 16.86 7.563e- 12 295-314 PR00378B 13.80 8.650e-10 166-
		G-PROTEIN BETA WD-40 REPEAT SIGNATURE INOSITOL PHOSPHATASE	10 577-592 PR00378D 16.86 7.563e- 12 295-314 PR00378B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		PROTEIN SIGNATURE	10 103-124
1433	BL01113	Clq domain proteins.	BL01113B 18.26 7.049e- 15 14-50 BL01113C 13.18 7.000e-12 82-102
1434	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 7.983e- 10 135-150
1436	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 1.000e- 12 84-103
1438	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.500e- 09 250-268 BL00290A 20.89 4.000e-09 188- 211
1440	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-
1441	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e- 09 88-102
1444	BL00422	Granins proteins.	BL00422D 19.48 1.000e- 08 114-138
1445	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841A 21.71 1.000e- 40 73-123 PD01841B 14.35 1.000e-40 144- 185 PD01841D 17.87 1.000e-40 206-258 PD01841F 13.36 1.000e- 40 296-345 PD01841G 24.26 1.000e-40 349- 403 PD01841I 23.00 1.000e-40 494-536 PD01841J 14.94 1.000e- 40 895-932 PD01841L 18.42 1.000e-40 1083- 1125 PD01841B 18.60 9.719e-38 258-296 PD01841K 14.81 1.000e- 35 1041-1071 PD01841H 21.30 3.189e-31 435- 472 PD01841C 13.78
			1.000e-25 185-206 PD01841M 10.82 1.250e- 20 1175-1194
1446	PF00816	H-NS histone family.	PF00816B 13.84 8.875e- 09 190-220
1447	PR00048 . ;	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.080e- 09 402-416
1448	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315D 18.40 7.393e- 09 23-67
1451	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 2.800e- 10 94-104
1454	DM01688	2 POLY-IG RECEPTOR.	DM01688D 13.44 7.146e-
1455	PF00777	Sialyltransferase family.	PF00777C 18.60 2.929e- 22 4-59
1457	BL00927	Trehalase proteins.	BL00927C 10.83 8.085e- 09 42-53
1460	BL00545	Aldose 1-epimerase proteins.	BL00545C 11.28 7.353e- 17 169-182 BL00545A 10.20 2.071e-15 73-89 BL00545B 13.10 3.942e- 09 140-153
1466	PR00097	ANTHRANILATE SYNTHASE COMPONENT II SIGNATURE	PR00097C 9.42 9.069e- 09 233-245
1472	BL01129	Hypothetical yabO/yceC/sfhB family proteins.	BL01129E 13.25 5.250e- 22 170-195 BL01129C 25.56 9.526e-18 63-106
1473	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.821e- 09 2114-2145
1475	PF00686	Starch binding domain proteins.	PF00686A 13.45 9.100e- 09 267-277

EQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
477	PF00566	Probable rabGAP domain proteins.	PF00566A 12.64 7.333e- 10 466-476
L478	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 9.400e- 10 43-53
1479	DM00406	GLIADIN.	DM00406 7.73 8.541e-10 292-305
1480	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.385e- 15 69-87 BL00290A 20.89 5.091e-11 12-35
1481	PR00150	PHOSPHOENOLPYRUVATE CARBOXYLASE SIGNATURE	PR00150F 10.45 9.039e- 09 21-51
1482	PF00780	Domain found in NIK1- like kinases, mouse citron and yeast ROM.	PF00780I 14.69 4.825e- 09 107-137
1483	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 1.153e- 09 108-162
1485	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 5.909e- 25 17-56
1486	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.529e- 09 34-50
1488	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 9.586e- 10 116-162
1490	BL00166	Enoyl-CoA hydratase/isomerase proteins.	BL00166D 22.87 2.607e- 24 190-226 BL00166C 18.93 5.500e-14 140- 167 BL00166B 16.92 9.357e-11 93-115
1491	BL00452	Guanylate cyclases proteins.	BL00452D 28.59 3.700e- 31 63-106 BL00452E 11.92 3.045e-13 115- 131
1492	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 3.667e- 09 532-546
1497	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 11 384-400 BL00107A 18.39 5.345e-11 322- 353
1500	PF00876	Ogre family.	PF00876E 7.99 1.947e- 10 107-117
1502	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e- 24 112-155
1503	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e- 24 112-155
1505	BL01177	Anaphylatoxin domain proteins.	BL01177E 20.64 5.800e- 24 448-475 BL01177C 17.39 5.333e-19 402- 421 BL01177B 13.61 7.840e-16 155-171 BL01177D 17.50 1.900e- 15 427-445
1506	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 5.500e- 14 311-336 BL00972A 11.93 7.429e-14 48-66 BL00972E 20.72 8.759e- 10 341-363
1512	BL00523	Sulfatases proteins.	BL00523E 19.27 4.536e- 22 76-106 BL00523D 9.89 1.563e-11 40-52 BL00523F 10.85 4.162e- 09 159-170 BL00523G 9.46 5.333e-09 256-266
1516	BL00914	Syntaxin / epimorphin family proteins.	BL00914 24.91 7.045e- 14 168-218
1518	BL00600	Aminotransferases class III pyridoxal-phosphate attachment si.	BL00600A 17.98 6.143e- 19 98-122 BL00600E 16.43 1.771e-17 302-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
CHG ID MO:	NO.		1230115
			331 BL00600G 12.43
			9.625e-17 377-396
			BL00600B 19.60 5.091e-
			15 160-186 BL00600C
			16.18 6.040e-12 190-
ł			206 BL00600F 8.77
		İ	1.000e-11 343-356
			BL00600D 8.71 1.000e-
			10 281-295
1523	PD00930	PROTEIN GTPASE DOMAIN	PD00930B 33.72 9.600e-
		ACTIVATION.	18 41-82
1528	PR00320	G-PROTEIN BETA WD-40	PR00320B 12.19 4.774e-
		REPEAT SIGNATURE	11 192-207 PR00320B
			12.19 8.839e-11 272-
			287 PR00320B 12.19
			9.743e-10 106-121
	ł		PR00320A 16.74 1.878e-
			09 192-207 PR00320A
	1	,	16.74 2.317e-09 106-
			121 PR00320A 16.74
	1		8.683e-09 272-287
	1	1	PR00320C 13.01 8.800e-
			09 106-121
1538	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 4.508e-
1536		ENDOSOMAL III.	15 171-184
1539	PF00781	Diacylglycerol kinase	PF00781D 11.11 7.593e-
		catalytic domain	10 103-127
1540	7770000	proteins (presumed).	7700005511 00 70 1 001
1540	PR00965	OCULAR ALBINISM TYPE 1	PR00965H 10.73 1.231e-
		PROTEIN SIGNATURE	29 312-334 PR00965E
			12.93 5.846e-29 172-
·			195 PR00965F 5.98 1.123e-28 209-231
		}	PR00965C 15.04 1.000e-
	<u> </u>		27 131-151 PR00965D
			5.84 1.000e-27 150-170
			PR00965G 8.52 2.440e-
	1		27 258-279 PR00965B
	Ì		4.80 8.650e-26 88-109
		·	PR00965A 12.52 1.000e-
:			25 35-55 PR00965I
			3.91 6.442e-25 385-406
1541	BL01013	Oxysterol-binding	BL01013D 26.81 9.719e-
		protein family proteins.	17 163-207
1543	PD02699	PROTEIN DNA-BINDING	PD02699C 24.84 1.000e-
		BINDING DNA.	40 599-646 PD02699A
			8.91 2.286e-34 219-248
:			PD02699B 18.28 6.143e-
<u> </u>	<u></u>		21 485-509
1544	PR00049	WILM'S TUMOUR PROTEIN	PR00049D 0.00 7.857e-
		SIGNATURE	10 182-197 PR00049D
			0.00 7.102e-09 67-82
1547	BL00951	ER lumen protein	BL00951C 19.35 1.000e-
	ĺ	retaining receptor	40 93-142 BL00951D
		proteins.	13.94 8.714e-40 142-
			177 BL00951A 15.10
			1.000e-38 2-38 .
			BL00951B 14.23 6.250e-
			33 38-69
1548	BL00536	Ubiquitin-activating	BL00536F 13.65 8.920e-
		enzyme proteins.	30 279-318 BL00536D
	!		22.91 5.737e-24 21-65
			BL00536E 16.94 4.696e-
			18 248-279
1549	PR00139	ASPARAGINASE/GLUTAMINASE	PR00139C 11.72 9.679e-
_ = =		FAMILY SIGNATURE	09 550-569
1553	PR00049	WILM'S TUMOUR PROTEIN	PR00049D 0.00 5.119e-
		SIGNATURE	09 58-73

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
.556	BL00061	Short-chain	BL00061B 25.79 6.276e-
.556	BE00001	dehydrogenases/reductase s family proteins.	13 67-105
		Hypothetical cof family	BL01228D 17.44 8.105e-
557	BL01228	proteins.	12 107-132 BL01228D 17.44 8.105e-
558	BL01228	Hypothetical cof family proteins.	12 107-132
.559	BL01228	Hypothetical cof family	BL01228D 17.44 8.105e-
.559	BB01220	proteins.	12 107-132 BT-00522C 11.90 6.600e-
.562	BL00522	DNA polymerase family X	18 412-436 BL00522B
		proteins.	27.30 1.738e-16 364-
		·	410 BL00522A 25.52
	1		6.000e-16 279-326 BL00522E 19.63 6.123e-
•	1		14 502-532 BL00522F
			14.90 2.385e-13 551-
		DD.	FF00651 15.00 1.947e-
1563	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	11 46-59
1564	BL00299	Ubiquitin domain	BL00299 28.84 2.823e-
•		proteins.	10 324-376 BL01013D 26.81 8.594e-
1566	BL01013	Oxysterol-binding	17 184-228 BL01013C
		protein family proteins.	9.97 4.906e-12 14-24
1567	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 3.400e-10
		proteins proteins.	378-389 BL00678 9.67 5.800e-10 418-429
			BL00678 9.67 8.800e-10
			295-306
1570	BL00479	Phorbol esters /	BL00479B 12.57 5.235e-
2370		diacylglycerol binding	17 297-313 BL00479A
		domain proteins.	19.86 6.625e-15 271- 294 BL00479A 19.86
			2.667e-14 147-170
			BL00479B 12.57 6.294e-
			12 173-189
1576	PR00665	OXYTOCIN RECEPTOR	PR00665G 12.36 4.673e- 24 364-384 PR00665D
		SIGNATURE	9.93 1.200e-22 138-155
•			PR00665F 11.73 4.000e-
		•	22 337-354 PR00665C
		• .	5.89 1.000e-20 65-80 PR00665B 5.29 4.337e-
			19 24-39 PRO0665E
-			5.60 2.929e-15 246-260
			PR00665A 5.99 5.622e-
		A law REED DEDUCTACE	15 11-25 DM00099B 14.73 9.308e-
1577	DM00099	4 kw A55R REDUCTASE TERMINAL	10 127-137
		DIHYDROPTERIDINE.	
1579	BL00524	Somatomedin B domain	BL00524A 9.65 6.776e- 14 52-73
	PD02004	proteins. HYDROLASE N4- PRECURSOR	PD02894B 13.93 6.959e-
1580	PD02894	PROTEIN SIGNAL BE.	16 182-215 PD02894A
			21.96 2.125e-10 57-103
1581	BL00411	Kinesin motor domain	BL00411C 15.04 5.292e- 12 32-54 BL00411H
		proteins.	15.66 4.441e-11 245-
1:	ŀ		276
1582	PR00604	CLASS IA AND IB	PR00604A 11.13 2.440e-
		CYTOCHROME C SIGNATURE	09 79-87 PF00651 15.00 1.000e-
1584	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	10 225-238
1585	DM01551	kw OSTEOINDUCTIVE YOPM	DM01551C 14.62 9.455e-
] 1003		MEMBRANE OUTER.	11 125-145
1586	DM01354	kw TRANSCRIPTASE REVERSE	DM01354S 11.61 7.750e-
	i	II ORF2.	U3 414-433

	·		1
SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1587	PR00072	MALIC ENZYME SIGNATURE	PR00072B 13.77 7.955e- 33 180-210 PR00072A
			12.75 6.040e-25 120-
			145 PR00072C 11.42
			2.286e-24 216-239
			PR00072D 10.77 3.400e- 22 276-295 PR00072E
			10.54 1.360e-19 301-
			318 PR00072G 10.45
			5.304e-19 433-450
			PR00072F 8.87 5.935e-
1589	BL00191	Cytochrome b5 family,	15 332-349 BL00191H 15.64 1.537e-
1509	Proorat	heme-binding domain	22 61-113 BL00191K
		proteins.	17.38 9.027e-12 398-
		-	442
1590	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 7.716e-
		ENDOSOMAL III.	13 211-224 DM01970B
1591	DM00517	5 kw NUCLEAR 60.7 NUP1	8.60 2.157e-12 94-107 DM00517B 10.96 6.625e-
1371	D:100317	CHROMOSOME.	16 1175-1193 DM00517A
			8.21 1.000e-11 1015-
<u> </u>		<u> </u>	1026
1592	BL00037	Myb DNA-binding domain	BL00037B 15.92 3.250e-
		proteins repeat proteins proteins.	27 116-142 BL00037A 16.68 2.500e-24 83-107
		proceins.	BL00037A 16.68 3.250e-
			12 31-55 BL00037B
			15.92 3.526e-11 64-90
			BL00037C 16.86 9.654e-
			10 146-164
1595	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.514e- 09 110-127
1598	PF00628	PHD-finger.	PF00628 15.84 3.250e-
			11 1667-1682
1599	PR00014	FIBRONECTIN TYPE III	PR00014D 12.04 5.500e- 09 980-995
1600	BL00518	REPEAT SIGNATURE Zinc finger, C3HC4 type	BL00518 12.23 6.571e-
1000	,	(RING finger), proteins.	10 30-39
1602	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 5.402e-
;		proteins.	10 136-187
1605	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 3.571e-
1607	BL00252	Interferon alpha, beta	BL00252A 18.49 6.657e-
1307	2200232	and delta family	23 20-57 BL00252B
	•	proteins.	19.78 9.125e-16 58-109
1610	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.000e-
	77.000.1	<u> </u>	08 61-94
1611	BL00904	Protein prenyltransferases alpha	BL00904C 8.98 7.353e- 10 91-125 BL00904D
		subunit repeat proteins	1.47 6.018e-09 127-168
		proteins.	
1612	PF00168	C2 domain proteins.	PF00168C 27.49 3.250e-
			09 365-391
1613	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 6.051e- 09 932-983 BL00412D
		proteins.	16.54 7.153e-09 933-
			984
1614	BL00559	Eukaryotic molybdopterin	BL00559I 13.63 3.531e-
	1	oxidoreductases	25 54-83 BL00559K
		proteins.	13.17 2.957e-18 197-
	1		224 BL00559J 19.63
			6.870e-16 124-176 BL00559L 13.60 9.000e-
	1		16 266-284
1615	PD01427	TRANSFERASE	PD01427B 22.45 3.025e-
	1	METHYLTRANSFERASE BI.	22 500-541 PD01427A
	<u> </u>		19.94 8.773e-18 439-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	1.0.		472
1616	BL00115	Eukaryotic RNA	BL00115Z 3.12 7.485e-
T0T0	BHOOTIS	polymerase II	09 152-201 BL00115Z
	į.	heptapeptide repeat	3.12 9.603e-09 145-194
		neptapeptide repeat	3.12 3.0030 03 110 101
		proteins.	250000 06 15 7 2500
1617	BL00303	S-100/ICaBP type calcium	BL00303B 26.15 7.750e-
		binding protein.	32 51-88 BL00303A
			21.77 1.947e-31 4-41
	BL01254	Fetuin family proteins.	BL01254F 10.02 8.754e-
1618	BT01724	recuin ramity processing	09 137-147
		PEPTIDE REDUCTASE	PD01888B 25.10 1.000e-
1619	PD01888		40 47-97 PD01888C
		PROTEIN METHI.	
			21.56 7.000e-30 125-
			155 PD01888A 12.84
		•	8.800e-15 7-23
	- DD 00000	MOLLUSCAN RHODOPSIN C-	PR00239E 1.58 3.455e-
1621	PR00239	MOLLOSCAN RHODOFSIN C	09 692-704 PR00239E
		TERMINAL TAIL SIGNATURE	
			1.58 4.580e-09 697-709
			PR00239E 1.58 4.580e-
	1		09 702-714 PR00239E
	J		1.58 5.193e-09 703-715
		- I I I I I I I I I I I I I I I I I I I	PR00860B 7.04 1.900e-
1622	PR00860	VERTEBRATE	18 27-41 PRO0860C
		METALLOTHIONEIN	18 27-41 PROUBBUC
	1	SIGNATURE	9.61 1.474e-14 41-51
			PR00860A 5.46 1.720e-
	1		14 5-18
		MITOCHONDRIAL BROWN FAT	PR00784D 15.86 8.027e-
1624	PR00784		
		UNCOUPLING PROTEIN	11 77-95
	.	SIGNATURE	
1626	BL00325	Actin-depolymerizing	BL00325B 21.66 1.000e-
1020	DB00323	proteins.	40 93-139 BL00325A
		process.	24.83 6.786e-23 61-93
			BL00064B 23.57 1.000e-
1631	BL00064	L-lactate dehydrogenase	BL00064B 23.57 1.000E-
		proteins.	40 82-130 BL00064C
		-	17.28 1.000e-40 137-
			182 BL00064E 27.20
			1.000e-40 223-275
			BL00064F 25.14 7.882e-
	ļ	1	36 286-331 BL00064A
			36 286-331 BL00084A
			21.16 1.000e-33 22-60
			BL00064D 14.19 6.500e-
•			31 182-212
		RIBOSOMAL PROTEIN L27	PR00063B 15.24 9.700e-
1632	PR00063	i .	11 59-84 PR00063A
	}	SIGNATURE	11 59-84 PRO0063A
	1		11.71 1.614e-09 34-59
1634	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239D 0.00 1.105e-
2004		TERMINAL TAIL SIGNATURE	11 36-49 PR00239C
	1		3.51 2.538e-09 37-45
			BL01210B 13.92 9.531e-
1636	BL01210	Caveolins proteins.	•
			10 133-183
1637	BL00982	Bacterial-type phytoene	BL00982A 18.41 5.388e-
,		dehydrogenase proteins.	11 11-43
		ubiE/COO5	BL01183B 21.31 8.144e-
1639	BL01183		
		methyltransferase family	14 134-111
		proteins.	1
1640	PR00015	GRAM-POSITIVE COCCUS	PR00015B 9.84 8.468e-
1010		SURFACE PROTEIN ANCHOR	10 128-149
		SIGNATURE	PR00320B 12.19 5.935e-
1641	PR00320	G-PROTEIN BETA WD-40	FKUU320B 12.19 5.9356-
		REPEAT SIGNATURE	11 364-379 PR00320A
			16.74 7.828e-11 364-
		•	379 PR00320C 13.01
ł			2.800e-10 279-294
	1		2.00VE-IU 2/3-234
l			PR00320C 13.01 2.800e-
1	i		10 364-379 PR00320B
1			12.19 5.114e-10 279-
1	1		294 PR00320A 16.74
!	1		1.659e-09 279-294
	1		1 1 659E-U9 2/J-274

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00320A 16.74 2.098e- 09 229-244
1642	PF00023	Ank repeat proteins.	PF00023A 16.03 6.464e- 09 114-130
1643	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.806e- 11 74-94
1644	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 109-120 BL00678 9.67 5.737e-09 528-539
1645	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 7.366e- 17 56-89
1646	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.270e- 21 103-125 PR00380D 9.93 6.308e-18 386-408 PR00380C 13.18 7.923e- 16 332-351 PR00380B 12.64 6.657e-15 292- 310
1647	DM01242	3 THREONINETRNA LIGASE.	DM01242C 17.15 9.791e- 37 340-381 DM01242E 23.00 5.071e-31 463- 505 DM01242D 23.29 3.925e-30 420-463 DM01242B 23.57 8.054e- 18 265-314 DM01242F 10.61 7.618e-14 526- 540
1649	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 5.500e- 10 13-34
1651	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.720e- 11 431-485
1652	BL00933	FGGY family of carbohydrate kinases proteins.	BL00933A 17.50 4.673e- 12 11-35 BL00933E 13.80 9.217e-09 456- 472
1653	BL00795	Involucrin proteins.	BL00795C 17.06 2.988e- 10 70-115
1654	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 302-334
1655	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 282-314
1656	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 1.391e- 16 607-630
1657	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.938e- 11 114-136
1658	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.889e- 10 442-455
1659	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 4.140e- 12 376-401 BL00972E 20.72 5.629e-09 446- 468
1660	BL00406	Actins proteins.	BL00406D 12.58 8.767e- 15 188-243
1661	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE	PR00105A 10.36 4.900e- 13 1140-1157 PR00105B 12.32 2.800e-12 1259- 1274 PR00105C 10.86 1.000e-10 1305-1319
1662	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 3.172e- 33 3119-3163
1663	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 5.714e-20 89-105 PR00319A 15.27 5.286e- 19 51-68 PR00319B 11.47 8.200e-19 70-85

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1664	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 5.050e-10 489-502
1667	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 8.500e- 38 7-46
1669	BL01153	NOL1/NOP2/sun family proteins.	BL01153D 19.69 1.188e- 17 115-141 BL01153C 13.67 8.977e-15 66-80 BL01153B 20.52 1.885e- 10 13-37
1671	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE	PR00678H 9.13 3.100e- 10 1146-1169
1672	ВL00598	Chromo domain proteins.	BL00598 14.45 8.500e- 20 27-49
1673	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.329e- 09 686-707
1674	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.580e- 11 343-358 PR00049D 0.00 1.286e-10 342-357
1676	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PR00747H 12.76 8.636e- 19 427-448 PR00747G 14.50 2.286e-18 368- 393 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e- 17 42-63 PR00747D 15.23 8.759e-17 163- 183 PR00747E 15.13 8.244e-15 254-272 PR00747B 7.65 S.355e-
			13 75-90 PR00747F 13.56 8.714e-10 311- 328
1677	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PR00747H 12.76 8.636e- 19 309-330 PR00747G 14.50 2.286e-18 250- 275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e- 17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e- 10 193-210
1680	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 4.600e-10 406-417 BL00678 9.67 6.684e-09 320-331
1681	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 4.600e-10 329-340 BL00678 9.67 6.684e-09 243-254
1683	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 1.346e- 13 389-410
1685	PR00646	RDC1 ORPHAN RECEPTOR SIGNATURE	PR00646H 6.32 4.188e- 09 755-771
1690	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e- 09 75-129
1691	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 7.281e- 10 418-433 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 8.125e- 10 420-435
1.00	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PRO0456E 3.06 7.281e- 10 487-502 PR00456E
1692		SIGNATORE	3.06 7.281e-10 488-503 PR00456E 3.06 8.125e- 10 489-504 BL00674C 22.60 8.043e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			4.46 4.000e-23 241-263 BL00674D 23.41 8.560e- 18 338-385 BL00674E 15.24 1.720e-15 414- 434
1697	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409F 12.70 4.388e- 10 427-447
1698	PR00466	CYTOCHROME B-245 HEAVY CHAIN SIGNATURE	PR00466C 10.17 3.443e- 13 187-208 PR00466B 5.03 5.500e-11 162-186 PR00466F 9.16 6.159e- 09 498-517
1699	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.217e- 12 283-300 BL00028 16.07 3.769e-11 255- 272 BL00028 16.07 5.154e-11 171-188 BL00028 16.07 5.500e- 11 227-244 BL00028 16.07 1.600e-10 199- 216
1700 ;	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 3.348e- 15 62-102 BL01019B 19.49 4.000e-15 107- 162
1703	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.484e- 12 200-239
1707	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.558e- 14 134-153
1710	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.565e- 10 116-130 PR00019B 11.36 4.600e-09 113- 127 PR00019B 11.36 7.120e-09 204-218
1711	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 6.523e- 11 232-247 BL01159 13.85 5.408e-10 613- 628
1712	PF00023	Ank repeat proteins.	PF00023A 16.03 7.000e- 10 187-203
1713	PF00642	Zinc finger C-x8-C-x5-C- x3-H type (and similar). Zinc finger C-x8-C-x5-C-	PF00642 11.59 9.550e- 11 230-241
1715	BL01115 .	x3-H type (and similar). GTP-binding nuclear	PF00642 11.59 9.550e- 11 230-241 BL01115A 10.22 7.129e-
1718	BL00353	protein ran proteins. HMG1/2 proteins.	09 7-51 BL00353C 14.83 6.018e- 10 136-183 BL00353B
1719	BL00412	Neuromodulin (GAP-43)	11.47 8.866e-09 86-136 BL00412D 16.54 5.408e-
1721	BL00038	proteins. Myc-type, 'helix-loop-helix' dimerization domain proteins.	09 432-483 BL00038B 16.97 8.448e- 12 79-100 BL00038A 13.61 4.000e-11 52-68
1723	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567C 9.17 8.500e-
1724	BL01279	Protein-L- isoaspartate(D- aspartate) O- methyltransferase signa.	BL01279A 24.27 5.663e- 12 233-281
1728	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.059e-11 73-86 BL00018 7.41 4.176e-11 157-170
1730	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 1.089e- 09 17-61

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1731	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e- 10 296-350
1732	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e- 10 316-370
1733	PF00850	Histone deacetylase family.	PF00850F 15.70 4.349e- 22 246-279 PF00850D 14.76 6.850e-20 177- 201 PF00850E 8.88 8.691e-18 209-235 PF00850G 22.75 4.098e- 14 281-323
1734	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 5.932e- 09 292-307
1735	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.263e- 10 492-502
1743	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e- 11 5-27 PR00449D 10.79 2.241e-10 109- 123 PR00449E 13.50 9.289e-10 144-167
1744	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e- 11 5-27 PR00449D 10.79 2.241e-10 109- 123 PR00449E 13.50 9.289e-10 144-167
1745	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 8.297e- 15 136-160
1746	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081B 10.38 6.727e- 11 45-57 PR00081E 17.54 3.935e-10 150- 168
1747	BL00439	Acyltransferases ChoActase / COT / CPT family proteins.	BL00439H 18.24 8.435e- 14 65-91 BL00439G 13.40 2.895e-12 3-14
1749	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 7.158e- 11 4-20
1751	PD00066	PROTEIN ZINC-FINGER METAL-BINDI	PD00066 13.92 3.400e- 14 33-46 PD00066
	;		13.92 1.000e-13 89-102 PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130
1753	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 6.516e- 18 33-77
1754	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318
1756	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.750e- 35 10-49
1758	DM00406	GLIADIN.	DM00406 7.73 7.600e-09 653-666
1762	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 4.529e- 09 224-278
1765	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 5.950e- 11 146-167
1775	PF00023	Ank repeat proteins.	PF00023A 16.03 3.077e- 14 523-539
1776	BL00942	glpT family of transporters proteins.	BL00942F 15.07 4.343e- 10 371-389 BL00942B 20.36 8.040e-09 94-137
1777	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.373e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1778	BL00084	Copper type II, ascorbate-dependent monooxygenases proteins.	BL00084D 25.11 3.700e- 20 169-224 BL00084B 24.26 8.134e-16 10-58 BL00084C 27.71 8.412e- 11 107-158
1779	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 3.758e- 18 611-655 BL01013A 25.14 2.881e-15 344- 380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e- 12 409-420
1783	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515
1784	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515

^{*} results include in order: accession number subtype; raw score; p-value; postion of signature in amino acid sequence.

TRADOCS:1416223.1(%CRJ0!!.DOC)

TABLE 4

NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
	ig	Immunoglobulin domain	2.1e-32	109.5
3	pkinase	Eukaryotic protein kinase	1.3e-29	110.7
<u> </u>	zf-C2H2	Zinc finger, C2H2 type	1.6e-21	84.9
	fn3	Fibronectin type III domain	0	1097.1
	fn3	Fibronectin type III domain	0	1035.0
7	fn3	Fibronectin type III domain	0	1090.4
3	fn3	Fibronectin type III domain	0	1097.1
}	TBC	TBC domain	4e-40	146.7
	p450	Cytochrome P450	9.5e-17	62.0
.0	ank	Ank repeat	6e-20	79.7
L2	iq	Immunoglobulin domain	1.7e-05	22.7
L4	zf-MYND	MYND finger	1.3e-06	35.4
15		MYND finger	1.3e-06	35.4
L6	zf-MYND	Zinc finger, C2H2 type	1.7e-99	343.9
1.7	zf-C2H2	CAP-Gly domain	1.2e-25	98.7
18	CAP_GLY	IMP dehydrogenase / GMP	1.6e-119	410.5
20	IMPDH_C	reductase C terminus	4.3e-102	352.6
21	IMPDH_C	IMP dehydrogenase / GMP reductase C terminus		
22	pkinase	Eukaryotic protein kinase domain	2.4e-79	277.0
23	pkinase	Eukaryotic protein kinase domain	8.4e-74	258.6
25	RNA_pol_A	RNA polymerase alpha subunit	Ö	1077.7
26	Clq	Clg domain	1.9e-10	44.4
27	Ribosomal_L2	Ribosomal protein L23	7.8e-32	111.2
28	Ribosomal_L2	Ribosomal protein L23	1e-29	104.2
30	zf-A20	A20-like zinc finger	1.5e-10	48.5
31	zf-A20	A20-like zinc finger	1.5e-10	48.5
32	FMN dh	FMN-dependent dehydrogenase	5.4e-179	608.1
34	PID	Phosphotyrosine interaction domain (PTB/PID)	3.8e-59	209.9
35	ig	Immunoglobulin domain	1.4e-13	48.8
36	ig	Immunoglobulin domain	1.4e-13	48.8
40	kinesin	Kinesin motor domain	6.7e-76	265.6
44	Ets	Ets-domain	1.4e-56	182.1
	Ets	Ets-domain	1.4e-56	182.1
45	LRR	Leucine Rich Repeat	1.7e-13	58.3
46		Zinc finger, C2H2 type	2.3e-162	552.8
48	zf-C2H2	Immunoreceptor tyrosine-based	1.4e-05	31.9
49	ITAM	activation mot		102.0
50	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	
	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
51			8.5e-45	162.3
	ras	Ras family		
52	ras PRK	Phosphoribulokinase	2.1e-65	230.7
	PRK myb_DNA-	Phosphoribulokinase Myb-like DNA-binding domain	2.1e-65 0.096	15.2
52 53 54	PRK myb_DNA- binding	Phosphoribulokinase Myb-like DNA-binding domain	2.1e-65 0.096	
52 53 54	PRK myb_DNA- binding voltage_CLC	Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels	2.1e-65 0.096	15.2
52 53 54 55 56	PRK myb_DNA- binding voltage_CLC sugar_tr	Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter	2.1e-65 0.096 3.3e-186	15.2 631.9
52 53 54 55 56 57	PRK myb_DNA- binding voltage_CLC sugar_tr TBC	Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter TBC domain	2.1e-65 0.096 3.3e-186 0.00015	15.2 631.9 -64.3
52 53 54 55 56 57 58	PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank	Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat	2.1e-65 0.096 3.3e-186 0.00015 2.2e-37 5.9e-25	15.2 631.9 -64.3 137.6
52 53 54 55 56 57	PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank ank PMP22_Claudi	Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat	2.1e-65 0.096 3.3e-186 0.00015 2.2e-37	15.2 631.9 -64.3 137.6 96.3
52 53 54 55 56 57 58 59 67	PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank ank PMP22_Claudi n	Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat PMP-22/EMP/MP20/Claudin family	2.1e-65 0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 5.9e-25 7.9e-49	15.2 631.9 -64.3 137.6 96.3 96.3
52 53 54 55 56 57 58 59 67	PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank ank PMP22_Claudi n C2	Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat PMP-22/EMP/MP20/Claudin family C2 domain	2.1e-65 0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 5.9e-25 7.9e-49	15.2 631.9 -64.3 137.6 96.3 96.3 175.6
52 53 54 55 56 57 58 59 67	PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank ank PMP22_Claudi n C2 C2	Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat PMP-22/EMP/MP20/Claudin family C2 domain C2 domain	2.1e-65 0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 5.9e-25 7.9e-49 7.9e-54 2.3e-54	15.2 631.9 -64.3 137.6 96.3 96.3 175.6
52 53 54 55 56 57 58 59 67	PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank ank PMP22_Claudi n C2	Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat PMP-22/EMP/MP20/Claudin family C2 domain	2.1e-65 0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 5.9e-25 7.9e-49	15.2 631.9 -64.3 137.6 96.3 96.3 175.6

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:		domain		SCORE
74	pkinase	Eukaryotic protein kinase	100000	
		domain	2.8e-38	140.6
76	zf- C4 Topoisom	Topoisomerase DNA binding C4 zinc fing	5.4e-54	192.8
83	Peptidase_S9	Prolyl oligopeptidase family	4.3e-10	36.8
84	fn3	Fibronectin type III domain	4.1e-51	183.2
86	SH2	Src homology domain 2	3.1e-22	67.7
88	ig	Immunoglobulin domain	0.0091	14.0
89	WD40	WD domain, G-beta repeat	2.1e-21	84.6
92	laminin_G	Laminin G domain	6.1e-27	98.5
93	AMP-binding	AMP-binding enzyme	2.4e-13	-37.2
95	pkinase	Eukaryotic protein kinase domain	1.4e-59	211.4
96	pkinase	Eukaryotic protein kinase domain	2.6e-51	183.9
97	adh_short	short chain dehydrogenase	2e-61	217.5
98	kinesin	Kinesin motor domain	2.2e-86	300.4
101	IRS	PTB domain (IRS-1 type)	5.4e-36	133.0
102	AAA	ATPases associated with various cellular act	6.8e-05	-5.2
104	pkinase	Eukaryotic protein kinase domain	2.7e-73	256.9
106	ras	Ras family	8.3e-24	92.5
107	FYVE	FYVE zinc finger	5.4e-27	100.7
108	Cyt_reductas e	FAD/NAD-binding Cytochrome reductase	7.7e-61	215.5
109	zf-C2H2	Zinc finger, C2H2 type	2.3e-122	420.0
113	pkinase	Eukaryotic protein kinase domain	4e-88	306.2
116	PH	PH domain	3.1e-11	45.2
117	lipocalin	Lipocalin / cytosolic fatty- acid binding pr	2.4e-14	53.5
118	pkinase	Eukaryotic protein kinase domain	4.5e-20	76.3
120	WD40	WD domain, G-beta repeat	2.4e-14	61.1
121	WD40	WD domain, G-beta repeat	2.4e-14	61.1
123	IF5_eIF4_eIF 2	eIF4-gamma/eIF5/eIF2-epsilon	1e-32	122.2
124	ig	Immunoglobulin domain	6.5e-08	30.6
127	mito_carr	Mitochondrial carrier proteins	3e-16	58.6
128	PP2C ATP1G1 PLM M	Protein phosphatase 2C	2.2e-71	250.6
	AT8	ATP1G1/PLM/MAT8 family	3.1e-20	80.6
130	pfkB	pfkB family carbohydrate kinase	4.5e-42	137.1
133	ACBP	Acyl CoA binding protein	4.6e-22	86.7
135	IO	RNA recognition motif. IQ calmodulin-binding motif	1.2e-31	118.5
136	ATP1G1 PLM M	ATPIGI/PLM/MAT8 family	2.6e-08	41.0
139	ATPIGI_PLM_W AT8	_	9.3e-22	85.7
140		Wiskott Aldrich syndrome homology region 2	0.0067	23.1
141	zf-C2H2 Peptidase_S2 6	Zinc finger, C2H2 type Signal peptidase I	1.7e-82 5.7e-10	35.7
143	arf	ADP-ribosylation factor family	1.2e-39	145.2
146	KRAB	KRAB box	7.3e-30	112.6
148	DUF6	Integral membrane protein DUF6	0.096	8.0
149	PDEase	3'5'-cyclic nucleotide phosphodiesterase	3.8e-80	231.1
151	S4	S4 domain	1.1e-08	42.3
153	tRNA-synt_1d	tRNA synthetases class I (R)	3.8e-103	356.1
154	Cyt_reductas e	FAD/NAD-binding Cytochrome reductase	7.8e-60	212.2
155	ras	Ras family	3.6e-28	107.0
157	actin	Actin	3.8e-26	87.1

NO:	PFAM NAME	DECORAL TAON	p-value	PFAM SCORE
158	Jacalin	Jacalin-like lectin domain	0.09	-24.9
	Zn carbOpept	Zinc carboxypeptidase	5e-138	471.9
.60		Eukaryotic protein kinase	5.1e-67	236.1
165	pkinase	domain	5.3e-07	27.0
167	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)		
168	Ribosomal_S1	Ribosomal protein S15	1.1e-06	29.0
169	DEAD	DEAD/DEAH box helicase	le-48	157.0
171	DUF59	Domain of unknown function	0.07	-17.4
		DUF59 Eukaryotic protein kinase	3.7e-15	58.6
172	pkinase	domain		67.4
173	globin	Globin	4.6e-18	
174	WW	WW domain	7.3e-06	32.9
175	ras	Ras family	1e-31	118.8
178	ATPIG1_PLM_M AT8	ATPIG1/PLM/MAT8 family	2.5e-17	71.0
179	zf-C2H2	Zinc finger, C2H2 type	1.5e-99	344.2
180	Clq	Clq domain	8.8e-72	251.9
190	Y_phosphatas	Protein-tyrosine phosphatase	4.9e-287	967.0
191	efhand	EF hand	7.5e-16	66.1
193	pkinase	Eukaryotic protein kinase domain	6.5e-82	285.6
104	bromodomain	Bromodomain	5.8e-31	111.4
194 195	PALP	Pyridoxal-phosphate dependent	2.5e-64	227.1
		enzyme	1.6e-38	141.4
197	DnaJ	DnaJ domain	0.00018	16.9
199	RrnaAD	Ribosomal RNA adenine dimethylases		
200	acid_phospha t	Histidine acid phosphatase	2.5e-10	37.2
201	WH2	Wiskott Aldrich syndrome homology region 2	0.00048	26.9
204	vATP- synt AC39	ATP synthase (C/AC39) subunit	1.3e-159	543.7
205	vATP- synt_AC39	ATP synthase (C/AC39) subunit	1.6e-139	476.9
206	ldl_recept_a	Low-density lipoprotein receptor domain	2.4e-25	97.6
209	ank	Ank repeat	1.4e-19	78.4
	Rhomboid	Rhomboid family	0.0035	1.2
210		Clq domain	1.6e-70	247.7
211	Clq	Ubiquitin-conjugating enzyme	7.4e-74	258.8
212	UQ con	Dordereru-couledactud envine		
		This moiting consideration on time	10-53	191.9
213	UQ_con	Ubiquitin-conjugating enzyme	1e-53	191.9
		Ubiquitin-conjugating enzyme DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family	1e-53 1.8e-43 4.5e-21	191.9 140.4 83.4
213 215	UQ_con DEAD	DEAD/DEAH box helicase	1.8e-43	140.4
213 215 216 218	UQ_con DEAD PMP22_Claudi n	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family Glycosyl transferases	1.8e-43 4.5e-21 4e-21	140.4 83.4 83.6
213 215 216	UQ_con DEAD PMP22_Claudi n Glycos_trans	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family Glycosyl transferases Immunoglobulin domain	1.8e-43 4.5e-21 4e-21	140.4 83.4 83.6
213 215 216 218	UQ_con DEAD PMP22_Claudi n Glycos_trans f_2	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family Glycosyl transferases Immunoglobulin domain WD domain, G-beta repeat	1.8e-43 4.5e-21 4e-21 0.092 7.4e-23	140.4 83.4 83.6 10.7 89.4
213 215 216 218 219	UQ_con DEAD PMP22_Claudi n Glycos_trans f_2 ig	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family Glycosyl transferases Immunoglobulin domain WD domain, G-beta repeat TPR Domain	1.8e-43 4.5e-21 4e-21 0.092 7.4e-23 1.2e-08	140.4 83.4 83.6 10.7 89.4 42.1
213 215 216 218 219 222	UQ_con DEAD PMP22_Claudi n Glycos_trans f_2 ig WD40	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family Glycosyl transferases Immunoglobulin domain WD domain, G-beta repeat TPR Domain DnaJ central domain (4 repeats)	1.8e-43 4.5e-21 4e-21 0.092 7.4e-23 1.2e-08 1.5e-38	140.4 83.4 83.6 10.7 89.4 42.1 141.5
213 215 216 218 219 222 224	UQ_con DEAD PMP22_Claudi n Glycos_trans f_2 ig WD40 TPR DnaJ_CXXCXGX	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family Glycosyl transferases Immunoglobulin domain WD domain, G-beta repeat TPR Domain	1.8e-43 4.5e-21 4e-21 0.092 7.4e-23 1.2e-08 1.5e-38	140.4 83.4 83.6 10.7 89.4 42.1 141.5
213 215 216 218 219 222 224 225	UQ_con DEAD PMP22_Claudi n Glycos_trans f_2 ig WD40 TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family Glycosyl transferases Immunoglobulin domain WD domain, G-beta repeat TPR Domain DnaJ central domain (4 repeats) DnaJ central domain (4 repeats)	1.8e-43 4.5e-21 4e-21 0.092 7.4e-23 1.2e-08 1.5e-38 1.5e-38	140.4 83.4 83.6 10.7 89.4 42.1 141.5 141.5
213 215 216 218 219 222 224 225 226	UQ_con DEAD PMP22_Claudi n Glycos_trans f_2 ig WD40 TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G HSP70	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family Glycosyl transferases Immunoglobulin domain WD domain, G-beta repeat TPR Domain DnaJ central domain (4 repeats) DnaJ central domain (4 repeats) Hsp70 protein	1.8e-43 4.5e-21 4e-21 0.092 7.4e-23 1.2e-08 1.5e-38	140.4 83.4 83.6 10.7 89.4 42.1 141.5
213 215 216 218 219 222 224 225 226 229 230	UQ_con DEAD PMP22_Claudi n Glycos_trans f_2 ig WD40 TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G HSP70 GSHPx	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family Glycosyl transferases Immunoglobulin domain WD domain, G-beta repeat TPR Domain DnaJ central domain (4 repeats) DnaJ central domain (4 repeats) Hsp70 protein Glutathione peroxidases	1.8e-43 4.5e-21 4e-21 0.092 7.4e-23 1.2e-08 1.5e-38 1.5e-38	140.4 83.4 83.6 10.7 89.4 42.1 141.5 141.5
213 215 216 218 219 222 224 225 226 229 230 231	UQ_con DEAD PMP22_Claudi n Glycos_trans f_2 ig WD40 TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G HSP70 GSHPx tsp_1	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family Glycosyl transferases Immunoglobulin domain WD domain, G-beta repeat TPR Domain DnaJ central domain (4 repeats) DnaJ central domain (4 repeats) Hsp70 protein Glutathione peroxidases Thrombospondin type 1 domain	1.8e-43 4.5e-21 4e-21 0.092 7.4e-23 1.2e-08 1.5e-38 1.5e-38 2.4e-54 3.4e-47 0.0075	140.4 83.4 83.6 10.7 89.4 42.1 141.5 141.5
213 215 216 218 219 222 224 225 226 229 230 231 233	UQ_con DEAD PMP22_Claudi n Glycos_trans f_2 ig WD40 TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G HSP70 GSHPx tsp_1 cyclin	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family Glycosyl transferases Immunoglobulin domain WD domain, G-beta repeat TPR Domain DnaJ central domain (4 repeats) DnaJ central domain (4 repeats) Hsp70 protein Glutathione peroxidases Thrombospondin type 1 domain Cyclin	1.8e-43 4.5e-21 4e-21 0.092 7.4e-23 1.2e-08 1.5e-38 1.5e-38 2.4e-54 3.4e-47 0.0075 4.6e-144	140.4 83.4 83.6 10.7 89.4 42.1 141.5 141.5 194.0 170.2 17.1 492.0
213 215 216 218 219 222 224 225 226 229 230 231 233 234	UQ_con DEAD PMP22_Claudi n Glycos_trans f_2 ig WD40 TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G HSP70 GSHPx tsp_1 cyclin ras	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family Glycosyl transferases Immunoglobulin domain WD domain, G-beta repeat TPR Domain DnaJ central domain (4 repeats) DnaJ central domain (4 repeats) Hsp70 protein Glutathione peroxidases Thrombospondin type 1 domain Cyclin Ras family	1.8e-43 4.5e-21 4e-21 0.092 7.4e-23 1.2e-08 1.5e-38 1.5e-38 2.4e-54 3.4e-47 0.0075 4.6e-144 4.8e-50	140.4 83.4 83.6 10.7 89.4 42.1 141.5 141.5 194.0 170.2 17.1 492.0 179.7
213 215 216 218 219 222 224 225 226 229 230 231 233	UQ_con DEAD PMP22_Claudi n Glycos_trans f_2 ig WD40 TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G HSP70 GSHPx tsp_1 cyclin	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family Glycosyl transferases Immunoglobulin domain WD domain, G-beta repeat TPR Domain DnaJ central domain (4 repeats) DnaJ central domain (4 repeats) Hsp70 protein Glutathione peroxidases Thrombospondin type 1 domain Cyclin Ras family Leucine Rich Repeat	1.8e-43 4.5e-21 4e-21 0.092 7.4e-23 1.2e-08 1.5e-38 1.5e-38 2.4e-54 3.4e-47 0.0075 4.6e-144 4.8e-50 1.2e-30	140.4 83.4 83.6 10.7 89.4 42.1 141.5 141.5 194.0 170.2 17.1 492.0 179.7 115.3
213 215 216 218 219 222 224 225 226 229 230 231 233 234	UQ_con DEAD PMP22_Claudi n Glycos_trans f_2 ig WD40 TPR DnaJ_CXXCXGX G DnaJ_CXXCXGX G HSP70 GSHPx tsp_1 cyclin ras	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family Glycosyl transferases Immunoglobulin domain WD domain, G-beta repeat TPR Domain DnaJ central domain (4 repeats) DnaJ central domain (4 repeats) Hsp70 protein Glutathione peroxidases Thrombospondin type 1 domain Cyclin Ras family	1.8e-43 4.5e-21 4e-21 0.092 7.4e-23 1.2e-08 1.5e-38 1.5e-38 2.4e-54 3.4e-47 0.0075 4.6e-144 4.8e-50	140.4 83.4 83.6 10.7 89.4 42.1 141.5 141.5 194.0 170.2 17.1 492.0 179.7

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:			p varae	SCORE
244	dCMP_cyt_dea	Cytidine and deoxycytidylate deaminase	2.5e-05	31.1
245	ig	Immunoglobulin domain	6.7e-08	30.5
248	wnt	wnt family of developmental signaling protei	9.1e-270	742.6
250	mito_carr	Mitochondrial carrier proteins	1.3e-55	193.6
254	adenylatekin ase	Adenylate kinase	1.8e-14	55.7
255	Cation_efflu x	Cation efflux family	2.8e-33	124.0
256	SH3	SH3 domain	3.9e-14	60.4
257	Aa_trans	Transmembrane amino acid	2.6e-52	187.2
	 	transporter protein	<u> </u>	
258	adenylatekin ase	Adenylate kinase	2.1e-110	380.2
259	HIT	HIT family	8.2e-07	25.3
260	Bacterial_PQ Q	PQQ enzyme repeat	1.6e-15	65.0
262	proteasome	Proteasome A-type and B-type	6.5e-64	225.7
267	pkinase	Eukaryotic protein kinase domain	6.3e-27	101.0
270	filament	Intermediate filament proteins	3.2e-150	512.5
271	Choline_kina se	Choline/ethanolamine kinase	2e-67	237.4
277	Ribosomal_S7	Ribosomal protein S7p/S5e	3.3e-20	80.6
279	pkinase	Eukaryotic protein kinase domain	3.3e-77	269.9
280	WD40	WD domain, G-beta repeat	7.8e-73	255.4
281	WD40	WD domain, G-beta repeat	7.8e-73	255.4
284	zf-DHHC	DHHC zinc finger domain	4.6e-24	93.4
287	Exonuclease	Exonuclease	1.4e-67	238.0
291	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
292	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
294	zf-C2H2	Zinc finger, C2H2 type	1.4e-29	111.7
295	zf-C2H2	Zinc finger, C2H2 type	2.2e-125	430.0
296	mito_carr	Mitochondrial carrier proteins	4.1e-59	205.5
302	HMG box	HMG (high mobility group) box Glycosyl transferase	6.7e-29	109.4
	Glycos_trans f_4	1 -	5e-87	302.5
304	tRNA-synt_2	tRNA synthetases class II (D, K and N)	1.1e-84	294.8
305	KRAB	KRAB box	2e-44	161.0
306 308	rrm	RNA recognition motif.	2.7e-44 5.2e-39	160.6
	7tm_1	7 transmembrane receptor (rhodopsin family)		126.1
309	DNA_polymera seX	DNA polymerase X family	2.4e-64	227.2
311	F-box	F-box domain.	9.5e-08	39.2
312	ig Ets	Immunoglobulin domain	6.8e-19	65.9
315	Kelch	Ets-domain Kelch motif	8.1e-60	192.3
317	arf	ADP-ribosylation factor family	1.3e-106 3.2e-35	367.6 130.4
318	sugar_tr	Sugar (and other) transporter	0.0003	-73.1
320	pkinase	Eukaryotic protein kinase domain	8.1e-83	288.6
322	pkinase	Eukaryotic protein kinase domain	4.9e-81	282.6
324	Xlink	Extracellular link domain	4.5e-143	331.5
326	ARID	ARID DNA binding domain	5.1e-37	136.4
327	HMG box	HMG (high mobility group) box	6.7e-29	109.4
328	cadherin	Cadherin domain	8.1e-81	281.9
331	chromo	'chromo' (CHRromatin Organization MOdifier)	4e-18	66.7
333	Peptidase M2	Glycoprotease family	1.2e-136	467.4
	2 -	•		

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
35	vwa	von Willebrand factor type A	2.3e-07	37.9
		Ras family	7.8e-07	-59.1
339	ras	Zinc finger, C2H2 type	8.2e-64	225.4
340	zf-C2H2	Zinc finger, C2H2 type	2.4e-85	297.0
342	zf-C2H2	Immunoglobulin domain	0.0005	18.0
343	ig	Eukaryotic protein kinase	6.5e-65	229.1
346	pkinase	domain		229.1
347	pkinase	Eukaryotic protein kinase domain	6.5e-65	
351	EGF	EGF-like domain	8.5e-20	79.2
352	ank	Ank repeat	2.5e-101	350.0
354	TBC	TBC domain	5.le-15	63.3
355	PHD	PHD-finger	3.2e-07	37.4
	DUF6	Integral membrane protein DUF6	0.033	15.8
358		Zinc finger, C2H2 type	7.4e-20	79.4
359	zf-C2H2		6.6e-34	126.1
361	ank	Ank repeat	4.7e-53	189.7
362	ArfGap	Putative GTP-ase activating protein for Arf		
363	efhand	EF hand	5.4e-10	46.6
367	LRR	Leucine Rich Repeat	8.8e-44	158.9
368	laminin G	Laminin G domain	1.5e-33	121.7
369	PP2C	Protein phosphatase 2C	5.3e-20	73.9
	LIM	LIM domain containing proteins	9.9e-15	57.1
372		KRAB box	4.8e-23	90.0 .
373	KRAB		2.9e-09	-4.2
376	ion_trans	Ion transport protein	4.9e-208	704.5
377	Beach	Beige/BEACH domain		
380	pkinase	Eukaryotic protein kinase domain	1.6e-94	327.5
381	AMP-binding	AMP-binding enzyme	1.4e-07	-140.3
382	HECT	HECT-domain (ubiquitin- transferase).	1.3e-07	-13.5
			2.5e-101	350.0
384	ank	Ank repeat	9.5e-06	23.6
386	ig	Immunoglobulin domain		154.6
388	zf-C2H2	Zinc finger, C2H2 type	1.7e-42	
389	ig	Immunoglobulin domain	2.8e-15	54.3
390	mito carr	Mitochondrial carrier proteins	3.5e-67	233.2
392	TPR	TPR Domain	6.1e-17	69.7
393	SH3	SH3 domain	3.5e-09	43.9
394	AAA	ATPases associated with various cellular act	4.1e-21	83.6
		Spectrin repeat	2.1e-67	237.3
396	spectrin		0.0066	23.1
397	zf-C2H2	Zinc finger, C2H2 type	4.1e-102	352.6
399	fn3	Fibronectin type III domain		
400	WD40	WD domain, G-beta repeat	0.00049	26.8
401	El_dehydrog	Dehydrogenase E1 component	3e-119	409.6
402	fn3	Fibronectin type III domain	0	1719.6
404	LRR	Leucine Rich Repeat	2.1e-10	48.0
405	cadherin	Cadherin domain	8.1e-81	281.9
406	zf-CXXC	CXXC zinc finger	5e-15	63.4
410	RhoGEF	RhoGEF domain	1.1e-23	92.1
	F-box	F-box domain.	4.2e-06	33.7
411	SNF2_N	SNF2 and others N-terminal	5.8e-16	61.6
415	CPSase_L_cha	domain Carbamoyl-phosphate synthase	1.5e-172	586.6
ļ	in	(CPSase)		
418	LRR	Leucine Rich Repeat	3.8e-24	93.6
419	DENN	DENN (AEX-3) domain	2e-58	207.5
	RasGEF	RasGEF domain	8.1e-43	155.7
420		Ank repeat	1.4e-153	523.7
421	ank		le-19	78.9
424	G-patch	G-patch domain	2.2e-31	117.1
425	pkinase	Eukaryotic protein kinase domain		
426	Plexin_repea	Plexin repeat	0.0023	24.6
				24.6

SCORE -11 39.2 5 214.0 -16 67.2 -114 393.5 -194 658.1 35 10.5 -256 866.0 -235 795.7 -65 230.9 012 -17.1 011 20.1 -18 75.2 -06 35.2
5 214.0 -16 67.2 -114 393.5 -194 658.1 35 10.5 -256 866.0 -235 795.7 -65 230.9 012 -17.1 011 20.1 -18 75.2
5 214.0 -16 67.2 -114 393.5 -194 658.1 35 10.5 -256 866.0 -235 795.7 -65 230.9 012 -17.1 011 20.1 -18 75.2
-16 67.2 -114 393.5 -194 658.1 35 10.5 -256 866.0 -235 795.7 -65 230.9 012 -17.1 011 20.1 -18 75.2
-114 393.5 -194 658.1 35 10.5 -256 866.0 -235 795.7 -65 230.9 012 -17.1 011 20.1 -18 75.2
-194 658.1 35 10.5 -256 866.0 -235 795.7 -65 230.9 012 -17.1 011 20.1 -18 75.2
35 10.5 -256 866.0 -235 795.7 -65 230.9 012 -17.1 011 20.1 -18 75.2
-256 866.0 -235 795.7 -65 230.9 012 -17.1 011 20.1 -18 75.2
795.7 65 230.9 012 -17.1 011 20.1 -18 75.2
230.9 012 -17.1 011 20.1 -18 75.2
012 -17.1 011 20.1 -18 75.2
011 20.1 -18 75.2
18 75.2
18 75.2
14 50.3
30.3
217 734.4
75 597.1
2 18.7
07 31.8
06 -26.3
107.9
20.7
21.0
18 73.0
118.8
66 232.0
11.4
74 259.6
47 171.9
153 521.9
222 751.6
10 48.8
22 77.6
-48.1
34 126.4
18 73.4
10 39.5
-3.6
62 219.0
145 496.3
56 201.5
06 27.0
06 27.0
09 38.5
63 221.4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
515	EGF	EGF-like domain	1.9e-18	74.7
		Surp module	4.3e-38	140.0
16	Surp	Immunoglobulin domain	3.3e-06	25.0
23	ig		1.le-34	128.6
26	UBX	UBX domain	2.7e-34	127.4
28	adh_zinc	Zinc-binding dehydrogenases	0.046	10.0
530	SAM	SAM domain (Sterile alpha motif)		
531	adh short	short chain dehydrogenase	0.0025	-34.1
532	mito_carr	Mitochondrial carrier proteins	2.5e-81	281.7
533	mito carr	Mitochondrial carrier proteins	2e-61	213.5
534	thiolase	Thiolase	3.5e-183	622.0
535	FMO-like	Flavin-binding monooxygenase-	0	1153.7
	10000	SCAN domain	4e-55	196.6
536	SCAN	tRNA synthetases class I (I, L,	3.1e-136	466.0
537	tRNA-synt_1	M and V)		466.0
538	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	
539	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	1.9e-117	403.6
540	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
541	vATP-synt E	ATP synthase (E/31 kDa) subunit	5.9e-85	295.7
543	zf-C2H2	Zinc finger, C2H2 type	5.5e-69	242.6
544	DUF101	Protein of unknown function	8.5e-38	139.0
545	TGFb_propept	TGF-beta propeptide	1.1e-67	238.2
547	WD40	WD domain, G-beta repeat	2.6e-32	120.8
548	RHD	Rel homology domain (RHD).	1.6e-238	686.2
	MMR HSR1	GTPase of unknown function	5.4e-67	236.0
549		HECT-domain (ubiquitin-	4.3e-127	435.6
551	HECT	transferase).	3.5e-74	259.8
554	MHC_II_alpha	Class II histocompatibility antigen, alp		
555	zf-UBR1	Putative zinc finger in N-recognin	3.3e-16	67.3
556	Kelch	Kelch motif	5.5e-29	109.7
561	AMP-binding	AMP-binding enzyme	2.8e-06	-163.7
562	PABP	Poly-adenylate binding protein, unique domai	4.9e-38	139.8
	1000 000	Gag P30 core shell protein	1.2e-67	238.2
564	Gag_p30	PWWP domain	8.1e-16	66.0
566	PWWP		7.3e-68	238.9
567	SCAN	SCAN domain	1.5e-84	294.3
569	pkinase	Eukaryotic protein kinase domain		
570	pkinase	Bukaryotic protein kinase domain	1.5e-84	294.3
571	CN_hydrolase	Carbon-nitrogen hydrolase	0.00081	-79.7
572	myosin_head	Myosin head (motor domain)	0	1495.2
573	myosin_head	Myosin head (motor domain)	0	1490.4
575	Surp	Surp module	1.7e-23	91.5
576	Surp	Surp module	1.7e-23	91.5
577	DNA pol B	DNA polymerase family B	0	1138.6
578	PDZ PDZ	PDZ domain (Also known as DHR	8.3e-09	42.7
		or GLGF).	4.9e-21	83.3
579	LRR	Leucine Rich Repeat	5.9e-177	601.3
580	neur_chan	Neurotransmitter-gated ion- channel		
583	sushi	Sushi domain (SCR repeat)	0	1673.0
584	DEAD	DEAD/DEAH box helicase	7.3e-36	116.3
. ~~ ~	KH-domain	KH domain	2.9e-13	57.5
586	I ver cometit		2.3e-14	61.2
586	G-patch	IG-patch domain	2.36-14	102.2
587	G-patch	G-patch domain		133.4
	G-patch LIM bromodomain	G-patch domain LIM domain containing proteins Bromodomain	2.3e-36 2.3e-36	

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
592	hormone_rec	Ligand-binding domain of nuclear hormone	3.5e-22	87.1
593	PHD	PHD-finger	3.8e-12	53.8
594	cadherin	Cadherin domain	4.2e-99	342.7
596	pkinase	Eukaryotic protein kinase domain	5e-92	319.2
597	WD40	WD domain, G-beta repeat	0.00054	26.7
600	FG-GAP	FG-GAP repeat	4.3e-75	262.9
602	G_Adapt_CT	Gamma-adaptin, C-terminus	1.1e-53	191.8
603	pkinase	Eukaryotic protein kinase domain	2.3e-86	300.4
605	Collagen	Collagen triple helix repeat (20 copies)	8e-42	152.4
606	mito_carr	Mitochondrial carrier proteins	6.3e-67	232.3
608	PWWP	PWWP domain	2.6e-28	107.5
609	PWWP	PWWP domain	2.6e-28	107.5
613	CAP_GLY	CAP-Gly domain	0.0046	20.1
615	RFX_DNA_bind ing	RFX DNA-binding domain	5.2e-54	192.9
616	kinesin	Kinesin motor domain	1.1e-81	284.8
617	kinesin	Kinesin motor domain	8.4e-80	278.5
618	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0098	13.1
620	MATH	MATH domain	7.8e-05	22.2
621	Y_phosphatas e	Protein-tyrosine phosphatase	1.4e-32	121.6
622	pkinase	Eukaryotic protein kinase domain	4.4e-40	146.6
623 .	BNR	BNR repeat	2.1e-11	51.3
624	molybdopteri n	Prokaryotic molybdopterin oxidoreductas	1.4e-12	42.2
625	TPR	TPR Domain	1.1e-17	72.2
627	cNMP_binding	Cyclic nucleotide-binding domain	3.7e-58	206.6
630	adh_short	short chain dehydrogenase	5e-17	70.0
631	zf-C2H2	Zinc finger, C2H2 type	2.1e-88	307.1
632	rrm	RNA recognition motif.	4e-05	30.5
635	pkinase	Eukaryotic protein kinase domain	1.6e-104	360.7
636	Fork_head	Fork head domain ,	5.9e-27	103.0
637	pkinase	Eukaryotic protein kinase domain	3.8e-70	246.5
642	TPR	TPR Domain	4.8e-08	40.1
643	efhand	EF hand	1.9e-27	104.6
647	SNF2_N	SNF2 and others N-terminal domain	1.2e-101	351.1
648	PseudoU_synt h_2	RNA pseudouridylate synthase	1.9e-55	197.6
650	zf-C2H2	Zinc finger, C2H2 type	0.0087	22.7
651	ank	Ank repeat	1.3e-17	71.9
652	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
653	neur_chan	Neurotransmitter-gated ion- channel	4.1e-171	581.8
654	tsp_1	Thrombospondin type 1 domain	4.1e-47	169.9
659	FH2	Formin Homology 2 Domain	1e-107	371.2
661	pou	Pou domain - N-terminal to homeobox domain	5.3e-45	162.9
662	C2	C2 domain	6.7e-19	76.2
663	C2	C2 domain	6.7e-19	76.2
664	C2	C2 domain	6.7e-19	76.2
667	GST	Glutathione S-transferases.	9.3e-34	114.4
668	LRR	Leucine Rich Repeat	9.3e-31	115.6
670	spectrin	Spectrin repeat	4e-57	203.2
671	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
672	ABC_tran	ABC transporter	5.3e-60	212.8
674	WD40	WD domain, G-beta repeat	4.8e-24	93.3

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
675	WD40	WD domain, G-beta repeat	4.8e-24	93.3
		Leucine Rich Repeat	0.0015	25.2
676	LRR			107.7
679	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-29	
680	zf-C2H2	Zinc finger, C2H2 type	5.2e-05	30.1
681	CH	Calponin homology (CH) domain	2.4e-17	71.1
	I	Dual specificity phosphatase,	4.3e-43	156.6
582	DSPc	catalytic doma		1
683	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.051	10.8
687	Synapsin	Synapsin	0	1890.8
689	PR55	Protein phosphatase 2A	0	1038.8
009	FR33	regulatory subunit PR	ļ	
			8.5e-30	112.4
691	homeobox	Homeobox domain		
696	Peptidase_M2	metallopeptidase family M24	2.6e-59	210.5
697	RhoGEF	RhoGEF domain	9.5e-35	128.9
698	PHD	PHD-finger	0.008	9.3
	zf-C2H2	Zinc finger, C2H2 type	5.5e-123	422.0
701			3e-231	781.6
702	Sulfatase	Sulfatase		79.8
703	zf-C2H2	Zinc finger, C2H2 type	5.7e-20	
707	Acyl_transf	Acyl transferase domain	1.1e-22	88.8
708	WD40	WD domain, G-beta repeat	4.8e-19	76.7
710	Ran BP1	RanBP1 domain.	8.4e-06	-7.3
		DEAD/DEAH box helicase	9.9e-42	134.9
713	DEAD			39.0
714	PH	PH domain	1.6e-09	
715	DSPC	Dual specificity phosphatase, catalytic doma	1.5e-37	138.2
717	Sialyltransf	Sialyltransferase family	7.5e-31	115.9
		Immunoglobulin domain	1e-29	100.8
718	ig		0	1125.4
719	integrin_B	Integrins, beta chain	1	32.4
720	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-08	
722	Peptidase_C2	Calpain family cysteine protease	3e-145	495.9
723	iq	Immunoglobulin domain	2.2e-05	22.4
724	F-box	F-box domain.	0.007	23.0
		Putative snoRNA binding domain	8.1e-58	205.5
725	Nop	Putative snorNA binding domain	8.1e-58	205.5
726	Мор	Putative snokNA binding domain		
727	WD40	WD domain, G-beta repeat	7.5e-26	99.3
730	dsrm	Double-stranded RNA binding motif	0.027	12.1
731	dynamin	Dynamin family	4.2e-16	66.9
		Zinc finger C-x8-C-x5-C-x3-H	2.8e-10	41.7
733	zf-CCCH	type		
735	CDP- OH P transf	CDP-alcohol phosphatidyltransferase	4.2e-26	100.1
738	DEAD	DEAD/DEAH box helicase	8.6e-57	182.5
739	TSC22	TSC-22/dip/bun family	6.5e-32	119.5
		Ras family	2.2e-100	346.9
742	ras	•	1.2e-243	822.9
743	PMI_typeI	Phosphomannose isomerase type I		279.4
747	trypsin	Trypsin	6.4e-88	
748	kazal	Kazal-type serine protease inhibitor domain	2.2e-52	187.4
749	efhand	EF hand	6.3e-06	33.1
			4.9e-16	66.7
751	PHD	PHD-finger		83.9
752	zf-C2H2	Zinc finger, C2H2 type	3.2e-21	
753	Hydrolase	haloacid dehalogenase-like hydrolase	6.le-11	49.8
754	Ribosomal_L3	Ribosomal L39 protein	0.00018	26.7
	9	PVI downdon	2 60-14	55.7
755	PH	PH domain	3.6e-14	
758	SCAN	SCAN domain	1.4e-53	191.5
759	PA	PA domain	0.0065	23.1
		ADP-ribosylation factor family	2.2e-19	77.8
760	arf	ADP-FIDOSYIACION LACCOL LAMELLY	1 2.20 27	

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
	Table Marie	DDD GREET TOW	p varue	SCORE
762	histone	Core histone H2A/H2B/H3/H4	9.9e-53	188.6
763	zf-MYND	MYND finger	4.1e-14	60.3
764	pou	Pou domain - N-terminal to	1e-52	188.6
	-	homeobox domain		
767	VWC	von Willebrand factor type C	2.9e-34	127.3
	1	domain	1	1
769	efhand	EF hand	4.8e-11	50.1
770	zf-C4	Zinc finger, C4 type (two	2.4e-53	181.6
	1	domains)	İ	
772	ras	Ras family	7e-90	312.0
773	Sulfatase	Sulfatase	le-142	487.5
775	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
776	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
777	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
778	rrm	RNA recognition motif.	2.1e-32	121.1
779	GGPD ·	Glucose-6-phosphate	1.5e-76	236.6
		dehydrogenase		1
780	spectrin	Spectrin repeat	3.7e-29	110.3
781	mito carr	Mitochondrial carrier proteins	4.6e-57	198.5
782	SCAN	SCAN domain	1.3e-24	95.2
783	PDZ	PDZ domain (Also known as DHR	4.1e-07	37.1
	1	or GLGF).	1	1
785	DEAD	DEAD/DEAH box helicase	6e-06	21.7
786	ras	Ras family	5.3e-39	143.0
787	RNase HII	Ribonuclease HII	2.5e-67	237.1
790	PI3 PI4 kina	Phosphatidylinositol 3- and 4-	5.4e-108	372.2
	se	kinases	3.14 200	1 3,2.2
795	cadherin	Cadherin domain	2.5e-40	147.4
796	ARID	ARID DNA binding domain	1.6e-20	81.6
797	trypsin	Trypsin	9.9e-20	64.8
799	CH	Calponin homology (CH) domain	3.7e-15	63.8
801	Gal-	Vertebrate galactoside-binding	4.1e-25	88.7
502	bind lectin	lectin	3.46-25	1 80.7
803	WD40	WD domain, G-beta repeat	0.00082	26.1
806	TBC	TBC domain	1.8e-26	101.4
807	TBC	TBC domain	1.8e-26	101.4
808	CN hydrolase	Carbon-nitrogen hydrolase	8.8e-80	278.5
811	CBFD NFYB HM	Histone-like transcription	6e-14	59.8
	F	factor	30 11	133.0
812	adh short	short chain dehydrogenase	8.1e-20	79.3
	1	Domain of unknown function	1	1
	IMP4		3.36-71	250 0
814 .	IMP4		3.3e-71 8.2e-66	250.0
814 815	zf-C2H2	Zinc finger, C2H2 type	8.2e-66	232.1
814 815	zf-C2H2 Pept_tRNA_hy		1	
814 815 816	zf-C2H2 Pept_tRNA_hy dro	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase	8.2e-66 1.6e-37	232.1 138.0
814 815 816 817	zf-C2H2 Pept_tRNA_hy dro ARID	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain	8.2e-66 1.6e-37 2.5e-18	232.1 138.0 74.3
814 815 816 817	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase	8.2e-66 1.6e-37	232.1 138.0
814 815 816 817 826	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon	8.2e-66 1.6e-37 2.5e-18 1.6e-32	232.1 138.0 74.3 121.5
814 815 816 817 826	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating	8.2e-66 1.6e-37 2.5e-18	232.1 138.0 74.3
814 815 816 817 826	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53	232.1 138.0 74.3 121.5
814 815 816 817 826 830	zf-C2H2 Pept_trNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53	232.1 138.0 74.3 121.5 191.3
814 815 816 817 826 830	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53	232.1 138.0 74.3 121.5
814 815 816 817 826 830 831	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V)	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53 2.1e-26 2e-57	232.1 138.0 74.3 121.5 191.3 101.1 204.2
814 815 816 817 826 830 831 832	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif.	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53 2.1e-26 2e-57	232.1 138.0 74.3 121.5 191.3 101.1 204.2
814 815 816 817 826 830 831 832	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V)	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53 2.1e-26 2e-57	232.1 138.0 74.3 121.5 191.3 101.1 204.2
814 815 816 817 826 830 831 832 839	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119	232.1 138.0 74.3 121.5 191.3 101.1 204.2 88.5 409.8
814 815 816 817 826 830 831 832 839	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53 2.1e-26 2e-57	232.1 138.0 74.3 121.5 191.3 101.1 204.2
814 815 816 817 826 830 831 832 839 840	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase domain	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119 3.4e-100	232.1 138.0 74.3 121.5 191.3 101.1 204.2 88.5 409:8
814 815 816 817 826 830 831 832 839 840	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase Ribosomal_L2	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119	232.1 138.0 74.3 121.5 191.3 101.1 204.2 88.5 409.8
814 815 816 817 826 830 831 832 839 840	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase Ribosomal_L2 2e	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase domain Ribosomal L22e protein family	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119 3.4e-100 1e-64	232.1 138.0 74.3 121.5 191.3 101.1 204.2 88.5 409:8 346.3
814 815 816 817 826 830 831 832 839 840 841	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase Ribosomal_L2 2e IBR	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase domain Ribosomal L22e protein family IBR domain	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119 3.4e-100 1e-64	232.1 138.0 74.3 121.5 191.3 101.1 204.2 88.5 409.8 346.3
814 815 816 817 826 830 831 832 839 840 841	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase Ribosomal_L2 2e	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase domain Ribosomal L22e protein family IBR domain Zinc finger, C3HC4 type (RING	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119 3.4e-100 1e-64	232.1 138.0 74.3 121.5 191.3 101.1 204.2 88.5 409:8 346.3
814 815 816 817 826 830 831 832 839 840 841 844	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase Ribosomal_L2 2e IBR zf-C3HC4	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase domain Ribosomal L22e protein family IBR domain Zinc finger, C3HC4 type (RING finger)	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119 3.4e-100 1e-64 9e-15 7.4e-07	232.1 138.0 74.3 121.5 191.3 101.1 204.2 88.5 409:8 346.3 228.4
814 815 816 817 826 830 831 832 839 840 841 844	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase Ribosomal_L2 2e IBR	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase domain Ribosomal L22e protein family IBR domain Zinc finger, C3HC4 type (RING finger) Zinc finger, C3HC4 type (RING	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119 3.4e-100 1e-64	232.1 138.0 74.3 121.5 191.3 101.1 204.2 88.5 409:8 346.3
814 815 816 817 826 830 831 832 839 840 841	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase Ribosomal_L2 2e IBR zf-C3HC4	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase domain Ribosomal L22e protein family IBR domain Zinc finger, C3HC4 type (RING finger)	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119 3.4e-100 1e-64 9e-15 7.4e-07	232.1 138.0 74.3 121.5 191.3 101.1 204.2 88.5 409:8 346.3 228.4
814 815 816 817 826 830 831 832 839 840 841 844 846 849	zf-C2H2 Pept_tRNA_hy dro ARID IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase Ribosomal_L2 2e IBR zf-C3HC4	Zinc finger, C2H2 type Peptidyl-tRNA hydrolase ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase domain Ribosomal L22e protein family IBR domain Zinc finger, C3HC4 type (RING finger) Zinc finger, C3HC4 type (RING finger)	8.2e-66 1.6e-37 2.5e-18 1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119 3.4e-100 1e-64 9e-15 7.4e-07 0.00016	232.1 138.0 74.3 121.5 191.3 101.1 204.2 88.5 409:8 346.3 228.4 62.5 26.5

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
10:				SCORE
		rich domain	0	1025.4
353	SRCR	Scavenger receptor cysteine- rich domain		
857	lactamase_B	Metallo-beta-lactamase superfamily	0.012	-6.0
858	COX6A	Cytochrome c oxidase subunit	3.4e-58	206.7
859	rrm	RNA recognition motif.	5.4e-45	162.9
861	PRK	Phosphoribulokinase	5.1e-62	219.4
863	mito carr	Mitochondrial carrier proteins	2.9e-53	185.5
864	HSP90	Hsp90 protein	4.7e-158	538.5
866	ig	Immunoglobulin domain	4e-12	44.1
867	zf-C2H2	Zinc finger, C2H2 type	7e-135	461.5
872	histone	Core histone H2A/H2B/H3/H4	4.9e-41	149.8
874	CPSase_L_cha	Carbamoyl-phosphate synthase (CPSase)	2.1e-218	739.0
879	Ribosomal_S1	Ribosomal protein S12e	2.1e-98	340.3
882	serpin	Serpins (serine protease inhibitors)	2.5e-42	145.7
883	Patatin	Patatin	1.2e-51	182.0
883	RA	Ras association (RalGDS/AF-6)	0.044	8.0
007	DUF92	Integral membrane protein DUF92	2.7e-12	.54.3
887 889	sugar_tr	Sugar (and other) transporter	8.2e-63	222.1
893	DUF28	Domain of unknown function	1.3e-43	158.3
		DUF28 Phosphatidylinositol transfer	6.5e-98	338.7
896	IP_trans	protein	1.5e-48	156.5
898	DEAD	DEAD/DEAH box helicase	7e-61	215.7
899	KE2	KE2 family protein	4.3e-51	183.2
900	KE2	KE2 family protein Zinc finger, C2H2 type	2.7e-57	203.8
901	zf-C2H2	Ras family	2.3e-75	263.8
902	TPR	TPR Domain	3.2e-22	87.2
904	GBP	Guanylate-binding protein	8.9e-253	853.1
908	GBP	Guanylate-binding protein	1.1e-239	809.6
908	WD40	WD domain, G-beta repeat	2.6e-26	100.8
909	PH	PH domain	1.3e-09	39.4
910	zf-C2H2	Zinc finger, C2H2 type	2.5e-39	144.1
913	Epimerase	NAD dependent epimerase/dehydratase family	5e-07	-88.5
921	TBC	TBC domain	1.5e-09	30.7
922	WD40	WD domain, G-beta repeat	1.6e-25	98.2
923	WD40	WD domain, G-beta repeat	8.2e-07	36.1
924	Hydrolase	haloacid dehalogenase-like hydrolase	2.9e-05	29.1
925	UQ con	Ubiquitin-conjugating enzyme	0.00033	-27.6
926	CH CH	Calponin homology (CH) domain	3.3e-53	190.2
928	WD40	WD domain, G-beta repeat	5.9e-48	172.7
929	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.1e-10	37.4
930	Ribul_P_3_ep	Ribulose-phosphate 3 epimerase family	7.2e-105	361.8
	Ribul P 3 ep	Ribulose-phosphate 3 epimerase family	1.2e-96	334.4
931				
	im	C2 domain	2.2e-62	220.7
931 936 937		C2 domain Nucleosome assembly protein	2.2e-62 1.1e-22	84.6
936 937	im C2 NAP_family	C2 domain Nucleosome assembly protein (NAP)	_	
936 937 940	im C2 NAP_family abhydrolase	C2 domain Nucleosome assembly protein (NAP) alpha/beta hydrolase fold	1.1e-22	84.6
936	im C2 NAP_family	C2 domain Nucleosome assembly protein (NAP) alpha/beta hydrolase fold Tropomyosins Eukaryotic protein kinase	1.1e-22 0.011	3.1
936 937 940 944	im C2 NAP_family abhydrolase Tropomyosin	C2 domain Nucleosome assembly protein (NAP) alpha/beta hydrolase fold Tropomyosins	0.011 3.2e-07	3.1 25.1

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:				SCORE
951	SAM	SAM domain (Sterile alpha motif)	0.014	14.5
954	GFO IDH MOCA	Oxidoreductase family	1.3e-11	52.0
955	BTB	BTB/POZ domain	7e-22	86.1
956	BTB	BTB/POZ domain	7e-22	86.1
957	CDP-	CDP-alcohol	0.053	-22.2
	OH_P_transf	phosphatidyltransferase		
959	ras	Ras family	2.4e-97	336.8
960	ras	Ras family	8.4e-43	155.6
961	Acetyltransf	Acetyltransferase (GNAT) family	1.2e-08	42.2
962	adh short	short chain dehydrogenase	2.4e-31	117.6
963	mutT	Bacterial mutT protein	5.6e-06	26.2
969 .	IF-2B	Initiation factor 2 subunit family	8.4e-193	653.9
970	RNase PH	3' exoribonuclease family	9e-24	92.4
975	WW	WW domain	5.7e-25	96.4
977	PDZ	PDZ domain (Also known as DHR or GLGF).	3.6e-21	83.7
978	Ribosomal_L1	Ribosomal protein L17	2.4e-20	81.0
979	LIM	LIM domain containing proteins	5.8e-42	152.8
980	Calsequestri n	Calsequestrin	1.7e-297	1001.7
982	HSP20	Hsp20/alpha crystallin family	1.2e-10	43.2
983	oxidored_q6	NADH ubiquinone oxidoreductase, 20 Kd sub	4.8e-63	222.9
988	TBC	TBC domain	2.2e-50	180.8
989	TBC	TBC domain	2.2e-50	180.8
993	tRNA_int_end	tRNA intron endonuclease	0.0017	-34.2
994	homeobox	Homeobox domain	4e-18	73.6
997	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	0.012	11.6
1000	mito carr	Mitochondrial carrier proteins	9.7e-123	421.2
1001	RA	Ras association (RalGDS/AF-6) domain	1.2e-15	65.4
1004	DUF81	Domain of unknown function DUF81	0.099	10.2
1005	actin	Actin	1.3e-174	574.3
1006	actin	Actin	3.1e-130	428.6
1007	cpn60_TCP1	TCP-1/cpn60 chaperonin family	3.7e-195	661.8
1008	TPR	TPR Domain	8.1e-44	159.0
1009	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1011	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1012	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.7e-15	53.1
1016	tRNA-synt_2c	tRNA synthetases class II (A)	2.3e-15	55.2
101B	RhoGAP	RhoGAP domain	1.6e-78	274.3
1022	PGAM	Phosphoglycerate mutase family	3.8e-18	69.7
1026	HMG_box	HMG (high mobility group) box	8.4e-20	79.2
1027	TBC	TBC domain	7.3e-45	162.5
1028	UQ_con	Ubiquitin-conjugating enzyme	1.4e-49	178.1
1032	PDZ	PDZ domain (Also known as DHR or GLGF).	0.028	16.3
1034	Hydrolase	haloacid dehalogenase-like hydrolase	2e-21	84.6
1037	KRAB	KRAB box	4.8e-06	32,4
1038	Cation_efflu x	Cation efflux family	7.1e-42	152.5
1040	ART	NAD:arginine ADP- ribosyltransferase	4.7e-47	169.1
	WD40	WD domain, G-beta repeat	1.9e-18	74.7
1042) WU40			
				93.7
1042 1043 1045	zf-C2H2	Zinc finger, C2H2 type	3.7e-24	93.7
1043				93.7 108.0 -25.1

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
NO:	<u> </u>		4.5e-80	279.4
1047	ligase-CoA	CoA-ligases	1.7e-09	35.6
1049	ig	Immunoglobulin domain		124.5
1050	Ribosomal_L2 4e	Ribosomal protein L24e	2e-33	
1054	Amidase	Amidase	4.3e-152	518.7
1055	rrm	RNA recognition motif.	3.8e-26	100.3
1058	annexin	Annexin	6.9e-44	159.2
1059		PMP-22/EMP/MP20/Claudin family	0.023	-23.6
1023	PMP22_Claudi n			117.2
1060	homeobox	Homeobox domain	3.2e-31	
1062	Acyltransfer ase	Acyltransferase	0.00065	10.5
1064	AMP-binding	AMP-binding enzyme	6.6e-100	345.3
1065	LRR	Leucine Rich Repeat	3.3e-14	60.6
1066	GTP1 OBG	GTP1/OBG family	4.8e-41	141.8
		Immunoglobulin domain	8.4e-48	159.1
1071	ig		6.8e-07	36.3
1072	PHD	PHD-finger	8.3e-33	121.5
1074	DENN	DENN (AEX-3) domain		149.8
1075	SCP	SCP-like extracellular protein	4.7e-41	
1077 ,	OLF	Olfactomedin-like domain	2.2e-66	234.0
1078	mito carr	Mitochondrial carrier proteins	1e-42	149.3
1079	WD40	WD domain, G-beta repeat	6.2e-45	162.7
1087	START	START domain	1.5e-48	174.7
1093	DSPC	Dual specificity phosphatase, catalytic doma	3.3e-63	223.4
	GGUP	Glutathione peroxidases	9.6e-41	148.8
1094	GSHPx	Domain of unknown function	2e-75	264.0
1095	DUF25	DUF25		262.4
1096	.DUF25	Domain of unknown function DUF25	6e-75	
1105	Nitroreducta se	Nitroreductase family	1.3e-13	58.6
1106	PTE	Phosphotriesterase family	1.3e-179	610.1
1107	DAGKC	Diacylglycerol kinase catalytic domain	0.00049	19.6
		Ras family	1.3e-15	40.7
1109	ras	Putative GTP-ase activating	9.7e-47	168.7
1115	ArfGap	protein for Arf		
1116	HMG14_17	HMG14 and HMG17	4.4e-21	83.5
1117	HMG14 17	HMG14 and HMG17	9.9e-12	52.4
1119	FAA_hydrolas	Fumarylacetoacetate (FAA) hydrolase fam	2e-83	290.6
1120	pkinase	Eukaryotic protein kinase	1.4e-94	327.6
		domain	9.2e-23	89.0
1123	abhydrolase	alpha/beta hydrolase fold	2.2e-56	197.1
1129	pro_isomeras e	Cyclophilin type peptidyl- prolyl cis-tr		
1131	DnaJ	DnaJ domain	1.6e-30	114.9
1132	WD40	WD domain, G-beta repeat	1.3e-19	78.6
1133	WD40	WD domain, G-beta repeat	1.8e-15	64.9
1134	PH	PH domain	0.0015	17.8
1134	Adap_comp_su	Adaptor complexes medium	1.2e-256	866.0
1137	Adap_comp_su	subunit family Adaptor complexes medium	2.5e-209	708.8
	b	subunit family		
1139	ras	Ras family	1.5e-86	301.0
1141	pkinase	Eukaryotic protein kinase domain	9.4e-74	258.4
1152	Acyltransfer ase	Acyltransferase	1.2e-05	29.9
1157	IRS	PTB domain (IRS-1.type)	5.4e-55	196.1
1153		Immunoqlobulin domain	1.3e-31	106.9
1155	Asparaginase	Asparaginase	6.4e-72	252.3
	_2	and the second	1 20 343	485.3
1159	GMC_oxred	GMC oxidoreductases	4.7e-142 0.00021	27.9
1160	zf-AN1	AN1-like Zinc finger		

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
1163	linkon highe	linkon histone Wi and We family	3.8e-14	SCORE 60.4
	linker_histo ne	linker histone H1 and H5 family		
1164	DED	Death effector domain	3.9e-05	30.5
1165	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1166	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1168	SAM	SAM domain (Sterile alpha motif)	0.04	10.5
1170	abhydrolase	alpha/beta hydrolase fold	0.098	-7.5
1174	SAP	SAP domain	3.9e-10	47.1
1177	PP2C	Protein phosphatase 2C	5.3e-31	112.5
1178	WD40	WD domain, G-beta repeat	4.7e-35	129.9
1180	Ets	Ets-domain	1.8e-09	33.3
1181	Collagen	Collagen triple helix repeat (20 copies)	0.00016	24.7
1182	TCL1_MTCP1	TCL1/MTCP1 family	9.5e-56	198.6
1184	RasGEF	RasGEF domain	1.7e-88	307.4
1185	mito_carr	Mitochondrial carrier proteins	1.5e-62	217.3
1187	UPAR_LY6	u-PAR/Ly-6 domain	0.0042	15.6
1188	Orn_DAP_Arg_ deC	Pyridoxal-dependent decarboxylase	6.2e-128	430.6
1193	Stathmin	Stathmin family	1.8e-90	314.0
1194	Stathmin	Stathmin family	1.8e-90	314.0
1195	Sec1	Sec1 family	3.2e-183	622.1
1196	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	3.1e-32	111.8
1197	Glyco_transf	Glycosyl transferase family 8	1.2e-09	45.5
1202	K_tetra	K+ channel tetramerisation domain	0.022	-16.8
1203	adh_short	short chain dehydrogenase	8.3e-45	162.3
1206	Ubie_methylt ran	ubiE/COQ5 methyltransferase family	1.3e-121	417.4
1208	7tm_3	7 transmembrane receptor	7.2e-09	29.0
1209	ank	Ank repeat	3.9e-15	63.7
1210	vATP- synt_AC39	ATP synthase (C/AC39) subunit	2.5e-128	439.7
1212	zf-C2H2	Zinc finger, C2H2 type	5.5e-17	69.9
1213	efhand	EF hand	3.2e-07	37.4
1219	rrm :	RNA recognition motif.	2.1e-40	147.7
1220	DUF6	Integral membrane protein DUF6	0.015	21.5
1222	SCAN	SCAN domain	1.5e-71	251.1
1223	G-gamma	GGL domain	3.6e-36	129.5
1227	catalase	Catalase	0	1158.9
1232	PX	PX domain	2.2e-15	64.5
1233	PX	PX domain	2.2e-15	64.5
1236 1241	FCH Peptidase M2	Fes/CIP4 homology domain Peptidase family M20/M25/M40	3.3e-09 2e-63	44.0 224.1
1243	WW	WW domain	0.044	17.9
1247	UPF0006	Metalloenzyme of unknown function UPF0006	6.3e-61	215.8
1248	Glycos_trans f_2	Glycosyl transferases	4.5e-10	46.9
1249	efhand	BF hand	4e-11	50.4
1254	UQ_con	Ubiquitin-conjugating enzyme	2.1e-73	257.3
1255	ras	Ras family	2.2e-62	220.7
1256	formyl_trans	Formyl transferase	4.9e-30	108.3
1259	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-13	46.4
		Dihydrofolate reductase	2.1e-69	241.7
1261	DiHfolate_re			
	<u> </u>	Gamma-glutamyltranspeptidase	1.8e-110	380.4
1261 1262 1263	d G_glu_transp	_		380.4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1266	SCP	SCP-like extracellular protein	6e-29	108.0
	K tetra	K+ channel tetramerisation	2.8e-27	104.0
L267	k_tetra	domain		
269	ras	Ras family	1.3e-85	297.9
275	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.2e-10	37.0
1276	abhydrolase	alpha/beta hydrolase fold	5.4e-23	89.8
1277	abhydrolase	alpha/beta hydrolase fold	5.6e-21	83.1
1279	trypsin	Trypsin	4.4e-41	132.0
L280	PBP	Phosphatidylethanolamine- binding protein	1.3e-13	58.7
1285	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.6e-14	49.6
1287	ank	Ank repeat	1.7e-52	187.8
1294	fn3	Fibronectin type III domain	0,026	20.9
		Guanylate-binding protein	0.00026	-70.0
1295	GBP	PMP-22/EMP/MP20/Claudin family	6.9e-41	149.3
1296	PMP22_Claudi			
1297	Rhodanese	Rhodanese-like domain	3.2e-14	60.7
1298	LIM	LIM domain containing proteins	5.8e-21	79.1
1301	rnaseA	Pancreatic ribonucleases	4.9e-43	145.2
1307	mito carr	Mitochondrial carrier proteins	2.1e-53	186.0
1308	WD40	WD domain, G-beta repeat	1.6e-17	71.6
1310	UPAR LY6	u-PAR/Ly-6 domain	7.1e-20	75.5
1313	thiored	Thioredoxin	3.6e-05	21.6
1314	Aa trans	Transmembrane amino acid	1.5e-67	237.9
1214	Aa_ctails	transporter protein		1.20 0 -
1316	trypsin	Trypsin	4.4e-41	132.0
1320	Ribosomal_L1	Ribosomal protein L13	3.9e-62	219.8
1327	Armadillo_se	Armadillo/beta-catenin-like repeats	0.0054	23.4
	g KRAB	KRAB box	0.052	-5.6
1328		RNA recognition motif.	2.1e-40	147.7
1329 1330	rrm Bcl-2	Apoptosis regulator proteins,	0.014	-1.6
		Bcl-2 family	<u> </u>	48.0
1331	PX	PX domain	2.1e-10	134.6
1333	KRAB	KRAB box	1.8e-36	
1334	UPP_syntheta	Putative undecaprenyl diphosphate synt	2.3e-89	310.3
1335	UPP syntheta	Putative undecaprenyl	1.8e-59	211.0
	'se	diphosphate synt		
1336	DSPC	Dual specificity phosphatase, catalytic doma	1.2e-31	118.6
1337	DSPc	Dual specificity phosphatase, catalytic doma	2.3e-12	54.5
1338	TPR	TPR Domain	0.00021	28.1
1340	metalthio	Metallothionein	0.013	20.3
	mutT	Bacterial mutT protein	5.8e-09	36.5
1341	,	FERM domain (Band 4.1 family)	1.3e-38	122.5
	Dand 41			
	Band_41		1.4e-44	161.5
1344	Kelch	Kelch motif	1.4e-44 1.2e-10	
1344 1345	Kelch Antifreeze	Kelch motif Antifreeze protein	1.2e-10	161.5
1344	Kelch	Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera	1.2e-10 0.086	161.5 48.8 -177.2
1344 1345	Kelch Antifreeze	Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain	1.2e-10 0.086 5.3e-28	161.5 48.8 -177.2
1344 1345 1347	Kelch Antifreeze 3Beta_HSD	Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6	1.2e-10 0.086 5.3e-28 0.033	161.5 48.8 -177.2 106.5 15.8
1344 1345 1347	Kelch Antifreeze 3Beta_HSD BTB	Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain)	1.2e-10 0.086 5.3e-28 0.033	161.5 48.8 -177.2 106.5 15.8 1088.7
1344 1345 1347 1348 1349	Kelch Antifreeze 3Beta_HSD BTB DUF6	Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated	1.2e-10 0.086 5.3e-28 0.033	161.5 48.8 -177.2 106.5 15.8
1344 1345 1347 1348 1349 1350	Kelch Antifreeze 3Beta_HSD BTB DUF6 myosin_head	Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium	1.2e-10 0.086 5.3e-28 0.033	161.5 48.8 -177.2 106.5 15.8 1088.7
1344 1345 1347 1348 1349 1350 1352	Kelch Antifreeze 3Beta_HSD BTB DUF6 myosin_head Nramp S_100	Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium binding domain	1.2e-10 0.086 5.3e-28 0.033 0 1.2e-202	161.5 48.8 -177.2 106.5 15.8 1088.7 686.6
1344 1345 1347 1348 1349 1350 1352 1353	Kelch Antifreeze 3Beta_HSD BTB DUF6 myosin_head Nramp S_100 DEAD	Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium binding domain DRAD/DEAH box helicase	1.2e-10 0.086 5.3e-28 0.033 0 1.2e-202 5.3e-23	161.5 48.8 -177.2 106.5 15.8 1088.7 686.6 89.9
1344 1345 1347 1348 1349 1350 1352 1353	Kelch Antifreeze 3Beta_HSD BTB DUF6 myosin_head Nramp S_100 DEAD C2	Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium binding domain DEAD/DEAH box helicase C2 domain	1.2e-10 0.086 5.3e-28 0.033 0 1.2e-202 5.3e-23 3.6e-65 2.4e-15	161.5 48.8 -177.2 106.5 15.8 1088.7 686.6 89.9
1344 1345 1347 1348 1349 1350 1352 1353	Kelch Antifreeze 3Beta_HSD BTB DUF6 myosin_head Nramp S_100 DEAD	Kelch motif Antifreeze protein 3-beta hydroxysteroid dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium binding domain DRAD/DEAH box helicase	1.2e-10 0.086 5.3e-28 0.033 0 1.2e-202 5.3e-23	161.5 48.8 -177.2 106.5 15.8 1088.7 686.6

				
SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:				SCORE
1362	SIS	SIS domain	3.8e-30	113.6
1363	SIS	SIS domain	1.3e-28	108.5
1364	ig	Immunoglobulin domain	0.00026	19.0
1368	K_tetra	K+ channel tetramerisation	1.1e-16	68.9
		domain		
1371	Collagen	Collagen triple helix repeat	2.2e-113	390.1
]	(20 copies)]	}
1372	DnaJ	DnaJ domain	6.6e-36	132.7
1376	KRAB	KRAB box	2.1e-38	141.0
1378	ELM2	ELM2 domain	2e-23	91.3
1380	thiored	Thioredoxin	1.2e-23	82.8
1381	ank	Ank repeat	2.3e-83	290.4
1382	BTB	BTB/POZ domain	3e-11	50.8
1383	WD40	WD domain, G-beta repeat	1.6e-19	78.3
1384	WD40	WD domain, G-beta repeat	6.3e-24	92.9
1387	zf-C3HC4	Zinc finger, C3HC4 type (RING	1.1e-09	35.6
2507	DI-COMOT	finger)	1.16-03	35.0
1389	zf-C2H2	Zinc finger, C2H2 type	5.5e-50	179.5
1390	zf-C2H2	Zinc finger, C2H2 type	2.5e-85	296.9
1393	1			
	kinesin	Kinesin motor domain	7.8e-188	637.4
1394	zf-C2H2	Zinc finger, C2H2 type	1.2e-49	178.4
1398	KRAB	KRAB box	5.1e-22	86.6
1402	bZIP	bZIP transcription factor	0.035	13.1
1405	sugar_tr	Sugar (and other) transporter	0.003	-101.5
1406	RhoGAP	RhoGAP domain	8.9e-47	168.8
1407	rrm	RNA recognition motif.	le-35	132.1
1408	LRR	Leucine Rich Repeat	2.1e-13	58.0
1409	Nebulin_repe	Nebulin repeat	6e-54	192.6
	at		1	1
1410	ank	Ank repeat	1.6e-17	71.6
1412	Ribosomal L5	ribosomal L5P family C-terminus	8.2e-58	205.5
	c])	1
1415	trypsin	Trypsin	4.7e-85	.270.4
1416	aminotran 1	Aminotransferases class-I	4.4e-05	-91.2
1417	S1	S1 RNA binding domain	1.6e-07	33.1
1419	WD40	WD domain, G-beta repeat	2.2e-09	44.6
1422	cadherin	Cadherin domain	8.3e-42	152.3
1424	SH3	SH3 domain	2.5e-80	280.3
1425	PHD	PHD-finger	3.2e-17	70.6
1426	PHD	PHD-finger	3.2e-17	70.6
1427	ArfGap	Putative GTP-ase activating		138.8
1427	Arreap	protein for Arf	1e-37	138.8
1428	helicase C		1 06	 _
1428	nelicase_C	i e	1e-26	102.2
7420	LID 4 0	domain		
1429	WD40	WD domain, G-beta repeat	3.9e-07	37.2
1430	inositol_P	Inositol monophosphatase family	2.5e-10	40.2
1431	mito_carr	Mitochondrial carrier proteins	4.3e-83	287.7
1433	Clq	Clq domain	2.9e-16	66.2
1434	WD40	WD domain, G-beta repeat	1.6e-13	58.3
1435	Inos-1-	Myo-inositol-1-phosphate	7e-228	770.4
	P_synth	synthase		[
1436	rrm	RNA recognition motif.	1.4e-34	128.3
1438	ig	Immunoglobulin domain	1.3e-12	45.6
1440	G_Adapt_CT	Gamma-adaptin, C-terminus	3.4e-67	236.7
1441	G Adapt CT	Gamma-adaptin, C-terminus	3.4e-67	236.7
1443	Kelch	Kelch motif	0.00013	28.7
1446	ARID	ARID DNA binding domain	1.8e-21	84.7
1447	zf-C2H2	Zinc finger, C2H2 type	9.4e-28	105.6
1448	AMP-binding		2.6e-07	-145.1
1451		AMP-binding enzyme		
	rrm	RNA recognition motif.	6.5e-21	82.9
1454	ig	Immunoglobulin domain	5.6e-44	146.7
1455	Sialyltransf	Sialyltransferase family	5.4e-21	83.2
1460	Aldose_epim	Aldose 1-epimerase	1.9e-35	131.2
	C2	C2 domain	4e-18	73.6
1461		L	46.40	L
1470	TIG	IPT/TIG domain	3.1e-19	77.3
		L		L

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
	h 2			
1474	DENN	DENN (AEX-3) domain	1.3e-44	161.6
475	Cation efflu	Cation efflux family	4.6e-49	176.4
.4/5	x Cacron_erriu	Callon elliar lamily		
477	TBC	TBC domain	8e-47	169.0
1478	rrm	RNA recognition motif.	2e-21	84.6
1480		Immunoglobulin domain	5.5e-06	24.3
	ig Telo_bind_al	Telomere-binding protein alpha	0.028	-225.9
1484	. – – 1	subuni	*****	}
1405	pha zf-C2H2	Zinc finger, C2H2 type	1.8e-68	240.9
1485		Eukaryotic protein kinase	9.5e-13	49.9
1486	pkinase	domain		
1400	helicase_C	Helicases conserved C-terminal	1.4e-15	65.2
1488	nelicase_c	domain		1
1400	DUF89	Protein of unknown function	0.079	-132.4
1489	פאיטע	DUF89		
	ECH	Enoyl-CoA hydratase/isomerase	5.2e-41	149.7
1490	ECH	family	0.20	
	7-1	Adenylate and Guanylate cyclase	5.9e-46	156.1
1491	guanylate_cy	catalyt	3.50 30	
1400	C	Leucine Rich Repeat	3.4e-19	77.2
1492	LRR zf-C3HC4	Zinc finger, C3HC4 type (RING	7.1e-10	36.3
1495	ZI-C3HC4	finger)	1	
	1.1.7	Eukaryotic protein kinase	1e-22	85.8
1497	pkinase	domain	10 22	1 33.5
	-	SH3 domain	9.3e-05	27.2
1500	SH3	Homeobox domain	0.084	13.8
1502	homeobox		0.084	13.8
1503	homeobox	Homeobox domain	2.7e-23	90.8
1505	EGF	EGF-like domain	2.7e-23	84.2
1506	UCH-2	Ubiquitin carboxyl-terminal	2.76-21	04.2
		hydrolase family	2.8e-28	101.8
1508	Peptidase_M2	Peptidase family M20/M25/M40	2.86-28	101.8
	0		1.9e-11	51.5
1511	PX	PX domain	2.8e-35	130.7
1512	Sulfatase	Sulfatase	0.011	-62.3
1516	Syntaxin	Syntaxin	9.7e-106	305.6
1518	aminotran_3	Aminotransferases class-III	9.7e-106	303.6
		pyridoxal-pho	0.075	11.0
1520	ig	Immunoglobulin domain	0.073	13.3
1521	RA	Ras association (RalGDS/AF-6)	0.013	13.3
		domain		10.7
1523	RhoGAP	RhoGAP domain	2.5e-05	18.7
1528	WD40	WD domain, G-beta repeat	5.4e-24	
1535	IMS	impB/mucB/samB family	7.8e-95	328.5
1538	FYVE	FYVE zinc finger	3.2e-27	101.5
1539	DAGKC	Diacylglycerol kinase catalytic	6e-07	36.5
		domain	ļ. <u></u>	1
1540	Ocular_alb	Ocular albinism type 1 protein	0	1184.7
1653	SAP	SAP domain	6e-06	33.2
1654	Amino_oxidas	Flavin containing amine oxidase	3.2e-43	157.0
	е		J	
1655	Amino_oxidas	Flavin containing amine oxidase	3.2e-43	157.0
	е			
1656	RhoGEF	RhoGEF domain	1.4e-24	95.1
1657	MMR_HSR1	GTPase of unknown function	0.0011	-45.5
1659	UCH-2	Ubiquitin carboxyl-terminal	2.5e-11	51.1
		hydrolase family	<u> </u>	
1660	actin	Actin	6.6e-21	69.9
1661	BAH	BAH domain	1.7e-82	287.5
1662	vwa	von Willebrand factor type A	0	1909.4
		domain		
1663	WD40	WD domain, G-beta repeat	1.4e-67	237.9
1667	zf-C2H2	Zinc finger, C2H2 type	1.3e-93	324.4
1669	Nol1_Nop2_Su	NOL1/NOP2/sun family	1.3e-23	84.3
2007	n n		1	1
1	SH2	Src homology domain 2	5.4e-15	46.9

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:			-	SCORE
1672	chromo	'chromo' (CHRromatin	2.1e-18	67.7
		Organization MOdifier)	}	ł
1674	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	0.0025	17.6
		type	<u> </u>	. }
1676	Glyco_hydro_	Glycosyl hydrolase family 47	1.8e-187	636.2
	47		<u> </u>	
1677	Glyco_hydro_	Glycosyl hydrolase family 47	4.5e-74	259.5
	47		<u> </u>	
1680	WD40	WD domain, G-beta repeat	1.1e-27	105.5
1681	WD40	WD domain, G-beta repeat	1.le-27	105.5
1683	MMR_HSR1	GTPase of unknown function	1.8e-78	274.1
1691	rrm	RNA recognition motif.	1.8e-37	137.9
1692	rrm	RNA recognition motif.	1.8e-37	137.9
1693	AAA	ATPases associated with various cellular act	1.3e-81	284.5
1697	Ferric reduc	Ferric reductase like	8.4e-82	285.2
1057	t t	transmembrane com	0.46-07	205.2
1698	Ferric reduc	Ferric reductase like	3.5e-53	190.1
_0,0	t t	transmembrane com	3.36-33	1 20.1
1699	zf-C2H2	Zinc finger, C2H2 type	4.4e-34	126.6
1700	arf	ADP-ribosylation factor family	9e-19	75.8
1702	GTP EFTU	Elongation factor Tu family	0.014	11.4
1702	SCAN SCAN	SCAN domain		
1703			1.8e-54	194.4
1/0/	pkinase	Eukaryotic protein kinase domain	1.2e-88	307.9
1709	WD40	WD domain, G-beta repeat	0.0035	24.0
1710	LRR	Leucine Rich Repeat	1.2e-30	115.3
1711	WW	WW domain	7.6e-12	52.8
1712	ank	Ank repeat	4.2e-34	126.7
1713	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	2.6e-09	38.3
1/13	ZI-CCCH	type .	2.68-09	38.3
1714	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	2.6e-09	38.3
		type	1	\
1715	ras	Ras family	4.4e-41	149.9
1718	HMG box	HMG (high mobility group) box	8.3e-21	82.6
1719	TBC	TBC domain	1.1e-45	165.2
1721	HLH	Helix-loop-helix DNA-binding	9.2e-10	45.9
		domain		}
1723	dsrm	Double-stranded RNA binding	2.9e-05	30.9
1704		motif		<u> </u>
1724	RrnaAD	Ribosomal RNA adenine	0.045	9.2
	l		1	1
	OTHER ST	dimethylases		
	CIDE-N	CIDE-N domain	5.9e-40	146.2
1726	HAT	CIDE-N domain HAT (Half-A-TPR) repeats	5.9e-40 2.9e-44	160.5
1726 1728	HAT efhand	CIDE-N domain HAT (Half-A-TPR) repeats EF hand	5.9e-40 2.9e-44 5.1e-20	160.5 79.9
1726 1728	HAT efhand Hist_deacety	CIDE-N domain HAT (Half-A-TPR) repeats	5.9e-40 2.9e-44	160.5
1728 1733	HAT efhand Hist_deacety 1	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family	5.9e-40 2.9e-44 5.1e-20 1.7e-104	160.5 79.9 360.6
1726 1728 1733	HAT efhand Hist_deacety 1 LRR	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat	5.9e-40 2.9e-44 5.1e-20 1.7e-104	160.5 79.9 360.6
1726 1728 1733	HAT efhand Hist_deacety 1	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific	5.9e-40 2.9e-44 5.1e-20 1.7e-104	160.5 79.9 360.6
1726 1728 1733 1735 1739	HAT efhand Hist_deacety 1 LRR PI-PLC-X	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023	160.5 79.9 360.6 126.6 16.1
1726 1728 1733 1735 1739	HAT efhand Hist_deacety 1 LRR PI-PLC-X ras	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023	160.5 79.9 360.6 126.6 16.1
1726 1728 1733 1735 1739 1743	HAT efhand Hist_deacety 1 LRR PI-PLC-X ras ras	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family Ras family	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023 3.7e-10 3.7e-10	160.5 79.9 360.6 126.6 16.1 -21.3
1726 1728 1733 1735 1739 1743 1744 1745	HAT efhand Hist_deacety 1 LRR PI-PLC-X ras ras RasGEF	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023 3.7e-10 3.7e-10 3.2e-49	160.5 79.9 360.6 126.6 16.1 -21.3 -21.3 176.9
1726 1728 1733 1735 1739 1743 1744 1745 1746	HAT efhand Hist_deacety 1 LRR PI-PLC-X ras ras RasGEF adh_short	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08	160.5 79.9 360.6 126.6 16.1 -21.3 -21.3 176.9 34.6
1726 1728 1733 1735 1739 1743 1744 1745 1746 1751	HAT efhand Hist_deacety 1 LRR PI-PLC-X ras ras RasGEF adh_short zf-C2H2	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39	160.5 79.9 360.6 126.6 16.1 -21.3 -21.3 176.9
1726 1728 1733 1735 1739 1743 1744 1745 1746 1751	HAT efhand Hist_deacety 1 LRR PI-PLC-X ras ras RasGEF adh_short zf-C2H2 fn3	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08	160.5 79.9 360.6 126.6 16.1 -21.3 -21.3 176.9 34.6
1726 1728 1733 1735 1739 1743 1744 1745 1746 1751 1754	HAT efhand Hist_deacety 1 LRR PI-PLC-X ras ras RasGEF adh_short zf-C2H2	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39	160.5 79.9 360.6 126.6 16.1 -21.3 -21.3 176.9 34.6 142.2
1726 1728 1733 1735 1739 1743 1744 1745 1746 1751 1754 1756 1758	HAT efhand Hist_deacety 1 LRR PI-PLC-X ras ras RasGEF adh_short zf-C2H2 fn3	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif.	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101	160.5 79.9 360.6 126.6 16.1 -21.3 -21.3 176.9 34.6 142.2 348.9
1726 1728 1733 1735 1739 1743 1744 1745 1746 1751 1754 1756 1758	HAT efhand Hist_deacety 1 LRR PI-PLC-X ras ras RasGEF adh_short zf-C2H2 fn3 zf-C2H2	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif.	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93	160.5 79.9 360.6 126.6 16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1
1726 1728 1733 1735 1739 1743 1744 1745 1746 1751 1754 1756 1758	HAT efhand Hist_deacety 1 LRR PI-PLC-X ras ras RasGEF adh_short zf-C2H2 fn3 zf-C2H2 rrm	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017	160.5 79.9 360.6 126.6 16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1 21.2
1726 1728 1733 1735 1739 1743 1744 1745 1746 1751 1754 1756 1758 1760 1761	HAT efhand Hist_deacety 1 LRR PI-PLC-X ras ras RasGEF adh_short zf-C2H2 fn3 zf-C2H2 rrm Nop	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain Putative snoRNA binding domain	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95 6.1e-95	160.5 79.9 360.6 126.6 16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8 328.8
1726 1728 1733 1735 1739 1743 1744 1745 1746 1751 1754 1756 1758 1760 1761 1765	HAT efhand Hist_deacety 1 LRR PI-PLC-X ras ras RasGEF adh_short zf-C2H2 fn3 zf-C2H2 rrm Nop Nop MMR_HSR1	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95 6.1e-95 6.4e-41	160.5 79.9 360.6 126.6 16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8 328.8 149.4
1726 1728 1733 1735 1739 1743 1744 1745 1746 1751 1754 1756 1758 1760 1761 1765 1769	HAT efhand Hist_deacety 1 LRR PI-PLC-X ras ras RasGEF adh_short zf-C2H2 fn3 zf-C2H2 rrm Nop Nop Nop MMR_HSR1 CN_hydrolase	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function Carbon-nitrogen hydrolase	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95 6.1e-95 6.4e-41 3e-06	160.5 79.9 360.6 126.6 16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8 328.8 149.4 -43.9
1726 1728 1733 1735 1739 1743 1744 1745 1746 1751 1754 1756 1758 1760 1761 1765 1769 1775	HAT efhand Hist_deacety l LRR PI-PLC-X ras ras RasGEF adh_short zf-C2H2 fn3 zf-C2H2 rrm Nop Nop Nop MMR_HSR1 CN_hydrolase ank	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function Carbon-nitrogen hydrolase Ank repeat	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95 6.1e-95 6.4e-41 3e-06 4.1e-07	160.5 79.9 360.6 126.6 16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8 328.8 149.4 -43.9 37.1
1726 1728 1733 1735 1739 1743 1744 1745 1746 1751 1754 1756 1758 1760 1761 1765 1769	HAT efhand Hist_deacety 1 LRR PI-PLC-X ras ras RasGEF adh_short zf-C2H2 fn3 zf-C2H2 rrm Nop Nop Nop MMR_HSR1 CN_hydrolase	CIDE-N domain HAT (Half-A-TPR) repeats EF hand Histone deacetylase family Leucine Rich Repeat Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function Carbon-nitrogen hydrolase	5.9e-40 2.9e-44 5.1e-20 1.7e-104 4.6e-34 0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95 6.1e-95 6.4e-41 3e-06	160.5 79.9 360.6 126.6 16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8 328.8 149.4 -43.9

263

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1785	rrm	RNA recognition motif.	6.4e-14	59.7

TRADOCS:1416227.1(%CRN011.DOC)

TABLE 5

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1	1-21	0.991	0.955
2	1-31	0.995	0.944
3	1-33	0.949	0.736
4	1-19	0.970	0.951
5	1-26	0.971	0.863
6	1-26	0.971	0.863
7	1-26	0.971	0.863
8	1-26	0.971	0.863
9	1-46	0.982	0.901
10	1-21	0.991	0.955
11	1-23	0.989	0.899
12	1-25	0.955	0.803
13	1-18	0.932	0.625
14	1-18	0.938	0.876
15	1-25	0.941	0.811
16	1-17	0.972	0.939
17	1-27	0.964	0.777
18	1-16	0.914	0.657
19	1-19	0.953	0.840
20	1-20	0.935	0.701
21	1-22	0.974	0.850
22	1-33	0.961	0.895
23	1-19	0.991	0.959
24	1-31	0.995	0.944
25	1-22	0.976	0.935
26	1-27	0.996	0.928
27	1-24	0.953	0.739
28	1-21	0.906	0.688
29	1-31	0.986	0.841
30	1-28	0.980	0.893
31	1-19	0.993	
32	1-19		0.976
35	1-33	0.998	0.736
36	1-33	0.949	0.736
46			
67	1-19	0.970	0.951
71		0.968	0.848
72	1-18		0.845
75		0.991	0.919
	1-29	0.958	0.854
88	1-20	0.986	0.945
94	1-33	0.994	0.943
97	1-46	0.964	0.595
103	1-49	0.983	0.570
108	1-26	0.978	0.885
111	1-23	0.989	0.899
126	1-25	0.955	0.803
129	1-19	0.963	0.918
138	1-29	0.971	0.844
143	1-18	0.914	0.628
148	1-20	0.969	0.904
156	1-25	0.941	0.811
158	1-22	0.979	0.927
160	1-17	0.972	0.939
161	1-48	0.903	0.571
162	1-25	0.937	0.729
168	1-16	0.939	0.826
171	1-27	0.964	0.777
178	1-21	0.945	0.825
180		0.981	0.941
100	1-27	0.901	0.741
187	1-27	0.982	0.936
		<u> </u>	
187	1-28	0.982	0.936

SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN SCORE)
	SIGNAL IN AMINO ACID SEQUENCE	SCORE)	3CORE/
199	1-20	0.935	0.701
200	1-23	0.977	0.773
206	1-30	0.984	0.890
207	1-19	0.990	0.924
208	1-22	0.974	0.850
210	1-40	0.940	0.849
211	1-28	0.986	0.956
216 218	1-33	0.961	0.895
219	1-19	0.970	0.871
221	1-19	0.904	0.553
222	1-21	0.917	0.555
230	1-19	0.991	0.959
231	1-26	0.953	0.800
232	1-25	0.988	0.826
239	1-23	0.969	0.828
240	1-17	0.982	0.955
241	1-17	0.982	0.722
245	1-30	0.976	0.935
249	1-23	0.968	0.940
252	1-18	0.971	0.923
261	1-24	0.883	0.587
265	1-18	0.939	0.868
272	1-24	0.953	0.739
283	. 1-21	0.906	0.688
284	1-29	0.997	0.854
290	1-31	0.986	0.841
302	1-28	0.980	0.635
304 312	1-16	0.993	0.976
313	1-17	0.930	0.753
323	1-22	0.998	0.909
324	1-17	0.982	0.954
328	1-19	0.971	0.865
329	1-22	0.963	0.924
330	1-33	0.978	0.841
331	1-24	0.920	0.712
332	1-24	0.975	0.881
333	1-19	0.984	0.567
334	1-20	0.942	0.813
335 336	1-20	0.952	0.850
337	1-38	0.942	0.653
338	1-27	0.973	0.772
339	1-36	0.979	0.804
340	1-27	0.888	0.597
343	1-19	0.971	0.865
344	1-22	0.994	0.928
345	1-17	0.966	0.687
346	1-19	0.936	0.822
347	1-22	0.963	0.966
349	1-24	0.982	0.815
351 352	1-31	0.918	0.912
354	1-31	0.974	0.839
355	1-29	0.932	0.632
356	1-15	0.994	0.969
357	1-33	0.935	0.726
360	1-27	0.938	0.827
361	1-25	0.954	0.674
362	1-22	0.929	0.788
363	1-21	0.881	0.715
364	1-33	10074	1 1) 1// 7

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
366	1-21	0.916	0.820
367	1-19	0.936	0.822
368		0.972	
370	1-29	0.920	0.874
371	1-24		
	1-24	0.961	0.773
372	1-27	0.919	0.768
373	1-19	0.986	0.945
375	1-32	0.994	0.932
376	1-34	0.987	0.810
377	1-17	0.995	0.950
378	1-49	0.971	0.749
380	1-20	0.968	0.874
381	1-20	0.928	0.782
382	1-19	0.986	0.934
383	1-28	0.965	0.829
384	1-39	0.970	0.551
386	1-24	0.975	0.881
388	1-30	0.989	0.868
389	1-19	0.984	0.941
390	1-26	0.971	0.782
392	1-20	0.981	0.900
393	1-16	0.968	0.890
394	1-23	0.937	0.701
397	1-22	0.985	0.854
399		l <u> </u>	<u> </u>
	1-46	0.977	0.698
401	1-20	0.899	0.567
402	1-22	0.967	0.931
403	1-27	0.992	0.934
404	1-19	0.991	0.973
405	1-23	0.994	0.921
407	1-35	0.987	0.658
408	1-39	0.976	0.551
409	1-33	0.897	0.570
410	1-25	0.990	0.962
411	1-38	0.977	0.827
412	1-20	0.944	0.768
413	1-20	0.988	0.965
414	1-46	0.993	0.638
415	1-23	0.981	0.940
417	1-29	0.941	0.672
418	1-20	0.952	0.850
419	1-19	0.986	0.967
420	1-29	0.965	0.861
421	1-22	0.889	0.785
422	1-48	0.889	0.785
424	1-19		
428	1-38	0.979	0.933
	±	0.942	0.653
430	1-18	0.947	0.595
432	1-33	0.957	0.789
433	1-26	0.979	0.904
434	1-27	0.962	0.777
435	1-24	0.998	0.977
436	1-27	0.973	0.772
443	1-15	0.966	0.940
448	1-36	0.979	0.804
453	1-41	0.958	0.609
455	1-33	0.943	0.606
457	1-27	0.888	0.597
462	1-16	0.925	0.681
486	1-27	0.972	0.845
495	1-24	0.917	0.636
498	1-26	0.917	0.890
505	1-20		
		0.976	0.926
507	1-17	0.966	0.687
510	1-23	0.930	0.593

SEQ ID NO:	POSITION OF	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
	SIGNAL IN AMINO ACID SEQUENCE	SCORE)	BCOKE,
311	1-23	0.930	0.593
12	1-23	. 0.930	0.593
15	1-18	0.978	0.956
23	1-19	0.936	0.822
29	1-22	0.963	0.924
45	1-24	0.982	0.966
50	1-30	0.933	0.713
52	1-21	0.973	0.912
554	1-23	0.969	0.784
571	1-21	0.918	0.815
574	1-31	0.988	0.912
80	1-39	0.925	0.556
594	1-31	0.974	0.839
808	1-29	0.932	0.632
509	1-29	0.932	0.632
510	1-21	0.990	0.948
621	1-15	0.994	0.969
523	1-33	0.935	0.726
653	1-27	0.938	0.827
668	1-22	0.929	0.788
677 .	1-16	0.948	0.807
685	1-21 .	0.881	
699	1-22	0.975	0.816
702	1-31	0.968	0.898
707	1-16	0.880	0.562
713	1-25	0.966	0.743
718	1-19	0.936	0.824
719	1-20	0.961	0.824
729	1-29	0.972	0.598
735	1-46	0.903	0.730
746	1-14	0.916	0.730
747	1-22	0.965	0.785
748	1-29	0.968	0.773
759	1-24	0.961	0.768
767	1-27	0.919	0.585
768	1-33	0.959	0.702
773	1-42	0.986	0.945
779	1-19	0.944	0.759
797	1-19	0.900	0.568
798	1-19	0.995	0.950
820		0.971	0.749
827	1-49	0.968	0.874
848	1-20	0.928	0.782
864	1-19	0.986	0.934
866	1-23	0.948	0.886
873 881	1-28	0.965	0.829
887	1-39	0.970	0.551
927	1-30	0.989	0.868
934	1-48	0.988	0.777
939	1-39	0.994	0.889
944	1-26	0.971	0.782
950	1-29	0.957	0.845
963	1-20	0.981	0.900
964	1-20	0.886	0.558
973	1-16	0.968	0.890
980	1-34	0.961	0.749
981	1-20	0.953	0.822
984	1-12	0.938	0.780
1015	1-22	0.985	0.854
1040	1-46	0.977	0.698
1052	1-18	0.969	0.842
1059	1-20	0.927	0.867
1065	1-33	0.983	0.918
1069	1-22	0.993	0.935

CEO TO NO.			· T
SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
	SIGNAL IN AMINO	SCORE)	SCORE)
1500	ACID SEQUENCE		
1075	1-27	0.992	0.934
1080	1-19	0.931	0.829
1092	1-19	0.991	0.973
1094	1-46	0.992	0.653
1095	1-30	0.974	0.929
1105	1-23	0.994	0.921
1123	1-35	0.987	0.658
1138	1-32	0.954	0.613
1140	1-38	0.989	0.789
1142	1-33	0.897	0.570
1152	1-25	0.990	0.962
1170	1-38	0.977	0.827
1176	1-20	0.944	0.768
1187	1-20	0.988	0.965
1189	1-35	0.967	
1192	_{		0.839
	1-46	0.993	0.638
1193	1-16	0.925	0.710
1197	1-29	0.985	0.853
1208	1-23	0.981	0.940
1225	1-29	0.941	0.672
1245	1-19	0.986	0.967
1258	1-29	0.965	0.861
1265	1-22	0.889	0.785
1266	1-20	0.944	0.809
1276	1-48	0.982	0.862
1292	1-19	0.979	0.933
1296	1-21	0.984	0.944
1297	1-19	0.984	0.953
1332	1-38	0.942	0.653
1358	1-18	0.947	0.595
1371	1-33	0.957	0.789
1380	1-26	0.979	0.904
1397	1-27	0.962	
1399	1-23		0.777
1404	<u> </u>	0.997	0.960
1410	1-24	0.998	0.977
1414	1-15	0.946	0.845
	1-24	0.913	0.588
1415	1-19	0.982	0.929
1416	1-12	0.931	0.891
1418	1-30	0.933	0.563
1420	1-20	0.881	0.561
1421	1-19	0.990	0.968
1423	1-17	0.968	0.863
1424	1-21	0.885	0.591
1425	1-24	0.913	0.588
1426	1-24	0.913	0.588
1428	1-25	0.967	0.899
1430	1-34	0.977	0.819
1431	1-28	0.979	0.923
1432	1-36	0.957	0.613
1433	1-32	0.921	0.753
1434	1-39	0.921	
1435	1-25		0.621
1436	1-42	0.910	0.631
		0.988	0.868
1437	1-22	0.998	0.980
1442	1-20	0.918	0.753
1448	1-12	0.931	0.891
1462	1-18	0.968	0.888
1490	1-20	0.881	0.561
1518	1-17	0.968	0.863
1525	1-21	0.885	0.591
1547	1-28	0.974	0.891
1561	1-25	0.967	0.899
1580	1-17	0.923	0.824
1593	1-28	0.979	0.923
	<u> </u>		

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1596	1-16	0.929	0.709
1601	1-36	0.957	0.613
1606	1-22	0.979	0.831
1607	1-20	0.974	0.770
1608	1-32	0.921	0.753
1614	1-33	0.969	0.829
1616	1-20	0.959	0.869
1625	1-39	0.983	0.621
1632	1-25	0.910	0.631
1636	1-33	0.897	0.591
1639	1-42	0.988	0.868
1645	1-20	0.927	0.568
1647	1-17	0.923	0.742
1648	1-22	0.998	0.980

TRADOCS:1416234.1(%CR%01!.DOC)

TABLE 6

SEQ ID NO:	SEQ ID	CEO TO NO.	L CEO ID	Driggitu	CPO ID
of full-	NO: of	SEQ ID NO: of contig	SEQ ID	Priority docket number	SEQ ID No:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	Bequence	sequence	priority	05/400,725
Doguoneo	sequence		bequence	application	
1	1787	3573	5359	784CIP2 1	1103
2	1788	3574	5360	784CIP2 2	2673
3	1789	3575	5361	784CIP2 3	4117
4	1790	3576	5362	784CIP2 4	5556
5	1791	3577	5363	784CIP2_4	5562
6	1792	3578	5364	784CIP2_5	5562
7	1793	3578	5365	784CIP2 7	5562
8	1794	3579	5366	784CIP2_7	5562
9	1795	<u> </u>		784CIP2_8 784CIP2_9	5563
		3581	5367		5564
10	1796	3582	5368	784CIP2_10	
11	1797	3583	5369	784CIP2_11	5565
12	1798	3584	5370	784CIP2_12	5689
13	1799	3585	5371	784CIP2_13	5729
14	1800	3586	5372	784CIP2_14	5745
15	1801	3587	5373	784CIP2_15	5777
16	1802	3588	5374	784CIP2_16	5777
17	1803	3589	5375	784CIP2_17	5789
18	1804	3590	5376	784CIP2_18	5792
19	1805	3591	5377	784CIP2_19	5804
20	1806	3592	5378	784CIP2_20	5805
21	1807	3593	5379	784CIP2_21	5805
22	1808	3594	5380	784CIP2_22	5844
23	1809	3595	5381	784CIP2_23	5844
24	1810	3596	5382	784CIP2_24	5850
25	1811	3597	5383	784CIP2_25	5867
26	1812	3598	5384	784CIP2_26	5973
27	1813	3599	5385	784CIP2_27	5995
28	1814	3600	5386	784CIP2_28	5995
29	1815	3601	5387	784CIP2_29	6005
30	1816	3602	5388	784CIP2_30	6007
31	1817	3603	5389	784CIP2_31	6007
32	1818	3604	5390	784CIP2_32	6009
33	1819	3605	5391	784CIP2 33	6012
34	1820	3606	5392	784CIP2 34	6015
. 35	1821	3607	5393	784CIP2 35	6016
36	1822	3608	5394	784CIP2 36	6016
37	1823	3609	5395	7B4CIP2 37	6018
38	1824	3610	5396	784CIP2 38	6018
39	1825	3611	5397	784CIP2 39	6018
40	1826	3612	5398	784CIP2_40	6023
41	1827	3613	5399	784CIP2_41	6070
42	1828	3614	5400	784CIP2_42	6081
43	1829	3615	5401	784CIP2 43	6089
44	1830	3616	5402	784CIP2 44	6118
45	1831	3617	5403	784CIP2 45	6118
46	1832	3618	5404	784CIP2 46	6130
47	1833	3619	5405	784CIP2 47	6177
48	1834	3620	5406	784CIP2 48	6189
49	1835	3621	5407	784CIP2 49	6191
50	1836	3622	5408	784CIP2 50	6204
51	1837	3623	5409	784CIP2 51 ·	6204
52	1838	3624	5410	784CIP2 52	6284
53	1839	3625	5411	784CIP2_53	6367
54	1840	3626	5412	784CIP2_53	6436
55	1841	3627	5413	784CIP2_55	6442
56	1842		5414	784CIP2_55	6445
57		3628			6457
	1843	3629	5415	784CIP2_57	
58 59	1844	3630	5416	784CIP2_58	6458
	1845	3631	5417	784CIP2 59	6458

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_ corresponding	NO:in U.S.S.N.
length	full-	nucleotide	of contig	SEQ ID NO: in	0.S.S.N. 09/488,725
nucleotide	length	sequence	peptide	priority	09/400,725
sequence	peptide		sequence	application	1
	sequence	3632	5418	784CIP2 60	6462
60	1846	3633	5419	784CIP2 61	6472
61	1847	3634	5420	784CIP2 62	6499
62	1849	3635	5421	784CIP2 63	6499
63	1850	3636	5422	784CIP2 64	6505
65	1851	3637	5423	784CIP2 65	6534
66	1852	3638	5424	784CIP2 66	6534
67	1853	3639	5425	784CIP2 67	6540
68	1854	3640	5426	784CIP2 68	6550
69	1855	3641	5427	784CIP2 69	6550
70	1856	3642	5428	784CIP2 70	6592
71	1857	3643	5429	784CIP2 71	6645
72	1858	3644	5430	784CIP2 72	6671
73	1859	3645	5431	784CIP2_73	6763
74	1860	3646	5432	784CIP2_74	6763
75	1861	3647	5433	784CIP2_75	6786
76	1862	3648	5434	784CIP2_76	6824
77	1863	3649	5435	784CIP2_77	6830
78	1864	3650	5436	784CIP2_78	6831
79	1865	3651	5437	784CIP2_79	6832
80	1866	3652	5438	784CIP2_80	6834
81	1867	3653	5439	784CIP2_81	6834
82	1868	3654	5440	784CIP2_82	6835
83	1869	3655	5441	784CIP2_83	6837
84	1870	3656	5442	784CIP2_84	6843
85	1871	3657	5443	784CIP2_85	6859
86	1872	3658	5444	784CIP2_86	6915
87	1873	3659	5445	784CIP2_87	6932
88	1874	3660	5446	784C1P2_88	6957
89	1875	3661	5447	784CIP2_89	6961
90	1876	3662	5448	784CIP2_90	6973
91	1877	3663	5449	784CIP2_91	6973 7007
92	1878	3664	5450	784CIP2_93	_1
93	. 1879	3665	5451	784CIP2_94	7018
94	1880	3666	5452	784CIP2_95	7020
95	1881	3667	5453	784CIP2_96	7020
96	1882	3668	5454	784CIP2_97 784CIP2_98	7021
97	1883	3669	5455	784CIP2_98	7023
98	1884	3670	5456	784CIP2_99	7023
99	1885	3671	5457		7028
100	1886	3672	5458 5459	784CIP2_101 784CIP2_102	7029
101	1887	3673	5460	784CIP2_102 784CIP2_103	7031
102	1888	3674 3675	5461	784CIP2_103	7032
103	1889	3675	5462	784CIP2_104	7033
104	1890	3677	5463	784CIP2_106	7035
105	1891	3678	5464	784CIP2 107	7036
106	1892	3678	5465	784CIP2 108	7039
107	1893	3680	5466	784CIP2 109	7043
108	1894	3680	5467	784CIP2 110	7044
109	1895	3682	5468	784CIP2_111	7046
110	1896	3683	5469	784CIP2 112	7054
111	1897	3684	5470	784CIP2 113	7061
112	1898	3685	5471	784CIP2 114	7077
113	1900	3686	5472	784CIP2 115	7092
114		3687	5473	784CIP2 116	7094
115	1901	3688	5474	784CIP2 117	7106
116	1902	3689	5475	784CIP2 118	7107
117	1903	3690	5476	784CIP2 119	7111
118	1904	3691	5477	784CIP2 120	7123
119 120	1905	3692	5478	784CIP2 121	7142
120	1 7300	3032	5479	784CIP2 122	7142

SEQ ID NO: of full-	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
length	NO: of full-	of contig	NO: of contig	docket number_ corresponding	NO:in U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	0.5.5.N. 09/488,725
sequence	peptide	sequence	sequence	priority	03/400,723
•	sequence			application	
122	1908	3694	5480	784CIP2 123	7154
123	1909	3695	5481	784CIP2_124	7160
124	1910	3696	5482	784CIP2_125	7169
125	1911	3697	5483	784CIP2_126	7185
126	1912	3698	5484	784CIP2_127	7197
127	1913	3699	5485	784CIP2_128	7219
128	1914	3700	5486	784CIP2_129	7226
129	1915	3701	5487	784CIP2_130	7229
130	1916	3702	5488	784CIP2_131	7234
131	1917	3703	5489	784CIP2_132	7235
132	1918	3704	5490	784CIP2_133	7235
133	1919	3705	5491	784CIP2_134	7238
134	1920	3706	5492	784CIP2_135	7247
135	1921	3707	5493	784CIP2_136	7261
136	1922	3708 3709	5494 5495	784CIP2_137 784CIP2_138	7262 7267
138	1923	3709	5495	784CIP2_138 784CIP2_139	7272
139	1925	3711	5497	784CIP2_139 784CIP2_140	7273
140	1925	3712	5498 .	784CIP2_140 784CIP2_141	72/3
141	1927	3713	5499	784CIP2 142	7288
142	1928	3714	5500	784CIP2 143	7291
143	1929	3715	5501	784CIP2 144	7293
144	1930	3716	5502	784CIP2 145	7294
145	1931	3717	5503	784CIP2 146	7299
146	1932	3718	5504	784CIP2 147	7300
147	1933	3719	5505	784CIP2 148	7312
148	1934	3720	5506	784CIP2 149	7313
149	1935	3721	5507	784CIP2_150	7315
150	1936	3722	5508	784CIP2_151	7318
151	1937	3723	5509	784CIP2_152	7321
152	1938	3724	5510	784CIP2_153	7330
153	1939	3725	5511	784CIP2_154	7331
154	1940	3726	5512	784CIP2_155	7333
155	1941	3727	5513	784CIP2_156	7350
156	1942	3728	5514	784CIP2_157	7352
157 158	1943	3729	5515	784CIP2_158	7384
159	1944 1945	3730 3731	5516 5517	784CIP2_159 784CIP2_160	7403 7431
160	1945	3732	5518	784CIP2_160 784CIP2_161	7441
161	1947	3733	5519	784CIP2_161 784CIP2_162	7453
162	1948	3734	5520	784CIP2 163	7467
163	1949	3735	5521	784CIP2 164	7471
164	1950	3736	5522	784CIP2 165	7493
165	1951	3737	5523	784CIP2 166	7502
166	1952	3738	5524	784CIP2 167	7511
167	1953	3739	5525	784CIP2_168	7514
168	1954	3740	5526	784CIP2_169	7520
169	1955	3741	5527	784CIP2_170	7541
170	1956	3742	5528	784CIP2_171	7570
171	1957	3743	5529	784CIP2_172	7578
172	1958	3744	5530	784CIP2_173	7583
173	1959	3745	5531	784CIP2_174	7592
174	1960	3746	5532	784CIP2_175	7601
175	1961	3747	5533	784CIP2_176	7602
176	1962	3748	5534	784CIP2_177	7608
177	1963	3749	5535	784CIP2_178	7615
178	1964	3750	5536	784CIP2_179	7617
179	1965	3751	5537	784CIP2_181	7624
180	1966	3752	5538	784CIP2_182	7626
181	1967	3753	5539	784CIP2_183	7640
182	1968	3754	5540	784CIP2_184	7641
183	1969	3755	5541	784CIP2_185	7641

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in U.S.S.N.
Length	full-	nucleotide	of contig	corresponding SEQ ID NO: in	0.5.5.N. 09/488,725
nucleotide	length	sequence	peptide	priority	03/400, 123
sequence	peptide		sequence	application	
	sequence	3756	5542	784CIP2 186	7641
184	1970	3756	5543	784CIP2 187	7642
185	1971	3757	5544	784CIP2 188	7649
186	1972	3758 3759	5545	784CIP2 189	7656
187	1973		5546	784CIP2 190	7657
188	1974	3760	5547	784CIP2 191	7657
189	1975	3761		784CIP2 192	7662
190	1976	3762	5548 5549	784CIP2 193	7668
191	1977	3763	5550	784CIP2 194	7673
192	1978	3764	5551	784CIP2 195	7690
193	1979	3765	5552	784CIP2 196	7700
194	1980	3766		784CIP2 197	7709
195	1981	3767	5553 5554	784CIP2 198	7736
196	1982	3768		784CIP2_198	7737
197	1983	3769	5555	784CIP2_200	7744
198	1984	3770	5556	784CIP2_200	7771
199	1985	3771	5557	784CIP2_201 784CIP2_202	7786
200	1986	3772	5558	784CIP2_202 784CIP2_203	7791
201	1987	3773	5559	784CIP2_203	7797
202	1988	3774	5560	784CIP2_204 784CIP2_205	7806
203	1989	3775	5561	784CIP2_203	7812
204	1990	3776	5562	784CIP2_206	7812
205	1991	3777	5563	784CIP2_207	7818
206	1992	3778	5564	784CIP2_208	7822
207	1993	3779	5565	784CIP2_209	7827
208	1994	3780	5566	784CIP2_210 784CIP2_211	7830
209	1995	3781	5567	784CIP2_211 784CIP2_212	7835
210	1996	3782	5568		7840
211	1997	3783	5569	784CIP2_214 784CIP2_215	7858
212	1998	3784	5570	784CIP2_215 784CIP2_216	7858
213	1999	3785	5571	784CIP2_216 784CIP2_217	7861
214	2000	3786	5572	784CIP2_217 784CIP2_218	7866
215	2001	3787	5573	784CIP2_218 784CIP2_219	7868
216	2002	3788	5574	784CIP2_219 784CIP2_220	7896
217	2003	3789	5575		7898
218	2004	3790	5576	784CIP2_221	7900
219	2005	3791	5577	784CIP2_222 784CIP2_223	7906
220	2006	3792	5578	784CIP2_223 784CIP2_224	7908
221	2007	. 3793	5579		7909
222	2008	3794	5580	784CIP2_225	7917
223	2009	3795	5581	784CIP2_226	7932
224	2010	3796	5582	784CIP2_227	7940
225	2011	3797	5583	784CIP2_228 784CIP2_229	7940
226	2012	3798	5584	784CIP2_229 784CIP2_230	7984
227	2013	3799	5585	784CIP2_230 784CIP2_231	7984
228	2014	3800	5586	784CIP2_231 784CIP2_232	8001
229	2015	3801	5587	1	8021
230	2016	3802	5588	784CIP2_233 784CIP2_234	8021
231	2017	3803	5589		8033
232	2018	3804	5590	784CIP2_235	8040
233	2019	3805	5591	784CIP2_236	8052
234	2020	3806	5592	784CIP2_237	8096
235	2021	3807	5593	784CIP2_238	8096
236	2022	3808	5594	784CIP2_239	8113
237	2023	3809	5595	784CIP2_240	
238	2024	3810	5596	784CIP2_241	8126
239	2025	3811	5597	784CIP2_242	8132
240	2026	3812	5598	784CIP2_243	8137
241	2027	3813	5599	784CIP2_244	8137
242	2028	3814	5600	784CIP2_245	8159
243	2029	3815	5601	784CIP2_246	8159
244	2030	3816	5602	784CIP2_247	
	2031	3817	5603	784CIP2_248	8176

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide sequence	length peptide	sequence	peptide sequence	SEQ ID NO: in priority	09/488,725
sequence	sequence		sequence	application	
246	2032	3818	5604	784CIP2 249	8196
247	2033	3819	5605	784CIP2 250	8200
248	2034	3820	5606	784CIP2 251	8212
249	2035	3821	5607	784CIP2 252	8220
250	2036	3822	5608	784CIP2 253	8238
251	2037	3823	5609	784CIP2 254	8254
252	2038	3824	5610	784CIP2 255	8255
253	2039	3825	5611	784CIP2 256	8288
254	2040	3826	5612	784CIP2_257	8296
255	2041	3827	5613	784CIP2_258	8329
256	2042	3828	5614	784CIP2_259	8362
257	2043	3829	5615	784CIP2_260	8429
258	2044	3830	5616	784CIP2_261	8436
259	2045	3831	5617	784CIP2_262	8448
260	2046	3832	5618	. 784CIP2_263	8472
261	2047	3833	5619	784CIP2_264	8502
262	2048	3834	5620	784CIP2_265	8504
263	2049	3835	5621	784CIP2_266	8507
264 :	2050	3836	5622	784CIP2_268	8509
265	2051	3837	5623	784CIP2_269	8515
266	2052	3838	5624	784CIP2_270	8519
267	2053	3839	5625	784CIP2_271	8530
268	2054	3840	5626	784CIP2_272	8532
269 270	2055 2056	3841 3842	5627	784CIP2_273	8532
271	2056	3842	5628 5629	784CIP2_274 784CIP2_275	8539
272	2058	3844	5630	784CIP2_275 784CIP2_276	8541 8543
273	2059	3845	5631	784CIP2_276	8593
274	2060	3846	5632	784CIP2 278	8595
275	2061	3847	5633	784CIP2_278	8615
276	2062	3848	5634	784CIP2_279	8620
277	2063	3849	5635	784CIP2 281	8621
278	2064	3850	5636	784CIP2 282	8623
279	2065	3851	5637	784CIP2 283	8625
280	2066	3852	5638	784CIP2 284	8628
281	2067	3853	5639	784CIP2 285	8628
282	2068	3854	5640	784CIP2 286	8629
283	2069	3855	5641	784CIP2 287	8630
284	2070	3856	5642	784CIP2_288	8631
285	2071	3857	5643	784CIP2_289	8633
286	2072	3858	5644	784CIP2_290	8634
287	2073	3859	5645	784CIP2_291	8635
288	2074	3860	5646	784CIP2_292	8636
289	2075	3861	5647	784CIP2_293	8659
290	2076	3862	5648	784CIP2_294	8660
291	2077	3863	5649	784CIP2_295	8667
292	2078	3864	5650	784CIP2_296	8667
293	2079	3865	5651	784CIP2_297	8685
294	2080	3866	5652	784CIP2_298	8805
295	2081	3867	5653	784CIP2_299	8896
296	2082	3868	5654	784CIP2_300	8978
297	2083	3869	5655	784CIP2_301	9046
298	2084	3870	5656	784CIP2_302	9048
300	2085	3871	5657	784CIP2_303	9116
	2086	3872	5658	784CIP2_304	9195
301	2087	3873	5659	784CIP2_305	9201
302	2088	3874 3875	5660	784CIP2_306	9307
303	2099	3876	5661	784CIP2_307	9321
	2091	3877	5662 5663	784CIP2_308 784CIP2 309	9397 9405
30⊑ '				. ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	. 74117
305 306	2092	3878	5664	784CIP2 310	9406

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length'	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	
	sequence			application	<u> </u>
308	2094	3880	5666	784CIP2_312	9494
309	2095	3881	5667	784CIP2_313	9512
310	2096	3882	5668	784CIP2_314	9632
311	2097	3883	5669	784CIP2_315	9661
312	2098	3884	5670	784CIP2_316	9664
313	2099	3885	5671	784CIP2_317	9691
314	2100	3886	5672	784CIP2_318	9700
315	2101	3887	5673	784CIP2_319	9716
316	2102	3888	5674	784CIP2_320	9721
317	2103	3889	5675	784CIP2 321	9870
318	2104	3890	5676	784CIP2 322	9887
319	2105	3891	5677	784CIP2 323	9923
320	2105	3892	5678	784CIP2 324	9938
		3893	5679	784CIP2_325	9964
321	2107	3894	5680	784CIP2 326	10007
322		3895	5681	784CIP2 327	10009
323	2109	3895	5682	784CIP2 328	10046
324	2110		5683	784CIP2 329	10156
325	2111	3897		784CIP2 330	10276
326	2112	3898	5684	784CIP2_330 784CIP2_331	10283
327	2113	3899	5685		152
328	2114	3900	5686	784CIP2B_1	167
329	2115	3901	5687	784CIP2B_2	205
330	2116	3902	5688	784CIP2B_3	I
331	2117	3903	5689	784CIP2B_4	210
332	2118	3904	5690	784CIP2B_5	225
333	2119	3905	5691	784CIP2B_6	226
334	2120	3906	5692	784CIP2B_7	264
335	2121	3907	5693	784CIP2B_8	268
336	2122	3908	5694	784CIP2B_9	293
337	2123	3909	5695	784CIP2B_10	293
338	2124	3910	5696	784CIP2B_11	293
339	2125	3911	5697	784CIP2B_12	302
340	2126	3912	5698	784CIP2B_13	311
341	2127	3913	5699	784CIP2B 14	352
342	2128	3914	5700	784CIP2B 15	358
343	2129	3915	5701	784CIP2B 16	368
344	2130	3916	5702	784CIP2B 17	3 9 3
345	2131	3917	5703	784CIP2B 18	477
	2132	3918	5704	784CIP2B_19	508
346		3919	5705	784CIP2B 20	508
347	2133	3920	5706	784CIP2B 21	515
348	2134		5707	784CIP2B 22	578
349	2135	3921	5708	784CIP2B_22	588
350	2136	3922		784CIP2B_23	591
351	2137	3923	5709	784CIP2B_24 784CIP2B_25	593
352	2138	3924	5710		594
353	2139	3925	5711	784CIP2B_26	
354	2140	3926	5712	784CIP2B_27	619
355	2141	3927	5713	784CIP2B_28	620
356	2142	3928	5714	784CIP2B_29	654
357	2143	3929	5715	784CIP2B_30	692
358	2144	3930	5716	784CIP2B_31	753
359	2145	3931	5717	784CIP2B_32	758
360	2146	3932	5718	784CIP2B_33	787
361	2147	3933	5719	784CIP2B_34	833
362	2148	3934	5720	784CIP2B_35	838
363	2149	3935	5721	784CIP2B 36	870
364	2150	3936	5722	784CIP2B 37	891
	2151	3937	5723	784CIP2B 38	891
365	2152	3938	5724	784CIP2B 39	921
366		3939	5725	784CIP2B 40	924
367	2153		5726	784CIP2B_40	932
368	2154	3940	3/20	10401141	942

SEQ ID NO:	SEQ ID	SEQ ID NO:	1 CDO YD	I was a series	1 0 0 0 0
of full-	NO: of	of contig	SEQ ID NO:	Priority docket number	SEQ ID NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	05,100,125
[sequence			application	
370	2156	3942	5728	784CIP2B 43	958
371	2157	3943	5729	784CIP2B 44	968
372	2158	3944	5730	784CIP2B 45	992
373	2159	3945	5731	784CIP2B 46	1025
374	2160	3946	5732	784CIP2B_47	1074
375	2161	3947	5733	784CIP2B_48	1104
376	2162	3948	5734	784CIP2B_49	1114
377	2163	3949	5735	784CIP2B_50	1144
378	2164	3950	5736	784CIP2B_51	1262
379	2165	3951	5737	784CIP2B_52	1318
380	2166	3952	5738	784CIP2B_53	1319
381	2167	3953	5739	784CIP2B_54	1328
382	2168	3954	5740	784CIP2B_55	1436
383	2169	3955	5741	784CIP2B_56	1464
384	2170	3956	5742	784CIP2B_57	1584
385	2171	3957	5743	784CIP2B_58	1617
386	2172	3958	5744	784CIP2B_59	1724
387	2173	3959	5745	784CIP2B_60	1728
388	2174	3960	5746	784CIP2B_61	1772
389	2175	3961	5747	784CIP2B_62	1809
390	2176	3962	5748	784CIP2B_63	1868
391	2177	3963	5749	784CIP2B_64	1898
392 393	2178	3964	5750	784CIP2B_65	1926
393	2179	3965	5751	784CIP2B_66	1965
395	2180	3966	5752	784CIP2B_67	1967
395	2181	3967	5753	784CIP2B_68	1995
396	2182	3968	5754	784CIP2B_69	2005.
398	2184	3969	5755	784CIP2B_70	2027
399	2184	3970 3971	5756 · 5757	784CIP2B_71	2055
400	2186	3971	5758	784CIP2B_72 784CIP2B_73	2103
401	2187	3972	5759	784CIP2B_73 784CIP2B_74	2106
402	2188	3974	5760	784CIP2B_74 784CIP2B_75	2166 2175
403	2189	3975	5761	784CIP2B_75	2176
404	2190	3976	5762	784CIP2B_78	2236
405	2191	3977	5763	784CIP2B_78	2250
406	2192	3978	5764	784CIP2B_73	2300 .
407	2193	3979	. 5765	784CIP2B_80	2323
408	2194	3980	5766	784CIP2B 82	2340
409	2195	3981	5767	784CIP2B 83	2371
410	2196	3982	5768	784CIP2B 84	2399
411	2197	3983	5769	784CIP2B 85	2411
412	2198	3984	5770	784CIP2B 86	2428
413	2199	3985	5771	784CIP2B 87	2430
414	2200	3986	5772	784CIP2B 88	2439
415	2201	3987	5773	784CIP2B 89	2447
416	2202	3988	5774	784CIP2B 90	2461
417	2203	3989	5775	784CIP2B 91	2487
418	2204	3990	5776	784CIP2B 92	2492
419	2205	3991	5777	784CIP2B 93	2512
420	2206	3992	5778	784CIP2B 94	2564
421	2207	3993	5779	784CIP2B 95	2678
422	2208	3994	5780	784CIP2B 96	2816
423	2209	3995	5781	784CIP2B 97	2818
424	2210	3996	5782	784CIP2B 98	2819
425	2211	3997	5783	784CIP2B_99	2943
426	2212	3998	5784	784CIP2B 100	3137
427	2213	3999	5785	784CIP2B 101	3137
428	2214	4000	5786	784CIP2B_102	3160
	2025	4004	5707	784CIP2B 103	3323
429	2215	4001	5787	/04CIP2B_103	3343
429 430 431	2216	4001	5788	784CIP2B_103	3360

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_ corresponding	NO:in U.S.S.N.
length	full-	nucleotide	of contig	SEQ ID NO: in	0.5.5.N. 09/488,725
nucleotide	length	sequence	peptide	priority	09/400,725
sequence	peptide	į	sequence	application	•
	sequence	4004	5790	784CIP2B 106	3417
432	2218	4004	5791	784CIP2B 107	3418
433	2219	4005	5792	784CIP2B 108	3442
434	2220	4008	5793	784CIP2B 109	3442
435	2221	4007	5794	784CIP2B 110	3444
436	2222	4009	5795	784CIP2B 111	3855
437	2223	4010	5796	784CIP2B_112	3863
438	2225	4011	5797	784CIP2B 113	4090
439	2225	4012	5798	784CIP2B 114	4105
441	2227	4013	5799	784CIP2B 115	4142
442	2228	4014	5800	784CIP2B 116	4142
443	2229	4015	5801	784CIP2B 117	4149
444	2230	4016	5802	784CIP2B 118	4196
445	2231	4017	5803	784CIP2B 119	4202
446	2232	4018	5804	784CIP2B_120	4274
447	2233	4019	5805	784CIP2B_121	4304
448	2234	4020	5806	784CIP2B_122	4306
449	2235	4021	5807	784CIP2B_123	4311
450	2236	4022	5808	784CIP2B_124	4321
451	2237	4023	5809	784CIP2B_125	4323
452	2238	4024	5810	784CIP2B_126	4332
453	2239	4025	5811	784CIP2B_127	4488
454	2240	4026	5812	784CIP2B_128	4588
455	2241	4027	5813	784CIP2B_129	5569
456	2242	4028	5814	784CIP2B_130	5573
457	2243	4029	5815	784CIP2B_131	5577
458	2244	4030	5816	784CIP2B_132	5579
459	2245	4031	5817	784CIP2B_133	5582
460	2246	4032	5818	784CIP2B_134	5583
461	2247	4033	5819	784CIP2B_135	5584
462	2248	4034	5820	784CIP2B_136	5585
463	2249	4035	5821	784CIP2B_137	5591
464	2250	4036	5822	784CIP2B_138	5593
465	2251	4037	5823	784CIP2B_139	5594
466	2252	4038	5824	784CIP2B_140	5594
467	2253	4039	5825	784CIP2B_141	5598
468	2254	4040	5826	784CIP2B_142	5602
469	2255	4041	5827	784CIP2B_143	5605 5608
470	2256	4042	5828	784CIP2B_144	
471	2257	4043	5829	784CIP2B_145	5617 5620
472	2258	4044	5830	784CIP2B_146	5622
473	2259	4045	5831	784CIP2B_147 784CIP2B_148	5623
474	2260	4046	5832	784CIP2B_148 784CIP2B_149	5624
475	2261	4047	5833	784CIP2B_149 784CIP2B_150	. 5625
476	2262	4048	5834	784CIP2B 150	5627
477	2263	4049	5835	784CIP2B_151 784CIP2B 152	5628
478	2264	4050	5836	784CIP2B_153	5630
479	. 2265	4051	5837	784CIP2B_153	5632
480	2266	4052	5838	784CIP2B_154	5640
481	2267	4053	5839 5840	784CIP2B 156	5641
482	2268	4054		784CIP2B_158	5643
483	2269	4055	5841	784CIP2B_157	5647
484	2270	4056	5842	784CIP2B_159	5649
485	2271	4057	5843	784CIP2B_139	5658
486	2272	4058	5844	784CIP2B_160	5659
487	2273	4059	5845	784CIP2B_161 784CIP2B 162	5667
488	2274	4060	5846	784CIP2B_162 784CIP2B 163	
489	2275	4061	5847 5848	784CIP2B_163 784CIP2B 164	5674
				/AU 1275 194	, ,,,,
490	2276	4062			5678
	2276 2277 2278	4062 4063 4064	5849 5850	784CIP2B_165 784CIP2B_166	

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	
	sequence			application	
494	2280	4066	5852	784CIP2B_168	5686
495	2281	4067	5853	784CIP2B_169	5694
496	2282	4068	5854	784CIP2B_170	5698
497	2283	4069	5855	784CIP2B_171	5699
499	2284	4070	5856	784CIP2B_172	5712
500	2286	4071 4072	5857 5858	784CIP2B_173	5719
501	2287	4073	5859	784CIP2B_174 784CIP2B_175	5720 5727
502	2288	4074	5860	784CIP2B_175	5730
503	2289	4075	5861	784CIP2B_176	5734
504	2290	4076	5862	784CIP2B_177	5738
505	2291	4077	5863	784CIP2B 178	5739
506	2292	4078	5864	784CIP2B_179	5740
507	2293	4079	5865	784CIP2B 181	5744
508	2294	4080	5866	784CIP2B_181	5748
509	2295	4081	5867	784CIP2B_182	5749
510	2296	4082	5868	784CIP2B 184	5750
511	2297	4083	5869	784CIP2B 185	5750
512	2298	4084	5870	784CIP2B 186	5750
513	2299	4085	5871	784CIP2B 187	5761
514	2300	4086	5872	784CIP2B 188	5762
515	2301	4087	5873	784CIP2B 189	5767
516	2302	4088	5874	784CIP2B 190	5773
517	2303	4089	5875	784CIP2B 191	5783
518	2304	4090	5876	784CIP2B 192	5784
519	2305	4091	5877	784CIP2B 193	5788
520	2306	4092	5878	784CIP2B 194	5798
521	2307	4093	5879	784CIP2B 196	5807
522	2308	4094	5880	784CIP2B 197	5818
523	2309	4095	5881	784CIP2B 198	5819
524	2310	4096	5882	784CIP2B_199	5827
525	2311	4097	5883	784CIP2B_200	5828
526	2312	4098	5884	784CIP2B_201	5842
527	2313	4099	5885	784CIP2B_202	5853
528	2314	4100	5886	784CIP2B_203	5861
529	2315	4101	5887	784CIP2B_204	5864
530	2316	4102	5888	784CIP2B_205	5865
531	2317	4103	5889	784CIP2B_206	5871
532	2318	4104	5890	784CIP2B_207	5873
533	2319	4105	5891	784CIP2B_208	5873
534	2320	4106	5892	784CIP2B_209	5875
535	2321	4107	5893	784CIP2B_210	5878
536	2322	4108	5894	784CIP2B_211	5879
537	2323	4109	5895	784CIP2B_212	5880
538	2324	4110	5896	784CIP2B_213	5880
539	2325	4111	5897	784CIP2B_214	5880
540	2326	4112	5898	784CIP2B_215	5880
541	2327	4113	5899	784CIP2B_216	5885
542	2328	4114	5900	784CIP2B_217	5895
543	2329	4115	5901	784CIP2B_218	5898
544	2330	4116	5902	784CIP2B_219	5902
545	2331	4117	5903	784CIP2B_220	5904
546	2332	4118	5904	784CIP2B_221	5918
547	2333	4119	5905	784CIP2B_222	5921
548	2334	4120	5906	784CIP2B_223	5927
549	2335	4121	5907	784CIP2B_224	5932
550	2336	4122	5908	784CIP2B_225	5939
551	2337	4123	5909	784CIP2B_226	5945
552	2338	4124	5910	784CIP2B_227	5946
553	2339	4125	5911	784CIP2B_228	5947
554	2340	4126	5912	784CIP2B_229	5956
555	2341	4127	5913	784CIP2B_230	5967

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority docket number	SEQ ID NO:in
of full-	NO: of	of contig	NO:	corresponding	U.S.S.N.
Length	full-	nucleotide	of contig	SEQ ID NO: in	09/488,725
nucleotide	length	sequence	peptide sequence	priority	05,100,120
sequence	peptide		Bequence	application	
556	sequence 2342	4128	5914	784CIP2B 232	5975
557	2342	4129	5915	784CIP2B 233	5977
558	2344	4130	5916	784CIP2B 234	5978
559	2345	4131	5917	784CIP2B_235	5979
560	2346	4132	5918	784CIP2B_236	5980
561	2347	4133	5919	784CIP2B_237	5988
562	2348	4134	5920	784CIP2B_238	5989
563	2349	4135	5921	784CIP2B_239	5991
564	2350	4136	5922	784CIP2B_240	5997
565	2351	4137	5923	784CIP2B_241	5998 .
566	2352	4138	5924	784CIP2B_242	6003
567	2353	4139	5925	784CIP2B_243	6004
568	2354	4140	5926	784CIP2B_244	6013
569	2355	4141	5927	784CIP2B_245	6028
570	2356	4142	5928	784CIP2B_246	6028
571	2357	4143	5929	784CIP2B_247	6029
572	2358	4144	5930	784CIP2B_248	6031
573	2359	4145	5931	784CIP2B_249	6031
574	2360	4146	5932	784CIP2B_250	6032
575	2361	4147	5933	784CIP2B_251	6037
576	2362	4148	5934	784CIP2B_252	6043
577	2363	4149	5935	784CIP2B_253	6044
578	2364	4150	5936	784CIP2B_254	6046
579	2365	4151	5937	784CIP2B_255 784CIP2B_256	6048
580	2366	4152	5938	784CIP2B_256 784CIP2B_257	6049
581	2367	4153	5939	784CIP2B_257	6051
582	2368	4154	5940	784CIP2B_258	6053
583	2369	4155	5941	784CIP2B_259	6060
584	2370	4156	5942 5943	784CIP2B 261	6063
585	2371	4157	5944	784CIP2B 262	6066
586	2372	4158	5945	784CIP2B_263	6067
587	2373	4159	5946	784CIP2B 264	6068
588	2374	4161	5947	784CIP2B 265	6073
589	2375	4162	5948	784CIP2B 266	6076
590	2376	4162	5949	784CIP2B 267	6076
591	2377	4164	5950	784CIP2B 268	6077
592	2378	4165	5951	784CIP2B 269	6079
593	2379	4166	5952	784CIP2B_270	6082
594 595	2381	4167	5953	784CIP2B 272	6088
	2382	4168	5954	784CIP2B 273	6091
596 597	2383	4169	5955	784CIP2B_274	6094
598	2384	4170	5956	784CIP2B_275	6101
599	2385	4171	5957	784CIP2B_276	6103
600	2386	4172	5958	784CIP2B_277	6104
601	2387	4173	5959	784CIP2B_278	6108
602	2388	4174	5960	784CIP2B_279	6112
603	2389	4175	5961	784CIP2B_280	6121
604	2390	4176	5962	784CIP2B_281	6125
605	2391	4177	5963	784CIP2B_282	6126
606	2392	4178	5964	784CIP2B_283	6128
607	2393	4179	5965	784CIP2B_284	6129
608	2394	4180	5966	784CIP2B_285	6133
609	2395	4181	5967	784CIP2B_286	6133
610	2396	4182	5968	784CIP2B_287	6135
611	2397	4183	5969	784CIP2B_288	6139
612	2398	4184	5970	784CIP2B_289	
613	2399	4185	5971	784CIP2B_290	
614	2400	4186	5972	784CIP2B_291	6146
615	2401	4187	5973	784CIP2B_292	6148
616	2402	4188	5974	784CIP2B_293	
1	2403	4189	5975	784CIP2B_294	6149

SEQ ID NO: of full- length	SEQ ID				
length	NO: of	SEQ ID NO: of contig	SEQ ID	Priority docket humber	SEQ ID NO:in
	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	_	sequence	priority	
	sequence			application	
618	2404	4190	5976	784CIP2B_295	6153
619	2405	4191	5977	784CIP2B_296	6159
620	2406	4192	5978	784CIP2B_297	6164
621	2407	4193	5979	784CIP2B_298	6167
622	2408	4194	5980	784CIP2B_299	6172
623	2409	4195	5981	784CIP2B_300	6173
624	2410	4196	5982	784CIP2B_301	6190
625	2411	4197	5983	784CIP2B_302	6194
626	2412	4198	5984	784CIP2B_303	6196
627	2413	4199	5985	784CIP2B_304	6197
628	2414	4200	5986	784CIP2B_305	6198
629	2415	4201	5987	784CIP2B_306	6198
630	2416	4202	5988	784CIP2B_308	6214
631	2417	4203	5989	784CIP2B_309	6215
632	2418	4204	5990	784CIP2B_310	6219
633	2419	4205	5991	784CIP2B_311	6226
634	2420	4206	5992	784CIP2B_312	6229
635	2421	4207	5993	784CIP2B_313	6234
636	2422	4208	5994	784CIP2B_314	6237
637	2423	4209	5995	784CIP2B_315	6238
638	2424	4210	5996	784CIP2B_316	6239
639	2425	4211	5997	784CIP2B_317	6239
640	2426	4212	5998	784CIP2B_318	6239
641	2427	4213	5999	784CIP2B_319	6240
642	2428	4214	6000	784CIP2B_320	6244
643	2429	4215	6001	784CIP2B_321	6245
644	2430	4216	6002	784CIP2B_322	6250
645	2431	4217	6003	784CIP2B_323	6252
646 647	2432	4218	6004	784CIP2B_324	6252
648	2433	4219	6005	784CIP2B_325	6256
649	2434 2435	4220 4221	6006	784CIP2B_326 784CIP2B 327	6260 6261
650	2435	4221	6008	784CIP2B_327	6264
651	2437	4223	6009	784CIP2B_328	6265
652	2438	4224	6010	784CIP2B_329	6266
653	2439	4225	6011	784CIP2B_330	6270
654	2440	4226	6012	784CIP2B_331	6271
655	2441	4227	6013	784CIP2B_332	6274
656	2442	4228	6014	784CIP2B 335	6276
657	2443	4229	6015	784CIP2B 336	6281
658	2444	4230	6016	784CIP2B 337	6281
659	2445	4231	6017	784CIP2B_337	6288
660	2446	4232	6018	784CIP2B_338	6292
661	2447	4233	6019	784CIP2B_333	6294
662	2448	4234	6020	784CIP2B 343	6312
663	2449	4235	6021	784CIP2B 344	6312
664	2450	4236	6022	784CIP2B 345	6312
665	2451	4237	6023	784CIP2B_345	6322
666	2452	4238	6024	784CIP2B_347	6324
667	2453	4239	6025	784CIP2B 349	6329
668	2454	4240	6026	784CIP2B_349	6331
669	2455	4241	6027	784CIP2B_350	6333
670	2456	4242	6027	784CIP2B_351	6334
671	2457	4243	6029	784CIP2B_352	6337
672	2458	4244	6030	784CIP2B_353	6339
673	2459	4245	6030	784CIP2B_354 784CIP2B_355	6346
· · · · · · · · · · · · · · · · · · ·	2460	4246	6032	784CIP2B_355	6348
674		4247	6032	784CIP2B_356 784CIP2B_357	6348
674	7467 1		ו נבטט	/04CIF4D 33/	0340
675	2461				
675 676	2462	4248	6034	784CIP2B_358	6350
675					

		1 676 YB 116	ODO TO	Deignitu	SEQ ID
SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority docket number	NO:in
of full-	NO: of	of contig	NO:	corresponding	U.S.S.N.
length	full-	nucleotide	of contig	SEO ID NO: in	09/488,725
nucleotide	length	sequence	peptide) — ·	09/400,723
sequence	peptide	1	sequence	priority	
	sequence			application	6368
680	2466	4252	6038	784CIP2B_362	6369
681	2467	4253	6039	784CIP2B_363	
682	2468	4254	6040	784CIP2B_364	6371
683	2469	4255	6041	784CIP2B_365	6376
684	2470	4256	6042	784CIP2B_366	6379
685	2471	4257	6043	784CIP2B_367	. 6380
686	2472	4258	6044	784CIP2B_368	6381
687	2473	4259	6045	784CIP2B_369	6392
688	2474	4260	6046	784CIP2B 370	6395
689	2475	4261	6047	784CIP2B 371	6397
690	2476	4262	6048	784CIP2B 372	6400
	2477	4263	6049	784CIP2B 373	6401
691		4264	6050	784CIP2B 374	6411
692	2478		6051	784CIP2B 375	6411
693	2479	4265		784CIP2B_375	6411
694	2480	4266	6052	784CIP2B_370	6416
695	2481	4267	6053	784CIP2B_377	6418
696	2482	4268	6054		
697	2483	4269	6055	784CIP2B_379	. 6422
698	2484	4270	6056·	784CIP2B_380	6423
699	2485	4271	6057	784CIP2B_381	6426
700	2486	4272	6058	784CIP2B_382	6427
701	2487	4273	6059	784CIP2B_383	6428
702	2488	4274	6060	784CIP2B_384	6429
703	2489	4275	6061	784CIP2B_385	6430
704	2490	4276	6062	784CIP2B 386	6432
705	2491	4277	6063	784CIP2B 387	6432
706	2492	4278	6064	784CIP2B 388	6438
707	2493	4279	6065	784CIP2B 389	6441
	2494	4280	6066	784CIP2B 390	6446
708		4281	6067	784CIP2B 391	6454
709	2495	4282	6068	784CIP2B_392	6459
710	2496	1	6069	784CIP2B 394	6461
711	2497	4283	1	784CIP2B 395	6467
712	2498	4284	6070		6468
713	2499	4285	6071	784CIP2B_396	6487
714	2500	. 4286	6072	784CIP2B_397	
715	2501	4287	6073	784CIP2B_398	6491
716	2502	4288	6074	784CIP2B_399	6506
717	2503	4289	6075	784CIP2B_401	6514
718	2504	4290	6076	784CIP2B_402	6519
719	2505	4291	6077	784CIP2B_403	6521
720	2506	4292	6078	784CIP2B_404	6532
721	2507	4293	6079	784CIP2B_405	6536
722	2508	4294	6080	784CIP2B_406	6543
723	2509	4295	6081	784CIP2B_407	6544
724	2510	4296	6082	784CIP2B_408	6548
725	2511	4297	6083	784CIP2B 409	6551
725	2512	4298	6084	784CIP2B 410	6551
	2512	4299	6085	784CIP2B 411	6552
727		4300	6086	784CIP2B 412	6554
728	2514		6087	784CIP2B 413	6556
729	2515	4301		784CIP2B 414	6560
730	2516	4302	6088	784CIP2B_414 784CIP2B_415	6563
731	2517	4303	6089		6564
732	2518	4304	6090	784CIP2B_416	
733	2519	4305	6091	784CIP2B_417	6567
734	2520	4306	6092	784CIP2B_418	6573
735	2521	4307	6093	784CIP2B_419	6575
736	2522	4308	6094	784CIP2B_420	6577
737	2523	4309	6095	784CIP2B_421	6593
738	2524	4310	6096	784CIP2B_422	6595
739	2525	4311	6097	784CIP2B_423	6599
740	2526	4312	6098	784CIP2B_424	6625
741	2527	4313	6099	784CIP2B 425	6625
1 ,47	1 2321	1 +2+2			!

SEQ ID NO:	SEQ ID	SEO ID NO:	SEQ ID	Priority	T-0-10-0-
of full-	NO: of	of contig	NO:	docket number	SEQ ID NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	_	sequence	priority	100,100,123
_	sequence			application	}
742	2528	4314	6100	784CIP2B 426	6626
743	2529	4315	6101	784CIP2B 427	6630
744	2530	4316	6102	784CIP2B 428	6631
745	2531	4317	6103	784CIP2B 429	6632
746	2532	4318	6104	784CIP2B 430	6633
747	2533	4319	6105	784CIP2B 431	6634
748	2534	4320	6106	784CIP2B 432	6638
749	2535	4321	6107	784CIP2B 433	6641
750	2536	4322	6108	784CIP2B 434	6644
751	2537	4323	6109	784CIP2B_435	6646
752	253B	4324	6110	784CIP2B_436	6648
753	2539	4325	6111	784CIP2B_437	6652
754	2540	4326	6112	784CIP2B_438	6654
755	2541	4327	6113	784CIP2B_439	6657
756	2542	4328	6114	784CIP2B_440	6658
757	2543	4329	6115	784CIP2B_441	6663
758	2544	4330	6116	784CIP2B_442	6664
·759	2545	4331	6117	784CIP2B_443	6668
760	2546	4332	6118	784CIP2B_444	6669
761	2547	4333	6119	784CIP2B_445	6673
762	2548	4334	6120	784CIP2B_446	6685
763	2549	4335	6121	784CIP2B_447	6687
764	2550	4336	6122	784CIP2B_448	6689
765	2551	4337	6123	784CIP2B_449	6693
766	2552	4338	6124	784CIP2B_450	6698
767	2553	4339	6125	784CIP2B_451	6699
768 .	2554	4340	6126	784CIP2B_452	6705
769	2555	4341	6127	784CIP2B_453	6711
770 .	2556	4342	6128	784CIP2B_454	67.13
771	2557	4343	6129	784CIP2B_455	6716
772	2558	4344	6130	784CIP2B_456	6725
773	2559	4345	6131	784CIP2B_457	6726
774	2560	4346	6132	784CIP2B_458	6727
775	2561	4347	6133	784CIP2B_459	6730
776	2562	4348	6134	784CIP2B_460	6730
777	2563	4349	6135	784CIP2B_461	6730
778	2564	4350	6136	784CIP2B_462	6732
. 779	2565	4351	6137	784CIP2B_463	6733
780 781	2566	4352	6138	784CIP2B_464	6737
	2567	4353	6139	784CIP2B_465	6745
782 783	2568	4354	6140	784CIP2B_466	6751
784	2569	4355	6141	784CIP2B_467	6754
785	2570 2571	4356	6142	784CIP2B_468	6758
786	2572	4357	6143	784CIP2B_469	6761
787	2572	4358		784CIP2B_470	6765
788		4359	6145	784CIP2B_471	6768
789	2574 2575	4360 4361	6146	784CIP2B_472	6773
790	2576	4362	6147	784CIP2B_473	6776
791	2576		6148	784CIP2B_474	6796
792	.2578	4363	6149	784CIP2B 475	6798
793	2579	4364	6150	784CIP2B_476	6823
794	2579	4365	6151	784CIP2B_477	6825
795	2580	4366	6152	784CIP2B_478	6826
796	2582	4367	6153	784CIP2B_479	6839
797	2583	4368	6154	784CIP2B_480	6844
798	2583	4369	6155	784CIP2B_482	6849
798		4370	6156	784CIP2B_483	6854
800	2585	4371	6157	784CIP2B_484	6857
	2586	4372	6158	784CIP2B_485	6861
801 802	2587	4373	6159	784CIP2B_486	6873
802	2588	4374	6160	784CIP2B_487	6875
003	2589	4375	6161	784CIP2B_488	6877

SEQ ID NO: SEQ ID NO: of full- nucleotide sequence SEQ ID NO: of contig nucleotide sequence 804 2590 4376 805 2591 4377 806 2592 4378 807 2593 4379 808 2594 4380 809 2595 4381 810 2596 4382 811 2597 4383 812 2598 4384	NO: of contig peptide sequence 6162 6163 6164 6165 6166 6167 6168 6169 6170 6171 6172 6173 6174	docket number_corresponding SEQ ID NO: in priority application 784CIP2B_489 784CIP2B_491 784CIP2B_491 784CIP2B_492 784CIP2B_494 784CIP2B_495 784CIP2B_496 784CIP2B_496 784CIP2B_497 784CIP2B_498	NO:in U.S.S.N. 09/488,725 6880 6885 6890 6894 6901 6904 6907 6914 6917
nucleotide sequence length peptide sequence sequence 804 2590 4376 805 2591 4377 806 2592 4378 807 2593 4379 808 2594 4380 809 2595 4381 810 2596 4382 811 2597 4383	peptide sequence 6162 6163 6164 6165 6166 6167 6168 6169 6170 6171 6172 6173	SEQ ID NO: in priority application 784CIP2B_489 784CIP2B_490 784CIP2B_491 784CIP2B_492 784CIP2B_493 784CIP2B_494 784CIP2B_495 784CIP2B_496 784CIP2B_497 784CIP2B_497	6880 6885 6890 6890 6894 6901 6904 6907 6914
sequence peptide sequence 804 2590 4376 805 2591 4377 806 2592 4378 807 2593 4379 808 2594 4380 809 2595 4381 810 2596 4382 811 2597 4383	6162 6163 6164 6165 6166 6167 6168 6169 6170 6171 6172 6173	priority application 784CIP2B_489 784CIP2B_490 784CIP2B_491 784CIP2B_492 784CIP2B_493 784CIP2B_494 784CIP2B_495 784CIP2B_496 784CIP2B_497 784CIP2B_497 784CIP2B_498	6880 6885 6890 6890 6894 6901 6904 6907 6914
sequence 804 2590 4376 805 2591 4377 806 2592 4378 807 2593 4379 808 2594 4380 809 2595 4381 810 2596 4382 811 2597 4383	6162 6163 6164 6165 6166 6167 6168 6169 6170 6171 6172 6173	application 784CIP2B_489 784CIP2B_490 784CIP2B_491 784CIP2B_492 784CIP2B_493 784CIP2B_494 784CIP2B_495 784CIP2B_496 784CIP2B_497 784CIP2B_498 784CIP2B_498	6885 6890 6890 6894 6901 6904 6907 6914
804 2590 4376 805 2591 4377 806 2592 4378 807 2593 4379 808 2594 4380 809 2595 4381 810 2596 4382 811 2597 4383	6163 6164 6165 6166 6167 6168 6169 6170 6171 6172 6173	784CIP2B 489 784CIP2B 490 784CIP2B 491 784CIP2B 492 784CIP2B 493 784CIP2B 494 784CIP2B 495 784CIP2B 496 784CIP2B 497 784CIP2B 497 784CIP2B 498 784CIP2B 499	6885 6890 6890 6894 6901 6904 6907 6914
805 2591 4377 806 2592 4378 807 2593 4379 808 2594 4380 809 2595 4381 810 2596 4382 811 2597 4383	6163 6164 6165 6166 6167 6168 6169 6170 6171 6172 6173	784CIP2B 490 784CIP2B 491 784CIP2B 492 784CIP2B 493 784CIP2B 494 784CIP2B 495 784CIP2B 496 784CIP2B 497 784CIP2B 498 784CIP2B 499	6885 6890 6890 6894 6901 6904 6907 6914
806 2592 4378 807 2593 4379 808 2594 4380 809 2595 4381 810 2596 4382 811 2597 4383	6164 6165 6166 6167 6168 6169 6170 6171 6172 6173	784CIP2B 491 784CIP2B 492 784CIP2B 493 784CIP2B 494 784CIP2B 495 784CIP2B 496 784CIP2B 497 784CIP2B 498 784CIP2B 498	6890 6890 6894 6901 6904 6907 6914
807 2593 4379 808 2594 4380 809 2595 4381 810 2596 4362 811 2597 4383	6165 6166 6167 6168 6169 6170 6171 6172 6173	784CIP2B 492 784CIP2B 493 784CIP2B 494 784CIP2B 495 784CIP2B 496 784CIP2B 497 784CIP2B 498 784CIP2B 499	6890 6894 6901 6904 6907 6914
808 2594 4380 809 2595 4381 810 2596 4382 811 2597 4383	6166 6167 6168 6169 6170 6171 6172 6173	784CIP2B 493 784CIP2B 494 784CIP2B 495 784CIP2B 496 784CIP2B 497 784CIP2B 498 784CIP2B 499	6894 6901 6904 6907 6914 6917
809 2595 4381 810 2596 4382 811 2597 4383	6167 6168 6169 6170 6171 6172 6173	784CIP2B 494 784CIP2B 495 784CIP2B 496 784CIP2B 497 784CIP2B 498 784CIP2B 499	6901 6904 6907 6914 6917
810 2596 4382 811 2597 4383	6168 6169 6170 6171 6172 6173	784CIP2B 495 784CIP2B 496 784CIP2B 497 784CIP2B 498 784CIP2B 499	6904 6907 6914 6917
811 2597 4383	6169 6170 6171 6172 6173	784CIP2B_496 784CIP2B_497 784CIP2B_498 784CIP2B_499	6907 6914 6917
012	6170 6171 6172 6173	784CIP2B_497 784CIP2B_498 784CIP2B_499	6914 6917
012 2592 4384	6171 6172 6173	784CIP2B_498 784CIP2B_499	6917
010	6172 6173	784CIP2B_499	l
813 2599 4385	6173	1	6923
814 2600 4386		784CTP2B 500	6929
815 2601 4387		784CIP2B_500 784CIP2B_501	6931
816 2602 4388			6935
. 817 2603 4389	6175		6940
818 2604 4390	6176	784CIP2B_503	6945
819 2605 4391	6177	784CIP2B_504 784CIP2B 505	6946
820 2606 4392	6178		6947
821 2607 4393	6179		6949
822 2608 4394	6180		6959
823 . 2609 4395	6181		6960
824 2610 4396 .	6182	784CIP2B_509	6962
825 2611 4397	6183	784CIP2B_510	6963
826 2612 4398	6184	784CIP2B_511	6967
827 2613 4399	6185	784CIP2B_512	6983
828 2614 4400	6186	784CIP2B_513	6988
829 2615 4401	6187	784CIP2B_514	
830 2616 4402	6188	784CIP2B_515	6996
831 2617 4403	6189	784CIP2B_516	7003
832 2618 4404	6190	784CIP2B_517	7016
833 2619 4405	6191	784CIP2B_518	7017 7025
834 2620 4406	6192	784CIP2B_519	
835 2621 4407	6193	784CIP2B_520	7025
836 2622 4408	6194	784CIP2B_521	7025
837 2623 4409	6195	784CIP2B_522	
838 2624 4410	6196	784CIP2B_523	7051
839 2625 4411	6197	784CIP2B_524	7055
840 2626 4412	6198	784CIP2B_525	7064
841 2627 4413	6199	784CIP2B_526	7067
842 2628 4414	6200 .	784CIP2B_527	7071
843 2629 4415	6201	784CIP2B_528	7072
844 2630 4416	6202	784CIP2B_529	7073
845 2631 4417	6203	784CIP2B_530	7076
846 2632 4418	6204	784CIP2B_531	7078
847 2633 4419	6205	784CIP2B_532	7089
848 2634 4420	6206	784CIP2B_533	7091
849 2635 4421	6207	784CIP2B_534 784CIP2B_535	7091
850 2636 4422	6208	784CIP2B_535	7104
851 2637 4423	6209	784CIP2B_536	7104
852 2638 4424	6210	784CIP2B_537	7105
853 2639 4425	6211	784CIP2B 538	7109
854 2640 4426	6212		7109
855 2641 4427	6213	784CIP2B_540	7109
856 2642 4428	6214	784CIP2B_541	7119
857 2643 4429	6215	784CIP2B_542	7120
858 2644 4430	6216	784CIP2B_543	7121
859 2645 4431	6217	784CIP2B_544	
860 2646 4432	6218	784CIP2B_545	7127
861 2647 4433	6219	784CIP2B_546	7130
862 2648 4434	6220	784CIP2B_547	7131
863 2649 4435	6221	784CIP2B_548	7144
864 2650 4436	6222	784CIP2B_549	7159
865 2651 4437	6223	784CIP2B_550	7163

SEQ ID NO:	CEO TO	SEQ ID NO:	LCEO TD	I But out to	LCDO TD
of full-	SEQ ID NO: of	of contig	SEQ ID	Priority docket number	SEQ ID NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	0.5.5.N.
sequence	peptide	sequence	sequence	priority	03/400,723
Bequence	sequence		sequence	application	İ
866	2652	4438	6224	784CIP2B 551	7175
867	2653	4439	6225	784CIP2B_551 784CIP2B 552	7175
				_	<u> </u>
868	2654	4440	6226	784CIP2B_553	7189
869	2655	4441	6227	784CIP2B_554	7190
870	2656	4442	6228	784CIP2B_555	7191
871	2657	4443	6229	784CIP2B_556	7203
872	2658	4444	6230	784CIP2B_557	7204
873	2659	4445	6231	784CIP2B_558	7208
874	2660	4446	6232	784CIP2B_559	7209
875	2661	4447	6233	784CIP2B_560	7210
876	2662	4448	6234	784CIP2B_561	7216
877	2663	4449	6235	784CIP2B_562	7221
878	2664	4450	6236	784CIP2B_563	7230
879	2665	4451	6237	784CIP2B_564	7237
880	2666	4452	6238	784CIP2B 565	7240
881 ·	2667	4453	6239	784CIP2B 566	7245
882	2668	4454	6240	784CIP2B_567	7250
883	2669	4455	6241	784CIP2B 568	7251
884	2670	4456	6242	784CIP2B 569	7255
885	2671	4457	6243	784CIP2B 570	7260
886	2672	4458	6244	784CIP2B 571	7265
887	2673	4459	6245	784CIP2B_572	7268
					l
888	2674	4460	6246	784CIP2B_573	7275
889	2675	4461	6247	784CIP2B_574	7279
890	2676	4462	6248	784CIP2B_575	7283
891	2677	4463	6249	784CIP2B_576	7283
892	2678	4464	6250	784CIP2B_577	7287
893	2679	4465	6251	784CIP2B_578	7301
894	2680	4466	6252	784CIP2B_579	7308
895	2681	4467	6253	784CIP2B_580	7308
896	2682	4468	6254	784CIP2B 581	7309
897	2683	4469	6255	784CIP2B 582	7319
898	2684	4470	6256	784CIP2B 583	7320
899	2685	4471	6257	784CIP2B 584	7326
900	2686	4472	6258	784CIP2B 585	7326
901	2687	4473	6259	784CIP2B 586	7334
902	2688	4474	6260	784CIP2B 587	7337
903	2689	4475	6261	784CIP2B 588	7339
904	2690	4476	6262	784CIP2B 589	7344
905	2691	4477	6263	784CIP2B_589	7355
906	2692	<u> </u>	6264		7363
		4478	L	784CIP2B_591	<u> </u>
907	2693	4479	6265	784CIP2B_592	7363
908	.2694	4480	6266	784CIP2B_593	7365
909	2695	4481	6267	784CIP2B_594	7368
910	2696	4482	6268	784CIP2B_595	7369
911	2697	4483	6269	784CIP2B_596	7372
912	2698	4484	6270	784CIP2B_599	7375
913	2699	4485	6271	784C1P2B_600	7381
914	2700	4486	6272	784CIP2B_601	7383
915	2701	4487	6273	784CIP2B_602	7387
916	2702	4488	6274	784CIP2B 603	7391
917	2703	4489	6275	784CIP2B 604	7393
918	2704	4490	6276	784CIP2B 605	7395
919	2705	4491	6277	784CIP2B 606	7397
920	2706	4492	6278	784CIP2B 607	7399
921	2707		1	784CIP2B 608	7405
	2707	4493	6279		7405
922		4494	6280	784CIP2B_609	
923	2709	4495	6281	784CIP2B_610	7406
924	2710	4496	6282	784CIP2B_611	7409
925	2711	4497	6283	784CIP2B_612	7410
	. 2712	4400	6284	784CIP2B 613	7411
926	2712 2713	4498 4499	6285	784CIP2B_613	7417

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority docket number	SEQ ID NO:in
of full-	NO: of	of contig	NO: of contig	corresponding	U.S.S.N.
length	full-	nucleotide sequence	peptide	SEQ ID NO: in	09/488,725
nucleotide	length peptide	sequence	sequence	priority	}
sequence	sequence	į	Doguesio	application	
928	2714	4500	6286	784CIP2B_615	7418
929	2715	4501	6287	784CIP2B_616	7421
930	2716	4502	6288	784CIP2B_617	7422
931	2717	4503	6289	784CIP2B_618	7422
932	2718	4504	6290	784CIP2B_619	7423
933	2719	4505	6291	784CIP2B_620	7424
934	2720	4506	6292	784CIP2B_621	7426
935	2721	4507	6293	784CIP2B_622	7427
936	2722	4508	6294	784CIP2B_623	7428
937	2723	4509	6295	784CIP2B_624	7430
938	2724	4510	6296	784CIP2B_625	7435
939	2725	4511	6297	784CIP2B_626	7437
940	2726	4512	6298	784CIP2B_627	7439
941	2727	4513	6299	784CIP2B_628	7440
942	2728	4514	6300	784CIP2B_629	7442
943	2729	4515	6301	784CIP2B_630	7450
944	2730	4516	6302	784CIP2B_631	7451
945	2731	4517	6303	784CIP2B_632	7452
946	2732	4518	6304	784CIP2B_633	7454
947	2733	4519	6305	784CIP2B_634	7457
948	2734	4520	6306	784CIP2B_635	7459
949	2735	4521	6307	784CIP2B_636	7461
950	2736	4522	6308	784CIP2B_637	7463
951	2737	4523	6309	784CIP2B_638	7466
952	2738	4524	6310	784CIP2B_639	7469
953	2739	4525	6311	784CIP2B_640	7473
954	2740	4526	6312	784CIP2B_641	7481
955	2741	4527	6313	784CIP2B_642	7482 7482
956	2742	4528	6314	784CIP2B_643	7482
957	2743	4529	6315	784CIP2B_644	7485
958	2744	4530	6316	784CIP2B_645	7486
959	2745	4531	6317	784CIP2B_646 784CIP2B_647	7487
960	2746	4532	6318	784CIP2B_647	7491
961	2747	4533	6319	784CIP2B_648	7492
962	2748	4534	6320	784CIP2B 650	7494
963	2749	4535	6321	784CIP2B 651	7498
964	2750	4536	6322	784CIP2B_652	7504
965	2751	4537 4538	6324	784CIP2B 653	7508
966	2752	4539	6325	784CIP2B 654	7516
967	2753 2754	4540	6326	784CIP2B 655	7518
968	2755	4541	6327	784CIP2B 656	7519
969		4542	6328	784CIP2B 657	7521
970	2756 2757	4543	6329	784CIP2B 658	7529
971		4544	6330	784CIP2B 659	7532
972	2758 2759	4545	6331	784CIP2B_660	7533
973	2760	4546	6332	784CIP2B 661	7535
974	2761	4547	6333	784CIP2B 662	7545
975 976	2762	4548	6334	784CIP2B 663	7546
976	2763	4549	6335	784CIP2B 664	7552
978	2764	4550	6336	784CIP2B 665	7554
	2765	4551	6337	784CIP2B 666	7567
979	2766	4552	6338	784CIP2B 667	7569
980	2767	4553	6339	784CIP2B 668	7575
981	2768	4554	6340	784CIP2B 669	7576
982	2769	4555	6341	784CIP2B_670	
983	2770	4556	6342	784CIP2B 671	7579
984	2771	4557	6343	784CIP2B 672	
985	2772	4558	6344	784CIP2B 673	
986	2773	4559	6345	784CIP2B 674	
987	2774	4560	6346	784CIP2B 675	

SEQ ID NO:	SEQ ID	SEO ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number	NO: in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	1 -	sequence	priority	', ' , '
	sequence	•		application	
990	2776	4562	6348	784CIP2B_677	7609
991	2777	4563	6349	784CIP2B_678	7609
992	2778	4564	6350	784CIP2B 679	7609
993	2779	4565	6351	784CIP2B 680	7613
994	2780	4566	6352	784CIP2B_681	7623
995	2781	4567	6353	784CIP2B_682	7629
996	2782	4568	6354	784CIP2B_683	7630
997	2783	4569	6355	784CIP2B_684	7633
998	2784	4570	6356	784CIP2B_685	7635
999	2785	4571	6357	784CIP2B_686	7638
1000	2786	4572	6358	784CIP2B_687	7639
1001	2787	4573	6359	784CIP2B_688	7646
1002	2788	4574	6360	784CIP2B_689	7647
1003	2789	4575	6361	784CIP2B_690	7648
1004	2790	4576	6362	784CIP2B_691	. 7658
1005	2791	4577	6363	784CIP2B_692	7664
1006	2792	4578 ·	6364	784CIP2B_693	7664
1007	2793	4579	6365	784CIP2B_695	7674
1008	2794	4580	6366	784CIP2B_696	7675
1009	2795	4581	6367	784CIP2B_697	7676
1010	2796	4582	6368	784CIP2B_698	7681
1011	2797	4583	6369	784CIP2B_699	7688
1012	2798	4584	6370	784CIP2B_700	7693
1013	2799	4585	6371	784CIP2B_701	7694
1014	2800	4586	6372	784CIP2B_702	7715
1015	2801	4587	6373	784CIP2B_703	7716
1016	2802	4588	6374	784CIP2B_704	7718
1017	2803	4589	6375	784CIP2B_705	7721
1018	2804	4590	6376	784CIP2B_706	7723
1019	2805	4591	6377	784CIP2B_707	7729
1020	2806	4592	6378	784CIP2B_708	7733
1021	2807	4593	6379	784CIP2B_709	7735
1022	2808	4594	6380	784CIP2B_710	7741
1023	2809	4595	6381	784CIP2B_711	7743
	2810	4596	6382	784CIP2B_712	7748
1025	2811	4597	6383	784CIP2B_713	7749
1026	2812 2813	4598	6384	784CIP2B_714	7750
1027		4599 4600	6385	784CIP2B_715	7757
	2814		6386	784CIP2B_716	7759
1029	2815	· 4601	6387	784CIP2B_717	7760
1030	2816 2817	4602 4603	6388	784CIP2B_718	7760
1031	2817	4604	6389	784CIP2B_719	7764
1032	2819	4605	6390 6391	784CIP2B_720	7765
1033	2820	4606	6392	784CIP2B_721	7766
1035	2821	4607	6392	784CIP2B_722	7767
1036	2822	4608	6394	784CIP2B_723	7769
1037	2823	4609		784CIP2B_724	7770
1037	2824	4610	6395	784CIP2B_725	7774
1039	2825.	4611	6396 6397	784CIP2B_726	7779
1040	2826	4612	6398	784CIP2B_727	7781
1041	2827	4612		784CIP2B_728	7782
1042	2828	4614	6399	784CIP2B_729	7783
1043	2829	4615	6401	784CIP2B_730	7787
1043	2830			784CIP2B_731	7792
1044	2831	4616	6402	784CIP2B_732	7795
1045	2832	4617	6403	784CIP2B_733	7801
1047	2833	4618 4619	6404	784CIP2B_734	7807
1047	2834		6405	784CIP2B_735	7808
1048		4620	6406	784CIP2B_736	7819
1050	2835	4621	6407	784CIP2B_737	7824
1050	2836	4622 4623	6408	784CIP2B_738	7826
	203/	#077	0403	784CIP2B_739	7829

of full- length Roll- nucleotide length sequence	SEQ ID NO:	LODO TO	SEO ID NO:	SEO ID	Priority	SEQ ID
Length Length Length Sequence Length Sequence Length Sequence Length Sequence		SEQ ID	_			
nucleotide sequence peptide sequence peptide sequence sequence sequence sequence peptide sequence SEQ ID NO: in peptide sequence peptide sequence SEQ ID NO: in peptide peptide sequence O9/488,725 peptide sequence PROFESS peptide sequence PRO	1				. –	
sequence sequence	, ,					
Sequence	1	, –	sequence	,		05/400,725
1052	boquence		1	bequeinee		
1053	1052		4624	6410		7832
1054						
1055		L	L.,		L _	
1055	L		l	<u> </u>		L
1087				1		
1059	1	<u> </u>				J
1059						L
1060			<u> </u>	1		
1061 2847		<u> </u>	L			
1062						
1063		L	}			<u> </u>
1064			L			
1065			I			i
1066		·				
1067	L		<u> </u>	<u> </u>		
1068	L	<u> </u>				
1069				L		1
1070			1	1		.L
1071						
1072						I
1073				<u> </u>		1
1074		1	L	· · · · · · · · · · · · · · · · · · ·		<u> </u>
1075	t	I	<u> </u>			
1076			L	J	<u> </u>	1
1077			<u> </u>	I	<u> </u>	<u> </u>
1078						·
1079			L	1	<u> </u>	
1080	i	<u> </u>	L	<u> </u>		1
1081 2867 4653 6439 784CIP2B_770 7942 1082 2868 4654 6440 784CIP2B_771 7945 1083 2869 4655 6441 784CIP2B_772 7946 1084 2870 4656 6442 784CIP2B_773 7948 1085 2871 4657 6443 784CIP2B_774 7951 1086 2872 4658 6444 784CIP2B_775 7952 1087 2873 4659 6445 784CIP2B_776 7953 1088 2874 4660 6446 784CIP2B_776 7953 1089 2875 4661 6447 784CIP2B_777 7954 1090 2876 4662 6448 784CIP2B_779 7958 1091 2877 4663 6449 784CIP2B_779 7958 1092 2878 4664 6450 784CIP2B_780 7961 1092 2878 4664 6450 784CIP2B_780 7965 1093 2879 4665 6451 784CIP2B_782 7966 1094 2880 4666 6452 784CIP2B_783 7979 1095 2881 4667 6453 784CIP2B_783 7979 1096 2882 4668 6454 784CIP2B_785 7986 1097 2883 4669 6455 784CIP2B_785 7986 1099 2885 4671 6457 784CIP2B_787 7991 1099 2886 4672 6458 784CIP2B_787 7992 1101 2887 4673 6459 784CIP2B_789 7992 1102 2888 4674 6460 784CIP2B_789 7992 1103 2889 4675 6451 784CIP2B_791 7992 1104 2890 4676 6462 784CIP2B_791 7992 1105 2891 4677 6463 784CIP2B_791 7992 1106 2892 4678 6464 784CIP2B_793 7992 1107 2893 4679 6456 784CIP2B_793 7992 1108 2894 4679 6466 784CIP2B_795 8016 1107 2893 4679 6465 784CIP2B_795 8016 1109 2895 4681 6467 784CIP2B_795 8016 1101 2897 4683 6466 784CIP2B_795 8016 1101 2896 4682 6468 784CIP2B_799 8022 1111 2897 4683 6469 784CIP2B_799 8022 1111 2897 4683 6469 784CIP2B_799 8022 1111 2898 4684 6470 784CIP2B_799 8022 1112 2898 4684 6470 784CIP2B_799 8022 1111 2898 4684 6470 784CIP2B_799 8022 1112 2898 4684 6470 784CIP2B_800 8028 1112 2898 4688 6469 784CIP2B_800 8028 1112 2898 46		<u> </u>	L	<u> </u>		1
1082 2868 4654 6440 784CIP2B 771 7945		<u> </u>	<u> </u>			
1083			t			<u> </u>
1084	t	1	L	I	<u> </u>	
1085 2871 4657 6443 784CIP2B_774 7951 1086 2872 4658 6444 784CIP2B_775 7952 1087 2873 4659 6445 784CIP2B_776 7953 1088 2874 4660 6446 784CIP2B_777 7954 1089 2875 4661 6447 784CIP2B_778 7957 1090 2876 4662 6448 784CIP2B_779 7958 1091 2877 4663 6449 784CIP2B_781 7965 1092 2878 4664 6450 784CIP2B_781 7965 1093 2879 4665 6451 784CIP2B_781 7965 1094 2880 4666 6452 784CIP2B_783 7979 1095 2881 4667 6453 784CIP2B_783 7979 1096 2882 4668 6454 784CIP2B_785 7986 1097 2883 4669 6455 784CIP2B_786 <		I	L	1	<u> </u>	1
1086 2872 4658 6444 784CIP2B_775 7952 1087 2873 4659 6445 784CIP2B_776 7953 1088 2874 4660 6446 784CIP2B_777 7954 1089 2875 4661 6447 784CIP2B_778 7957 1090 2876 4662 6448 784CIP2B_780 7961 1091 2877 4663 6449 784CIP2B_780 7961 1092 2878 4664 6450 784CIP2B_780 7961 1093 2879 4665 6451 784CIP2B_781 7965 1093 2879 4666 6452 784CIP2B_783 7979 1095 2881 4667 6453 784CIP2B_783 7979 1095 2881 4667 6453 784CIP2B_783 7979 1096 2882 4668 6454 784CIP2B_785 7986 1097 2883 4669 6455 784CIP2B_785 <		I				
1087 2873 4659 6445 784CIP2B_776 7953 1088 2874 4660 6446 784CIP2B_777 7954 1089 2875 4661 6447 784CIP2B_778 7957 1090 2876 4662 6448 784CIP2B_779 7958 1091 2877 4663 6449 784CIP2B_780 7961 1092 2878 4664 6450 784CIP2B_781 7965 1093 2879 4665 6451 784CIP2B_781 7966 1094 2880 4666 6452 784CIP2B_783 7979 1095 2881 4667 6453 784CIP2B_783 7979 1095 2881 4667 6453 784CIP2B_783 7979 1096 2882 4658 6454 784CIP2B_785 7986 1097 2883 4669 6455 784CIP2B_785 7991 1099 2885 4671 6457 784CIP2B_788 <			1		<u> </u>	
1088 2874 4660 6446 784CIP2B_777 7954 1089 2875 4661 6447 784CIP2B_778 7957 1090 2876 4662 6448 784CIP2B_779 7958 1091 2877 4663 6449 784CIP2B_780 7961 1092 2878 4664 6450 784CIP2B_781 7965 1093 2879 4665 6451 784CIP2B_782 7966 1094 2880 4666 6452 784CIP2B_783 7979 1095 2881 4667 6453 784CIP2B_784 7986 1096 2882 4668 6454 784CIP2B_785 7986 1097 2883 4669 6455 784CIP2B_786 7988 1098 2884 4670 6456 784CIP2B_786 7981 1099 2885 4671 6457 784CIP2B_787 7991 1099 2886 4672 6458 784CIP2B_789 <			1	J	<u> </u>	1
1089 2875 4661 6447 784CIP2B_778 7957 1090 2876 4662 6448 784CIP2B_779 7958 1091 2877 4663 6449 784CIP2B_780 7961 1092 2878 4664 6450 784CIP2B_781 7965 1093 2879 4665 6451 784CIP2B_782 7966 1094 2880 4666 6452 784CIP2B_783 7979 1095 2881 4667 6453 784CIP2B_783 7979 1096 2882 4668 6454 784CIP2B_783 7979 1096 2882 4668 6454 784CIP2B_784 7986 1097 2883 4669 6455 784CIP2B_785 7988 1098 2884 4670 6456 784CIP2B_787 7991 1099 2885 4671 6457 784CIP2B_789 7992 1100 2886 4672 6458 784CIP2B_789 <						
1090 2876 4662 6448 784CIP2B_779 7958 1091 2877 4663 6449 784CIP2B_780 7961 1092 2878 4664 6450 784CIP2B_781 7965 1093 2879 4665 6451 784CIP2B_783 7976 1094 2880 4666 6452 784CIP2B_783 7979 1095 2881 4667 6453 784CIP2B_784 7986 1096 2882 4668 6454 784CIP2B_785 7986 1097 2883 4669 6455 784CIP2B_785 7986 1097 2883 4669 6455 784CIP2B_786 7988 1098 2884 4670 6456 784CIP2B_787 7991 1099 2885 4671 6457 784CIP2B_789 7992 1100 2886 4672 6458 784CIP2B_789 7992 1101 2887 4673 6459 784CIP2B_790 <			<u> </u>	<u> </u>	1 . - .	1
1091 2877 4663 6449 784CIP2B_780 7961 1092 2878 4664 6450 784CIP2B_781 7965 1093 2879 4665 6451 784CIP2B_782 7966 1094 2880 4666 6452 784CIP2B_783 7979 1095 2881 4667 6453 784CIP2B_784 7986 1096 2882 4668 6454 784CIP2B_785 7986 1097 2883 4669 6455 784CIP2B_786 7988 1098 2884 4670 6456 784CIP2B_787 7991 1099 2885 4671 6457 784CIP2B_787 7991 1009 2886 4672 6458 784CIP2B_789 7992 1101 2887 4673 6459 784CIP2B_790 7992 1102 2888 4674 6460 784CIP2B_791 7992 1103 2889 4675 6461 784CIP2B_792 <			L		I	· · · ·
1092 2878 4664 6450 784CIP2B_781 7965 1093 2879 4665 6451 784CIP2B_782 7966 1094 2880 4666 6452 784CIP2B_783 7979 1095 2881 4667 6453 784CIP2B_784 7986 1096 2882 4668 6454 784CIP2B_785 7986 1097 2883 4669 6455 784CIP2B_786 7988 1098 2884 4670 6456 784CIP2B_787 7991 1099 2885 4671 6457 784CIP2B_788 7992 1100 2886 4672 6458 784CIP2B_789 7992 1101 2887 4673 6459 784CIP2B_789 7992 1102 2888 4674 6460 784CIP2B_791 7992 1103 2889 4675 6461 784CIP2B_792 8003 1104 2890 4676 6462 784CIP2B_793 8014 1105 2891 4677 6463 784CIP2B_795						
1093 2879 4665 6451 784CIP2B_782 7966 1094 2880 4666 6452 784CIP2B_783 7979 1095 2881 4667 6453 784CIP2B_784 7986 1096 2882 4668 6454 784CIP2B_785 7986 1097 2883 4669 6455 784CIP2B_786 7988 1098 2884 4670 6456 784CIP2B_787 7991 1099 2885 4671 6457 784CIP2B_788 7992 1100 2886 4672 6458 784CIP2B_789 7992 1101 2887 4673 6459 784CIP2B_790 7992 1102 2888 4674 6460 784CIP2B_791 7992 1103 2889 4675 6461 784CIP2B_792 8003 1104 2890 4676 6462 784CIP2B_793 8014 1105 2891 4677 6463 784CIP2B_794 <		1				
1094 2880 4666 6452 784CIP2B 783 7979 1095 2881 4667 6453 784CIP2B 784 7986 1096 2882 4668 6454 784CIP2B 785 7986 1097 2883 4669 6455 784CIP2B 786 7988 1098 2884 4670 6456 784CIP2B 787 7991 1099 2885 4671 6457 784CIP2B 788 7992 1100 2886 4672 6458 784CIP2B 789 7992 1101 2887 4673 6459 784CIP2B 790 7992 1102 2888 4674 6460 784CIP2B 791 7992 1103 2889 4675 6461 784CIP2B 791 7992 1103 2889 4675 6461 784CIP2B 792 8003 1104 2890 4676 6462 784CIP2B 793 8014 1105 2891 4677 6463 784CIP2B 795 <			l		<u></u>	1
1095 2881 4667 6453 784CIP2B 784 7986 1096 2882 4668 6454 784CIP2B 785 7986 1097 2883 4669 6455 784CIP2B 786 7988 1098 2884 4670 6456 784CIP2B 787 7991 1099 2885 4671 6457 784CIP2B 788 7992 1100 2886 4672 6458 784CIP2B 789 7992 1101 2887 4673 6459 784CIP2B 790 7992 1102 2888 4674 6460 784CIP2B 791 7992 1103 2889 4675 6461 784CIP2B 791 7992 1103 2889 4675 6461 784CIP2B 791 7992 1104 2890 4676 6462 784CIP2B 792 8003 1104 2891 4677 6463 784CIP2B 793 8014 1105 2891 4678 6464 784CIP2B 795 <			<u> </u>	<u> </u>	<u> </u>	<u> </u>
1096 2882 4668 6454 784CIP2B_785 7986 1097 2883 4669 6455 784CIP2B_786 7988 1098 2884 4670 6456 784CIP2B_787 7991 1099 2885 4671 6457 784CIP2B_789 7992 1100 2886 4672 6458 784CIP2B_789 7992 1101 2887 4673 6459 784CIP2B_790 7992 1102 2888 4674 6460 784CIP2B_791 7992 1103 2889 4675 6461 784CIP2B_791 7992 1104 2890 4676 6462 784CIP2B_792 8003 1104 2890 4676 6462 784CIP2B_793 8014 1105 2891 4677 6463 784CIP2B_794 8015 1106 2892 4678 6464 784CIP2B_795 8016 1107 2893 4679 6465 784CIP2B_796 <			<u> </u>	<u> </u>		L
1097 2883 4669 6455 784CIP2B_786 7988 1098 2884 4670 6456 784CIP2B_787 7991 1099 2885 4671 6457 784CIP2B_78B 7992 1100 2886 4672 6458 784CIP2B_789 7992 1101 2887 4673 6459 784CIP2B_790 7992 1102 2888 4674 6460 784CIP2B_791 7992 1103 2889 4675 6461 784CIP2B_791 7992 1104 2890 4676 6462 784CIP2B_792 8003 1104 2890 4676 6462 784CIP2B_793 8014 1105 2891 4677 6463 784CIP2B_794 8015 1106 2892 4678 6464 784CIP2B_795 8016 1107 2893 4679 6465 784CIP2B_796 8017 1108 2894 4680 6466 784CIP2B_797 <		<u> </u>				
1098 2884 4670 6456 784CIP2B_787 7991 1099 2885 4671 6457 784CIP2B_78B 7992 1100 2886 4672 6458 784CIP2B_789 7992 1101 2887 4673 6459 784CIP2B_790 7992 1102 2888 4674 6460 784CIP2B_791 7992 1103 2889 4675 6461 784CIP2B_792 8003 1104 2890 4676 6462 784CIP2B_793 8014 1105 2891 4677 6463 784CIP2B_793 8015 1106 2892 4678 6464 784CIP2B_795 8016 1107 2893 4679 6465 784CIP2B_795 8016 1107 2893 4680 6466 784CIP2B_797 8019 1109 2895 4681 6467 784CIP2B_798 8020 1110 2896 4682 6468 784CIP2B_799 <				<u> </u>		
1099 2885 4671 6457 784CIP2B_788 7992 1100 2886 4672 6458 784CIP2B_789 7992 1101 2887 4673 6459 784CIP2B_790 7992 1102 2888 4674 6460 784CIP2B_791 7992 1103 2889 4675 6461 784CIP2B_792 8003 1104 2890 4676 6462 784CIP2B_793 8014 1105 2891 4677 6463 784CIP2B_794 8015 1106 2892 4678 6464 784CIP2B_795 8016 1107 2893 4679 6465 784CIP2B_796 8017 1108 2894 4680 6466 784CIP2B_797 8019 1109 2895 4681 6467 784CIP2B_798 8020 1110 2896 4682 6468 784CIP2B_799 8022 1111 2897 4683 6469 784CIP2B_800 <					_	. I
1100 2886 4672 6458 784CIP2B_789 7992 1101 2887 4673 6459 784CIP2B_790 7992 1102 2888 4674 6460 784CIP2B_791 7992 1103 2889 4675 6461 784CIP2B_792 8003 1104 2890 4676 6462 784CIP2B_793 8014 1105 2891 4677 6463 784CIP2B_794 8015 1106 2892 4678 6464 784CIP2B_795 8016 1107 2893 4679 6465 784CIP2B_796 8017 1108 2894 4680 6466 784CIP2B_797 8019 1109 2895 4681 6467 784CIP2B_798 8020 1110 2896 4682 6468 784CIP2B_799 8022 1111 2897 4683 6469 784CIP2B_800 8022 1112 2898 4684 6470 784CIP2B_801 <				1	<u> </u>	
1101 2887 4673 6459 784CIP2B_790 7992 1102 2888 4674 6460 784CIP2B_791 7992 1103 2889 4675 6461 784CIP2B_792 8003 1104 2890 4676 6462 784CIP2B_793 8014 1105 2891 4677 6463 784CIP2B_794 8015 1106 2892 4678 6464 784CIP2B_795 8016 1107 2893 4679 6465 784CIP2B_796 8017 1108 2894 4680 6466 784CIP2B_797 8019 1109 2895 4681 6467 784CIP2B_798 8020 1110 2896 4682 6468 784CIP2B_799 8022 1111 2897 4683 6469 784CIP2B_800 8022 1112 2898 4684 6470 784CIP2B_801 8028			I			<u> </u>
1102 2888 4674 6460 784CIP2B 791 7992 1103 2889 4675 6461 784CIP2B 792 8003 1104 2890 4676 6462 784CIP2B 793 8014 1105 2891 4677 6463 784CIP2B 794 8015 1106 2892 4678 6464 784CIP2B 795 8016 1107 2893 4679 6465 784CIP2B 796 8017 1108 2894 4680 6466 784CIP2B 797 8019 1109 2895 4681 6467 784CIP2B 798 8020 1110 2896 4682 6468 784CIP2B 799 8022 1111 2897 4683 6469 784CIP2B 800 8022 1112 2898 4684 6470 784CIP2B 801 8028			<u> </u>			
1103 2889 4675 6461 784CIP2B_792 8003 1104 2890 4676 6462 784CIP2B_793 8014 1105 2891 4677 6463 784CIP2B_794 8015 1106 2892 4678 6464 784CIP2B_795 8016 1107 2893 4679 6465 784CIP2B_796 8017 1108 2894 4680 6466 784CIP2B_797 8019 1109 2895 4681 6467 784CIP2B_798 8020 1110 2896 4682 6468 784CIP2B_799 8022 1111 2897 4683 6469 784CIP2B_800 8022 1112 2898 4684 6470 784CIP2B_801 8028			L			
1104 2890 4676 6462 784CIP2B_793 8014 1105 2891 4677 6463 784CIP2B_794 8015 1106 2892 4678 6464 784CIP2B_795 8016 1107 2893 4679 6465 784CIP2B_796 8017 1108 2894 4680 6466 784CIP2B_797 8019 1109 2895 4681 6467 784CIP2B_798 8020 1110 2896 4682 6468 784CIP2B_799 8022 1111 2897 4683 6469 784CIP2B_800 8022 1112 2898 4684 6470 784CIP2B_801 8028						
1105 2891 4677 6463 784CIP2B_794 8015 1106 2892 4678 6464 784CIP2B_795 8016 1107 2893 4679 6465 784CIP2B_796 8017 1108 2894 4680 6466 784CIP2B_797 8019 1109 2895 4681 6467 784CIP2B_798 8020 1110 2896 4682 6468 784CIP2B_799 8022 1111 2897 4683 6469 784CIP2B_800 8022 1112 2898 4684 6470 784CIP2B_801 8028				<u> </u>		
1106 2892 4678 6464 784CIP2B_795 8016 1107 2893 4679 6465 784CIP2B_796 8017 1108 2894 4680 6466 784CIP2B_797 8019 1109 2895 4681 6467 784CIP2B_798 8020 1110 2896 4682 6468 784CIP2B_799 8022 1111 2897 4683 6469 784CIP2B_800 8022 1112 2898 4684 6470 784CIP2B_801 8028						
1107 2893 4679 6465 784CIP2B_796 8017 1108 2894 4680 6466 784CIP2B_797 8019 1109 2895 4681 6467 784CIP2B_798 8020 1110 2896 4682 6468 784CIP2B_799 8022 1111 2897 4683 6469 784CIP2B_800 8022 1112 2898 4684 6470 784CIP2B_801 8028						
1108 2894 4680 6466 784CIP2B_797 8019 1109 2895 4681 6467 784CIP2B_798 8020 1110 2896 4682 6468 784CIP2B_799 8022 1111 2897 4683 6469 784CIP2B_800 8022 1112 2898 4684 6470 784CIP2B_801 8028						
1109 2895 4681 6467 784CIP2B_798 8020 1110 2896 4682 6468 784CIP2B_799 8022 1111 2897 4683 6469 784CIP2B_800 8022 1112 2898 4684 6470 784CIP2B_801 8028				<u> </u>		
1110 2896 4682 6468 784CIP2B_799 8022 1111 2897 4683 6469 784CIP2B_800 8022 1112 2898 4684 6470 784CIP2B_801 8028				·		<u> </u>
1111 2897 4683 6469 784CIP2B_800 8022 1112 2898 4684 6470 784CIP2B_801 8028	1109	2895	4681	6467	784CIP2B_798	
1112 2898 4684 6470 784CIP2B_801 8028	1110	2896	4682	6468		
	1111	2897	4683	6469	784CIP2B_800	8022
1117 2000 4605 6471 5045700 600	1112		4684	6470	784CIP2B_801	
1113 2099 4685 64/1 784CIP2B_802 8030	1113	2899	4685	6471	784CIP2B_802	8030

SEQ ID NO:	SEQ ID	GEO TE NO	SEQ ID	Charles Carles	1 270 70
of full-	NO: of	SEQ ID NO: of contig	NO:	Priority docket number	SEQ ID NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	0.5.5.N.
sequence	peptide	sequence	sequence	priority	03/400,125
5544555	sequence	ľ	sequence	application	
1114	2900	4686	6472	784CIP2B 803	8038
1115	2901	4687	6473	784CIP2B_803	8042
1116	2902	4688	6474	784CIP2B_804 784CIP2B_805	<u>1</u>
1117	2902	4689			8045
1118	2903	.1	6475	784CIP2B_806	8045
		4690	6476	784CIP2B_807	8046
1119	2905	4691	6477	784CIP2B_808	8047
1120	2906	4692	6478	784CIP2B_809	8051
1121	2907	4693	6479	784CIP2B_810	8059
1122	2908	4694	6480	784CIP2B_811	8064
1123	2909	4695	6481	784CIP2B_812	8069
1124	2910	4696	6482	784CIP2B_813	8074
1125	2911	4697	6483	784CIP2B_814	8077
1126	2912	4698	6484	784CIP2B_815	8078
1127	2913	4699	6485	784CIP2B_816	8079
1128	2914	4700	6486	784CIP2B_817	8084
1129	2915	4701	6487	784CIP2B_818	8088
1130	2916	4702	6488	784CIP2B_819	8090
1131	2917	4703	6489	784CIP2B 820	8091
1132	2918	4704	6490	784CIP2B 821	8099
1133	2919	4705	6491	784CIP2B 822	8099
1134	2920	4706	6492	784CIP2B 823	8100
1135	2921	4707	6493	784CIP2B 824	8102
1136	2922	4708	6494	784CIP2B 825	8103
1137	2923	4709	6495	784CIP2B 826	8103
1138	2924	4710	6496	784CIP2B 827	8104
1139	2925	4711	6497	784CIP2B 828	8108
1140	2926	4712	6498	784CIP2B 829	8110
1141	2927	4713	6499	784CIP2B 830	8116
1142	2928	4714	6500	784CIP2B 831	8117
1143	2929	4715	6501	784CIP2B 832	8123
1144	2930	4716	6502	784CIP2B 833	8130
1145	2931	4717	6503		
1146	2932	4718	6504	784CIP2B_834 784CIP2B_835	8130
1147	2933	L			8143 8143
1148	2934	4719	6505	784CIP2B_836	
1149	2934	4720	6506	784CIP2B_837	8154
		4721	6507	784CIP2B_838	8155
1150	2936	4722	6508	784CIP2B_839	8162
1151	. 2937	4723	6509	784CIP2B_840	8163
1152	2938	4724	6510	784CIP2B_841	8172
1153	2939	4725	6511	784CIP2B_842	8173
1154	2940	4726	6512	784CIP2B_843	8179
1155	2941	4727	6513	784CIP2B_844	8182
1156	2942	4728	6514	784CIP2B_845	8183
1157	2943	4729	6515	784CIP2B_846	8184
1158	2944	4730	6516	784CIP2B_847	8185
1159	2945	4731	6517	784CIP2B_848	8187
1160	2946	4732	6518	784CIP2B_849	8188
1161	2947	4733	6519	784CIP2B_850	8190
1162	2948	4734	6520	784CIP2B_851	8190
1163	2949	4735	6521	784CIP2B 852	8192
1164	2950	4736	6522	784CIP2B 853	8193
1165	2951	4737	6523	784CIP2B 854	8197
1166	2952	4738	6524	784CIP2B 855	8197
1167	2953	4739	6525	784CIP2B 856	8199
1168	2954	4740	6526	784CIP2B_857	8202
1169	2955	4741	6527	784CIP2B 858	8203
1170	2956	4742	6528	784CIP2B 859	8208
1171	2957	4743	. 6529	784CIP2B_859 784CIP2B_860	8209
1172	2958	4744	6530	784CIP2B_860 784CIP2B_861	
1173	2959	4744	6531		8211
1174	2960			784CIP2B_862	8214
		4746	6532	784CIP2B_863	8217
1175	2961	4747	6533	784CIP2B_864	8223

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority docket number	SEQ ID NO:in
of full-	NO: of	of contig	NO:	corresponding	U.S.S.N.
Length	full-	nucleotide	of contig	SEQ ID NO: in	09/488,725
ucleotide	length	sequence	peptide sequence	priority	05,155,7-5
equence	peptide sequence		sequence	application	
1176	.2962	4748	6534	784CIP2B_865	8224
1177	2963	4749	6535	784CIP2B 866	8226 .
1178	2964	4750	6536	784CIP2B_867	8227
1179	2965	4751	6537	784CIP2B_868	8229
1180	2966	4752	6538	784CIP2B_869	8232
1181	2967	4753	6539	784CIP2B_870	8236
1182	2968	4754	6540	784CIP2B_871	8239
1183	2969	4755	6541	784CIP2B_872	8244
1184	2970	4756	6542	784CIP2B_873	8245
1185	2971	4757	6543	784CIP2B_874	8248
1186	2972	4758	6544	784CIP2B_875	8251
1187	2973	4759	6545	784CIP2B_876	8253 8260
1188	2974	4760	6546	784CIP2B_877	8262
1189	2975	4761	6547	784CIP2B_878	8268
1190	2976	4762	6548	784CIP2B_879 784CIP2B 880	8270
1191	2977	4763	6549	784C1P2B_880 784C1P2B_881	8270
1192	2978	4764	6550	784C1P2B_881 784C1P2B_882	8274
1193	2979	4765	6551	784CIP2B 883	8274
1194	2980	4766	6552 6553	784CIP2B 884	8275
1195	2981	4767	6554	784CIP2B 885	8277
1196	2982	4768 4769	6555	784CIP2B 886	8281
1197	2983	4770	6556	784CIP2B 887	8283
1198	2984 2985	4771	6557	784CIP2B 888	8289
1199	2985	4772	6558	784CIP2B_889	8295
1200	2987	4773	6559	784CIP2B 890	8300
1201	2988	4774	6560	784CIP2B_891	8303
1202	2989	4775	6561	784CIP2B 892	8304
1204	2990	4776	6562	784CIP2B_893	8305
1205	2991	4777	6563	784CIP2B_894	8309
1205	2992	4778	6564	784CIP2B_895	8318
1207	2993	4779	6565	784CIP2B_896	8319
1208	2994	4780	6566	784CIP2B_897	8321
1209	2995	4781	6567	784CIP2B_898	8322
1210	2996	4782	6568	784CIP2B_899	8323
1211	2997	4783	6569	784CIP2B_900	8325
1212	2998	4784	6570	784CIP2B_901	8331
1213	2999	4785	6571	784CIP2B_902	8332
1214	3000	4786	6572	784CIP2B_903	8333
1215	3001	4787	6573	784CIP2B_904	8335
1216	3002	4788	6574	784CIP2B_905	8336
1217	3003	4789	6575	784CIP2B_906 784CIP2B_907	8340
1218	3004	4790	6576	784CIP2B_907	8343
1219	3005	4791	6577	784CIP2B 909	8347
1220	3006	4792	6578	784CIP2B_909	8349
1221	3007	4793 4794	6579	784CIP2B_911	8351
1222	3008	4794	6581	784CIP2B_912	8353
1223	3009	4796	6582	784CIP2B 913	8355
1224	3010	4797	6583	784CIP2B 914	8361
1225	3011	4798	6584	784CIP2B 915	8365
1226	3012	4799	6585	784CIP2B_916	8367
1227	3013	4800	6586	784CIP2B 917	8369
1228	3014	4801	6587	784CIP2B_919	8375
1230	3015	4802	6588	784CIP2B_920	8387
1230	3017	4803	. 6589	784CIP2B 921	8391
1231	3017	4804	6590	784CIP2B_922	8393
1232	3019	4805	6591	784CIP2B_923	8393
1234	3020	4806	6592	784CIP2B_924	8394
1235	3021	4807	6593	784CIP2B_925	8395
1236	3022	4808	6594	784CIP2B_926	8396
	3023	4809	6595	784CIP2B 927	8398

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	
	sequence		<u> </u>	application	
1238	3024	4810	6596	784CIP2B_928	8402
1239	3025	4811	6597	784CIP2B_929	8402
1240	3026	4812	6598	784CIP2B_930	8405
1241	3027	4813	6599	784CIP2B_931	8406
1242	3028	4814	6600	784CIP2B_932	8409
1243	3029	4815	6601	784CIP2B_933	8410
1244	3030	4816	6602	784CIP2B_934	8414
1245	3031	4817	6603	784CIP2B_935	8415
1246	3032	4818	6604	784CIP2B_936	8419
1247	3033	4819	6605	784CIP2B_937	8426
1248	3034 3035	4820	6606	784CIP2B_938	8430
1250	3035	4821 4822	6607	784CIP2B_939	8431
1250	3036		6608	784CIP2B_940 784CIP2B_941	8432 8433
1252		4823	6609		8433
1252	3038	4824 4825	6610 6611	784CIP2B_942 784CIP2B_943	8434
1254	3039	4825	6612	784CIP2B_943 784CIP2B_944	8438
1255	3041	4827	6613	784CIP2B_944 784CIP2B_945	8439
1256	3042	4828	6614	784CIP2B_945	8450
1257	3042	4829	6615	784CIP2B_948 784CIP2B 947	8451
1258	3044	4830	6616	784CIP2B 948	8452
1259	3045	4831	6617	784CIP2B_948	8460
1260	3046	4832	6618	784CIP2B 950	8461 .
1261	3047	4833	6619	784CIP2B_951	8462
1262	3048	4834	6620	784CIP2B 952	8464
1263	3049	4835	6621	784CIP2B 953	8465
1264	3050	4836	6622	784CIP2B 954	8467
1265	3051	4837	6623	784CIP2B 955	8470
1266	3052	4838	6624	784CIP2B 956	8471
1267	3053	4839	6625	784CIP2B 957	8473
1268	3054	4840	6626	784CIP2B 958	8474
1269	3055	4841	6627	784CIP2B 959	8475
1270	3056	4842	6628	784CIP2B 960	8476
1271	3057	4843	6629	784CIP2B 961	8480
1272	3058	4844	6630	784CIP2B 962	8482
1273	3059	4845	6631	784CIP2B 963	8482
1274	3060	4846	6632	784CIP2B 964	8486
1275	3061	4847	6633	784CIP2B_965	8488
1276	3062	4848	6634	784CIP2B_966	8492
1277	3063	4849	6635	784CIP2B_967	8494
1278	3064	4850	6636	784CIP2B_968	8496
1279	3065	4851	6637	784CIP2B_969	8497
1280 .	3066	4852	6638	784CIP2B_970	8499
1281	3067	4853	6639	784CIP2B_971	8513
1282	3068	4854	6640	784CIP2B_972	8522
1283	3069	4855	6641	784CIP2B_973	8526
1284	3070	4856	6642	784CIP2B_974	8531
1285	3071	4857	6643	784CIP2B_975	8533
1286	3072	4858	6644	784CIP2B_976	8542
1287	3073	4859	6645	784CIP2B_977	8544
1288	3074	4860	6646	784CIP2B_978	8565
1289	3075	4861	6647	784CIP2B_979	8565
1290	3076	4862	6648	784CIP2B_980	8572
1291	3077	4863	6649	784CIP2B_981	8576
1292	3078	4864	6650	784CIP2B_982	8578
1293	3079	4865	6651	784CIP2B_983	8584
1294	3080	4866	6652	784CIP2B_984	8598
1295	3081	4867	6653	784CIP2B_985	8602
1296	3082	4868	6654	784CIP2B_986	8604
		4000	CCCC	784CIP2B 987	8609
1297	3083	4869	6655		
1297 1298 1299	3083 3084 3085	4869 4870 4871	6656 6657	784CIP2B_988 784CIP2B_989	8612 8637

		100 TO NO.	000 70	Priority	SEQ ID
SEQ ID NO:	SEQ ID	SEQ ID NO: of contig	SEQ ID NO:	docket number	NO:in
of full-	NO: of full-	nucleotide	of contig	corresponding	U.S.S.N.
length		sequence	peptide	SEQ ID NO: in	09/488,725
nucleotide	length	sequence	sequence	priority	05/400/125
sequence	peptide		sequence	application	
	sequence	4072	6658	784CIP2B 990	8640
1300	3086	4872		784CIP2B_990	8643
1301	3087	4873	6659		8645
1302	3088	4874	6660	784CIP2B_992	
1303	3089	4875	6661	784CIP2B_993	8650
1304	3090	4876	6662	784CIP2B_994	8651
1305	3091	4877	6663	784CIP2B_995	8654
1306	3092	4878	6664	784CIP2B_996	8655
1307	3093	4879	6665	784CIP2B_997	8657
1308	3094	4880	6666	784CIP2B_998	8665
1309	3095	4881	6667	784CIP2B_999	8668
1310	3096	4882	6668	784CIP2B_1000	8671
1311	3097	4883	6669	784CIP2B 1001	8672
1312	3098	4884	6670	784CIP2B 1002	8692
1313	3099	4885	6671	784CIP2B 1003	8706
1313	3100	4886	6672	784CIP2B 1004	8716
	3101	4887	6673	784CIP2B 1005	8719
1315	3102	4888	6674	784CIP2B 1006	8743
1316		1	6675	784CIP2B 1007	8764
1317	3103	4889	6676	784CIP2B_1007	8764
1318	3104		1	784CIP2B 1008	8764
1319	3105	4891	6677		8774
1320	3106	4892	6678	784CIP2B_1010	
1321	3107	4893	6679	784CIP2B_1011	8782
1322	3108	4894	6680	784CIP2B_1012	8796
1323	3109	4895	6681	784CIP2B_1013	8827
1324	3110	4896	6682	784CIP2B_1014	8842
1325	3111	4897	6683	784CIP2B_1015	8842
1326	3112	4898	6684	784CIP2B_1016	8858
1327	3113	4899	6685	784CIP2B_1017	8871
1328	3114	4900	6686	784CIP2B_1018	8921
1329	3115	4901	6687	784CIP2B 1019	8927
1330	3116	4902	6688	784CIP2B 1020	8942
1331	3117	4903	6689	784CIP2B 1021	8994
1332	3118	4904	6690	784CIP2B 1022	9023
1333	3119	4905	6691	784CIP2B 1023	9028
1334	3120	4906	6692	784CIP2B 1024	9058
1335	3121	4907	6693	784CIP2B 1025	9058
	3122	4908	6694	784CIP2B 1026	9079
1336		4909	6695	784CIP2B 1027	9079
1337	3123		6696	784CIP2B 1028	9082
1338	3124	4910		784CIP2B_1029	9084
1339	3125	4911	6697		· · · · · · · · · · · · · · · · · · ·
1,340	3126	4912	6698	784CIP2B_1030	9093
1341	3127	4913	6699	784CIP2B_1031	9101
1342	3128	4914	6700	784CIP2B_1032	9103
1343	3129	4915	6701	784CIP2B_1033	9105
1344	3130	4916	6702	784CIP2B_1034	9151
1345	3131	4917	6703	784CIP2B_1035	9161
1346	3132	4918	6704	784CIP2B_1036	9172
1347	3133	4919	6705	784CIP2B_1037	9174
1348	3134	4920	6706	784CIP2B_1038	9204
1349	3135	4921	6707	784CIP2B_1039	9234
1350	3136	4922	6708	784CIP2B 1040	9235
1351	3137	4923	6709	784CIP2B 1041	9239
1352	3138	4924	6710	784CIP2B 1042	9256
	3139	4925	6711	784CIP2B 1043	9276
1353		4925	6712	784CIP2B_1043	9345
1354	3140			784CIP2B_1044 784CIP2B 1045	9379
1355	3141	4927	6713		9435
1356	3142	4928	6714	784CIP2B_1046	9437
1357	3143	4929	6715	784CIP2B_1047	
1358	3144	4930	6716	784CIP2B_1048	9469
				- 2010TD2D 1010	9500
1359	3145	4931	6717	784CIP2B_1049	
	3145 3146	4931 4932 4933	6718 6719	784CIP2B_1050 784CIP2B_1050	9502 9520

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	
1362	sequence 3148	4934	6720	application 784CIP2B 1052	0543
1363	3149	4935	6721		9541 9541
1364	3150	4936	6722	784CIP2B_1053 784CIP2B 1054	
1365	3150	4937	6723	784CIP2B_1054	9548 9556
1366	3152	4938	6724	784CIP2B_1055	9556
1367	3153	4939	6725	784CIP2B_1056	9575
1368	3154	4940	6726	784CIP2B 1057	9589
1369	3155	4941	6727	784CIP2B_1058	9599
1370	3156	4942	6728	784CIP2B_1059	9602
1371	3157	4943	6729	784CIP2B_1060	9606
1372	3158	4944	6730	784CIP2B_1061	9622
1373	3159	4945	6731	784CIP2B 1063	9623
1374	3160	4946	6732	784CIP2B 1064	9646
1375	3161	4947	6733	784CIP2B 1065	9747
1376	3162	4948	6734	784CIP2B 1066	9773
1377	3163	4949	6735	784CIP2B 1067	9785
1378	3164	4950	6736	784CIP2B 1068	9801
1379	3165	4951	6737	784CIP2B 1069	9811
1380	3166	4952	6738	784CIP2B 1070	9843
1381	3167	4953	6739	784CIP2B 1071	9854
1382	3168	4954	6740	784CIP2B 1072	9854
1383	3169	4955	6741	784CIP2B 1073	9864
1384	3170	4956	6742	784CIP2B 1074	9864
1385	3171	4957	6743	784CIP2B 1075	9871
1386	3172	4958	6744	784CIP2B 1076	9879
1387	3173	4959	6745	784CIP2B 1077	9881
1388	3174	4960	6746	784CIP2B 1078	9885
1389	3175	4961	6747	784CIP2B 1079	9901
1390	3176	4962	6748	784CIP2B_1080	9912
1391	3177	4963	6749	784CIP2B_1081	9916
1392	3178	4964	6750	784CIP2B_1082	9921
1393	3179	4965	6751	784CIP2B_1083	9925
1394	3180	4966	6752	784CIP2B_1084	9930
1395	3181	4967	6753	784CIP2B_1085	9949
1396	3182	. 4968	6754	784CIP2B_1086	9951
1397	3183	4969	6755	784CIP2B_1087	9959
1398	3184	4970	6756	784CIP2B_1088	9973
1399	3185	4971	6757	784CIP2B_1089	9982
1400	3186	4972	6758	784CIP2B_1090	9994
1401	3187	4973	6759	784CIP2B_1091	10021
1402	3188	4974	6760	784CIP2B_1092	10041
1403	3189	4975	6761	784CIP2B_1094	10067
1404	3190	4976	6762	784CIP2B_1095	10073
1405	3191	4977	6763	784CIP2B_1096	10112
1406	3192	4978	6764	784CIP2B_1097	10117
1407	3193	4979	6765	784CIP2B_1098	10132
1408	3194	4980	6766	784CIP2B_1099	10169
1409	3195	4981	6767	784CIP2B_1100	10217
1410	3196	4982	6768	784CIP2B_1101	10226
1411	3197	4983	6769	784CIP2B_1102	10232
1412	3198	4984	6770	784CIP2B_1103	10237
1413	3199	4985	6771	784CIP2B_1104	10279
1414	3200	4986	6772	784CIP2C_1	33
1415	3201	4987	6773	784CIP2C_2	271
1416	3202	4988	6774	784CIP2C_3	848
1417	3203	4989	6775	784CIP2C_4	849
1418	3204	4990	6776	784CIP2C_5	864
	3205	4991	6777	784CIP2C_6	953
1419					
1419 1420	3206	4992	6778	784CIP2C_7	980
1419		4992 4993 4994	6778 6779 6780	784CIP2C_7 784CIP2C_8 784CIP2C_9	980 1595 1697

		1 000 70 110	1 252 25	I was a sale was	LCRO TR
SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID NO:	Priority docket number	SEQ ID NO:in
of full-	NO: of full-	of contig	of contig	corresponding	U.S.S.N.
length nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	boquomeo	sequence	priority	
boquomeo	sequence		1	application	
1424	3210	4996	6782	784CIP2C_11	1937
1425	3211	4997	6783	784CIP2C_12	1955
1426	3212	4998	6784	784CIP2C_13	1955
1427	3213	4999	6785	784CIP2C_14	2185
1428	3214	5000	6786	784CIP2C_15	2889
1429	3215	5001	6787	784CIP2C_16	2901
1430	3216	5002	6788	784CIP2C_17	2902
1431	3217	5003	6789	784CIP2C_18	2905
1432	3218	5004	6790	784CIP2C_19	2948
1433	3219	5005	6791	784CIP2C_20	2956
1434	3220	5006	6792	784CIP2C_21	2959
1435	3221	5007	6793	784CIP2C_22	2965
1436	3222	5008	6794	784CIP2C_23	2966
1437	3223	5009	6795	784CIP2C_24	2970
1438	3224	5010	6796	784CIP2C_25	2985
1439	3225	5011	6797	784CIP2C_26	2987
1440	3226	5012	6798	784CIP2C_27	2993
1441	3227	5013	6799	784CIP2C_28	2993
1442	3228	5014	6800	784CIP2C_29	3017
1443	3229	5015	6801	784CIP2C_30	3046 3050
1444	3230	5016	6802	784CIP2C_31	3357
1445	3231	5017	6803	784CIP2C_32 784CIP2C 33	3357
1446	3232	5018	6804	784CIP2C_33	3432
1447	3233	5019	6805 6806	784CIP2C_34	3438
1448	3234	5020	6807	784CIP2C 36	3439
1449	3235	5021	6808	784CIP2C_38	3463
1450	3236	5022 5023	6809	784CIP2C_33	3466
1451	3237	5024	6810	784CIP2C_40	3466
1452 1453	3238 3239	5025	6811	784CIP2C_41	3467
1454	3239	5026	6812	784CIP2C 43	3468
1455	3241	5027	6813	784CIP2C 44	3483
1456	3242	5028	6814	784CIP2C 45	3484
1457	3242	5029	6815	784CIP2C 46	3488
1458	3244	5030	6816	784CIP2C 47	3491
1459	3245	5031	6817	784CIP2C 48	3493
1460	3246	5032	6818	784CIP2C 49	3494
1461	3247	5033	6819	784CIP2C 50	3495
1462	3248	5034	6820	784CIP2C 51	3496
1463	3249	5035	6821	784CIP2C_52	3503
1464	3250	5036	6822	784CIP2C_53	3503
1465	3251	5037	6823	784CIP2C_54	3504
1466	3252	5038	6824	784CIP2C_55	3511
1467	3253	5039	6825	784CIP2C_56	3531
1468	3254	5040	6826	784CIP2C_57	3536
1469	3255	5041	6827	784CIP2C_58	3546
1470	3256	5042	6828	784CIP2C_59	3548
1471	3257	5043	6829	784CIP2C_60	3551
1472	3258	5044	6830	784CIP2C_61	3553
1473	3259	5045	6831	784CIP2C_62	3564
1474	3260	5046	6832	784CIP2C_63	3567
1475	3261	5047	6833	784CIP2C_64	3572
1476	3262	5048	6834	784CIP2C_65	3573
1477	3263	5049	6835	784CIP2C_66	3574
1478	3264	5050	6836	784CIP2C_67	3583
1479	3265	5051	6837	784CIP2C_68	3615
1480	3266	5052	6838	784CIP2C_69	3623
1481	3267	5053	6839	784CIP2C_70	3629
1482	3268	5054	6840	784CIP2C_71	3666
1483	3269	5055	6841	784CIP2C_72	3667
1484	3270	5056	6842	784CIP2C_73	3906
1485	3271	5057	6843	784CIP2C 74	3912

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full- length	NO: of full-	of contig	NO: of contig	docket number_ corresponding	NO:in U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	0.S.S.N. 09/488,725
sequence	peptide	sequence	sequence	priority	05/400,725
	sequence		Doquec	application	
1486	3272	5058	6844	784CIP2C 75	3924
1487	3273	5059	6845	784CIP2C_76	3928
1488	3274	5060	6846	784CIP2C_77	3935
1489	3275	5061	6847	784CIP2C_78	3959
1490	3276	5062	6848	784CIP2C_79	3981
1491	3277	5063	6849	784CIP2C_80	3989
1492	3278	5064	6850	784CIP2C_81	4295
1493	3279	5065	6851	784CIP2C_82	4300
1494	3280	5066	6852	784CIP2C_83	4360
1495	3281	5067	6853	784CIP2C_84	4362
1496	3282	5068	6854	784CIP2C_85	4371
· 1497	3283	5069	6855	784CIP2C_86	4373
1498	3284 3285	5070 5071	6856 6857	784CIP2C_87 784CIP2C 89	4376 4378
1500	3286	5072	6858	784CIP2C_89	43/8
1501	3286	5073	6859	784CIP2C_90 784CIP2C_91	4409
1502	3288	5074	6860	784CIP2C_91	4421
1503	3289	5075	6861	784CIP2C_92	4421
1504	3290	5076	6862	784CIP2C 94	4426
1505	3291	5077	6863	784CIP2C 95	4430
1506	3292	5078	6864	784CIP2C 96	4435
1507	3293	5079	6865	784CIP2C 97	4436
1508	3294	5080	6866	784CIP2C_98	4439
1509	3295	5081	6867	784CIP2C_99	4440
1510	3296	5082	6868	784CIP2C_100	4441
1511	3297	5083	6869	784CIP2C_101	4442
1512	3298	5084	6870	784CIP2C_102	4455
1513	3299	5085	6871	784CIP2C_103	4462
1514	3300	5086	6872	784CIP2C_104	4466
1515	3301	5087	6873	784CIP2C_105	4469
1516	3302	5088	6874	784CIP2C_106	4477
1517	3303	5089	6875	784CIP2C_107	4481
1518 1519	3304 3305	5090	6876	784CIP2C_108	4483
1520	3305	5091 5092	6877 6878	784CIP2C_109 784CIP2C 110	4484
1521	3306	5092	6879	784CIP2C_110 784CIP2C_111	4490
1522	3308	5094	6880	784CIP2C_111 784CIP2C 112	4499
1523	3309	5095	6881	784CIP2C 113	4503
1524	3310	5096	6882	784CIP2C 114	4506
1525	3311	5097	6883	784CIP2C 115	4509
1526	3312	5098	6884	784CIP2C 116	4514
1527	3313	5099	6885	784CIP2C_117	4516
1528	3314	5100	6886	784CIP2C_118	4522
1529	3315	5101	6887	784CIP2C_119	4525
1530	3316	5102	6888	784CIP2C_120	4527
1531	3317	5103	6889	784CIP2C_121	4528
1532	3318	5104	6890	784CIP2C_122	4529
1533	3319	5105	6891	784CIP2C_123	4532
1534	3320	, 5106	6892	784CIP2C_124	4537
1535	3321	5107	6893	784CIP2C_125	4538
1536	3322	5108	6894	784CIP2C_126	4551
1537	3323	5109	6895	784CIP2C_127	4552
1538 1539	3324	5110	6896	784CIP2C 128	4559
1540	3325 3326	5111	6897	784CIP2C_129	4567
1541	3326	5112 5113	6898 6899	784CIP2C_130 784CIP2C 132	4568 4585
1542	3328	5113	6900	784CIP2C_132 784CIP2C_133	4592
1543	3329	5114	6901	784CIP2C_133	4609
1544	3330	5116	6902	784CIP2C_134 784CIP2C 135	4616
1545	3331	5117	6903	784CIP2C 136	4617
	3332	5118	6904	784CIP2C 137	4618
1546	222	3 7110			

		1 000 TD NO	L GEO. TD	Priority	SEQ ID
SEQ ID NO:	SEQ ID	SEQ ID NO: of contig	SEQ ID NO:	docket number	NO:in
of full-	NO: of	nucleotide	of contig	corresponding	U.S.S.N.
length	full-	t -	peptide	SEQ ID NO: in	09/488,725
nucleotide	length	sequence	sequence	priority	05/100//25
sequence	peptide		sequence	application	
	sequence	5120	6906	784CIP2C 139	4624
1548	3334		6907	784CIP2C 140	4632
1549	3335	5121		784CIP2C 141	4634
1550	3336	5122	6908		4638
1551	3337	5123	6909	784CIP2C_142	
1552	3338	5124	6910	784CIP2C_143	4639
1553	3339	5125	6911	784CIP2C_144	4643
1554	3340	5126	6912	784CIP2C_145	4644
1555	3341	5127	6913	784CIP2C_146	4655
1556	3342	5128	6914	784CIP2C_147	4668
1557	3343	5129	6915	784CIP2C_148	4677
1558	3344	5130	6916	784CIP2C_149	4677
1559	3345	. 5131	6917	784CIP2C_150	4677
1560	3346	5132	6918	784CIP2C_152	4682
1561	3347	5133	6919	784CIP2C_153	4690
1562	3348	5134	6920	784CIP2C_154	4691
1563	3349	5135	6921	784CIP2C 155	4727
1564	3350	5136	6922	784CIP2C 156	4730
1565	3351	5137	6923	784CIP2C 157	4734
1566	3352	5138	6924	784CIP2C 158	4757
	3353	5139	6925	784CIP2C 159	4764
1567			6926	784CIP2C 160	4786
1568	3354	5140	6927	784CIP2C 161	4793
1569	3355	5141		784CIP2C_161 784CIP2C_162	4825
1570	3356	5142	6928		4826
1571	3357	5143	6929	784CIP2C_163	
1572	3358	5144	6930	784CIP2C_164	4850
1573	3359	5145	6931	784CIP2C_165	4853
1574	3360	5146	6932	784CIP2C_166	4855
1575	3361	5147	6933	784CIP2C_167	4856
1576	3362	5148	6934	784CIP2C_168	4867
1577	3363	5149	6935	784CIP2C_169	4869
1578	3364	5150	6936	784CIP2C_170	4878
1579	3365	5151	6937	784CIP2C_171	4880
1580	3366	5152	6938	784CIP2C 172	4942
1581	3367	5153	6939	784CIP2C 173	4945
1582	3368	5154	6940	784CIP2C 174	4950
1583	3369	5155	6941	784CIP2C 175	4952
1584	3370	5156	6942	784CIP2C 176	4954
1585	3371	5157	6943	784CIP2C 177	4958
	3372	5158	6944	784CIP2C 178	4961
1586				784CIP2C 179	5590
1587	3373	5159	6945	784CIP2C 180	5599
1588	3374	5160	6946	784CIP2C 181	5692
1589	3375	5161	6947	784CIP2C 181	5732
1590	3376	5162	6948		5765
1591	3377	5163	6949	784CIP2C_183	1
1592	3378	5164	6950	784CIP2C_184	5771
1593	3379	5165	6951	784CIP2C_185	5774
1594	3380	5166	6952	784CIP2C_186	5793
1595	3381	5167	6953	784CIP2C_187	5806
1596	3382	5168	6954	784CIP2C_188	5852
1597	3383	5169	6955	784CIP2C_189	5892
1598	3384	5170	6956	784CIP2C_190	6057
1599	3385	5171	6957	784CIP2C_191	6061
1600	3386	5172	6958	784CIP2C 192	6109
1601	3387	5173	6959	784CIP2C 193	6160
<u> </u>	3388	5174	6960	784CIP2C 194	6297
1602	_		6961	784CIP2C 195	6398
1603	3389	5175		784CIP2C_193	6398
1604	3390	5176	6962		6415
1605	3391	5177	6963	784CIP2C_197	6448
1606	3392	5178	6964	784CIP2C_198	6469
1607	3393	5179	6965	784CIP2C_199	1
1608	3394	5180	6966	784CIP2C_200	6476
1609	3395	5181	6967	784CIP2C 201	6561

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	1	sequence	priority	}
1610	sequence	F		application	
1610	3396	5182	6968	784CIP2C_202	6574
1611	3397	5183	6969	784CIP2C_203	6578
1612	3398 3399	5184 5185	6970 6971	784CIP2C_204	6662
1613	3400	5185		784CIP2C_205	6672
1615	3400	5187	6972	784CIP2C_206	6691 6695
1616	3402	5188	6973 6974	784CIP2C_207 784CIP2C_208	6746
1617	3403	5189	6975	784CIP2C_208	6898
1618	3404	5190	6976	784CIP2C_209	6938
1619	3405	5191	6977	784CIP2C_210 784CIP2C_211	6943
1620	3406	5192	6978	784CIP2C_211 784CIP2C_212	7110
1621	3407	5193	6979	784CIP2C 213	7200
1622	3408	5194	6980	784CIP2C 214	7212
1623	3409	5195	6981	784CIP2C 215	7218
1624	3410	5196	6982	784CIP2C 216	7249
1625	3411	5197	6983	784CIP2C 217	7500
1626	3412	5198	6984	784CIP2C 218	7509
1627	3413	5199	6985	784CIP2C 219	7523
1628	3414	5200	6986	784CIP2C 220	7544
1629	3415	5201	6987	784CIP2C 221	7564
1630	3416	5202	6988	784CIP2C 222	7568
1631	3417	5203	6989	784CIP2C 223	7631
1632	3418	5204	6990	784CIP2C 224	7813
1633	3419	5205	6991	784CIP2C 225	7831
1634	3420	5206	6992	784CIP2C 226	7843
1635	3421	5207	6993	784CIP2C 227	7907
1636	3422	5208	6994	784CIP2C 228	7943
1637	3423	5209	6995	784CIP2C 229	8175
1638	3424	5210	6996	784CIP2C_230	8216
1639	3425	5211	6997	784CIP2C_231	8225
1640	3426	5212	6998	784CIP2C_232	8271
1641	3427	5213	6999	784CIP2C_233	8397
1642	3428	5214	7000	784CIP2C_234	8466
1643	3429	5215	7001	784CIP2C_235	8503
1644	3430	5216	7002	784CIP2C_236	8953
1645	3431	5217	7003	784CIP2C_237	9106
1646	3432	5218	7004	784CIP2C_238	9139
1647	3433	5219	7005	784CIP2C_239	9555
1648	3434	5220	7006	784CIP2C_240	9650
1649	3435	5221	7007	784CIP2C_241	9889
1650	3436	5222	7008	784CIP2C_242	9933
1651	3437	5223	7009	784CIP2C_243	9953
1652	3438	5224	7010	784CIP2C_244	9981
1653	3439	5225	7011	784CIP2D_1	746
1654	3440	5226	7012	784CIP2D_2	3558
1655	3441	5227	7013	784CIP2D_3	3558
1656	3442	5228	7014	784CIP2D_4	3633
1657	3443	5229	7015	784CIP2D_5	3658
1658	3444	5230	7016	784CIP2D_6	3732
1659	3445	5231	7017	784CIP2D_7	4004
1660	3446	5232	7018	784CIP2D_8	4700
1661	3447	5233	7019	784CIP2D_9	4703
1662 1663	3448	5234	7020	784CIP2D_10	4774
	3449	5235	7021	784CIP2D_11	4894
1664	3450	· 5236	7022	784CIP2D_12	4918
1665	3451	5237	7023	784CIP2D_13	5159
1666	3452	5238	7024	784CIP2D_14	7443
	3453	5239	7025	784CIP2D_15	8673
1667	2454	E040	"AAA" '	70407000	
1667 1668	3454	5240	7026	784CIP2D 16	8679
1667	3454 3455 3456	5240 5241 5242	7026 7027 7028	784CIP2D 16 784CIP2D 17 784CIP2D 18	8679 8727 8734

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	
	sequence		<u> </u>	application	
1672	3458	5244	7030	784CIP2D_20	8818
1673	3459	5245	7031	784CIP2D_21	8844
1674	3460	5246	7032	784CIP2D_22	8846
1675	3461	5247	7033	784CIP2D_23	8912
1676	3462	5248	7034	784CIP2D_24	8918
1677	3463	5249	7035	784CIP2D_25	8918
1678	3464	5250	7036	784CIP2D_26	8941
1679	3465	5251	7037	784CIP2D_27	8941
1680	3466	5252	7038	784C1P2D_28	8951
1681	3467	5253	7039	784CIP2D_29	8951
1682	3468	5254	7040	784CIP2D_30	9007
1683	3469	5255	7041	784CIP2D_31	9012
1684	3470	5256	7042	784CIP2D_32	9013
1685	3471	5257	7043	784CIP2D_33	9025
1686	3472	5258	7044	784CIP2D_34 784CIP2D_35	9053
1687	3473	5259	7045 7046	784CIP2D_35 784CIP2D_36	9054
1688	3474	5260		<u> </u>	9054
1689	3475	5261	7047	784CIP2D_37 784CIP2D 38	9113
1690	3476	5262	7048 7049	784C1P2D_38 784C1P2D_39	9134
1691	3477	5263 5264		784CIP2D_39	9152
1692	3478 3479	5264	7050 7051	784CIP2D_40 784CIP2D 41	9211
1693	3479	5265	7051	784CIP2D_41 784CIP2D_42	9223
1694		5267	7052	784CIP2D_42	9223
1695	3481	5268	7054	784CIP2D 44	9231
1696	3482	<u> </u>	7055	784CIP2D_44 784CIP2D 45	9236
1697	3483	5269 5270	7056	784CIP2D_45	9236
1698	3484 3485		7057	784CIP2D_45	9303
1699	1	5271	7057	784CIP2D 47	9309
1700 1701	3486 3487	5272 5273	7059	784CIP2D_48	9314
1701	3488	5274	7060	784CIP2D_49	9326
1702	3488	5275	7061	784CIP2D 51	9339
1704	3490	5276	7062	784CIP2D_52	9348
1704	3491	5277	7063	784CIP2D 53	9376
1706	3492	5278	7064	784CIP2D 54	9382
1707	3493	5279	7065	784CIP2D 55	9407
1708	3494	5280	7066	784CIP2D 56	9414
1709	3495	5281	7067	784CIP2D 57	9439
1710	3496	5282	7068	784CIP2D_58	9485
1711	3497	5283	7069	784CIP2D 59	9493
1712	3498	5284	7070	784CIP2D 60	9501
1713	3499	5285	7071	784CIP2D 61	9526
1714	3500	5286	7072	784CIP2D 62	9526
1715	3501	5287	7073	784CIP2D 63	9551
1716	3502	5288	7074	784CIP2D 64	9557
1717	3503	5289	7075	784CIP2D 65	9568
1718	3504	5290	7076	784CIP2D 66	9588
1719	3505	5291	7077	784CIP2D 67	9597
1720	3506	5292	7078	784CIP2D 68	9615
1721	3507	5293	7079	784CIP2D 69	9628
1722	3508	5294	7080	784CIP2D 70	9649
1723	3509	5295	7081	784CIP2D 71	9652
1724	3510	5296	7082	784CIP2D 72	9660
1725	3511	5297	7083	784CIP2D 73	9662
1726	3512	5298	7084	784CIP2D 74	9725
1727	3513	5299	7085	784CIP2D 75	9746
1728	3514	5300	7086	784CIP2D 76	9777
1729	3515 .	5301	7087	784CIP2D 77	9787
	3516	5302	7088	784CIP2D 78	9790
	1 JJIO				
1730	.l			784CIP2D 79	9842
	3517 3518	5302 5303 5304	7089 7090	784CIP2D_79 784CIP2D_80	9842 9842

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEO ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number	NO: in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	•	sequence	priority	1 557, 3007, 725
1	sequence		•	application	
1734	3520	5306	7092	784CIP2D 82	9867
1735	3521	5307	7093	784CIP2D 83	10010
1736	3522	5308	7094	784CIP2D 84	10011
1737	3523	5309	7095	784CIP2D 85	10052
1738	3524	5310	7096	784CIP2D 86	10057
1739	3525	5311	7097	784CIP2D 87	10085
1740	3526	5312	7098	784CIP2D 89	10139
1741	3527	5313	7099	784CIP2D 90	10142
1742	3528	5314	7100	784CIP2D 92	10165
1743	3529	5315	7101	784CIP2D 93	10173
1744	3530	5316	7102	784CIP2D 94	10173
1745	3531	5317	7103	784CIP2D 95	10273
1746	3532	5318	7104	784CIP2E 1	3121
1747	3533	5319	7105	784CIP2E 2	3628
1748	3534	5320	7106	784CIP2E 4	3673
1749	3535	5321	7107	784CIP2E 5	4018
1750	3536	5322	7108	784CIP2E 6	4467
1751	3537	5323	7109	784CIP2E 7	4865
1752	3538	5324	7110	784CIP2E 8	4916
1753	3539	5325	7111	784CIP2E 9	4923
1754	3540	5326	7112	784CIP2E 10	4926
1755	3541	5327	7113	784CIP2B 11	4962
1756	3542	5328	7114	784CIP2B 12	4963
1757	3543	5329	7115	784CIP2B 13	4964
1758	3544	5330	7116	784CIP2E 14	4988
1759	3545	5331	7117	784CIP2B 15	5835
1760	3546	5332	7118	784CIP2E 16	7682
1761	3547	5333	7119	784CIP2E 17	7682
1762	3548	5334	7120	784CIP2E 18	7699
1763	3549	5335	7121	784CIP2E 19	7707
1764	3550	5336	7122	784CIP2E 20	7707
1765	3551	5337	7123	784CIP2E 21	7752
1766	3552	5338	7124	784CIP2E 22	8357
1767	3553	5339	7125	784CIP2E 23	9065
1768	3554	5340	7126	784CIP2E 24	9324
1769	3555	5341	7127	784CIP2F 1	2976
1770	3556	5342	7128	784CIP2F 2	3559
1771	3557	5343	7129	784CIP2F 3	4021
1772	3558	5344	7130	784CIP2F 4	4474
1773	3559	5345	7131	784CIP2F 5	4566
1774	3560	5346	7132	784CIP2F 6	4705
1775	3561	5347	7133	784CIP2F 7	4707
1776	3562	5348	7134	784CIP2F 8	4712
1777	3563	5349	7135	784CIP2F 9	5008
1778	3564	5350	7136	784CIP2F 10	5009
1779	3565	5351	7137	784CIP2F 11	5015
1780	3566	5352	7138	784CIP2F 12	5015
1781	3567	5353	7139	784CIP2F 13	7724
1782	3568	5354	7140	784CIP2F_14	7725
1783	3569	5355	7141	784CIP2F 15	8828
1784	3570	5356	7142	784CIP2F 16	8830
1785	3571	5357	7143	784CIP2F 17	9739
1786	3572	5358	7144	784CIP2F 18	9896
				.0101121_10	7070

TRADOCS:1416247.1(%CS7011.DOC)

TABLE 7

WO 01/53312

1 A	BLE 7		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location .	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine; M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	residue of	amino acid	Codon, /=possible nucleotide deletion,
ł	amino acid	sequence	Codon, /=possible nucleotide delection,
1	sequence		\=possible nucleotide insertion)
5359	337	1131	AHLSARLSALILDEVAILPAPQNLSVLSTNMKHLLMWSPVIAPG
Ì	l	(ETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITA
1	ł		TVPYNLRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI
l l		1	TKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIP
1	Ì		VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPL
-	1		VLALFAFVGFMLILVVVPLFVWKMGRLLQ/YLLLPRGGSSQTPW
1		ł	KITOF
	 	1115	PRVRSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLK
5360	2	1112	CVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPED
1			
1	1	1	SGKYTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVD
1 .	1	[FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKF
I	1	1	VVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYS
1		[FRSAFLTVLPDPKPPGPPVASSSSATSLPWPVVIGIPAGAVFIL
1	1	1.	GTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPSL
1			AALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTGHS
1			TPHTYTHPPPSCQLNSSHS
5361	3	925	HEGSISSANILLDDQFQPKLTDFAMAHFRSHLEHQSCTINMTSS
1 3302		1	SSKHLWYMPEEYIRQGKLSIKTDVYSFGIVIMEVLTGCRVVLDD
1			PKHIQLRDLLRELMEKRGLDSCLSFLDKKVPPCPRNFSAKLFCL
1			AGRCAATRAKLRPSMDEVLNTLESTQASLYFAEDPPTSLKSFRC
-			PSPLFLENVPSIPVEDDESQNNNLLPSDEGLRIDRMTQKTPFEC
- 1	1	1	SQSEVMFLSLDKKPESKRNEEACNMPSSSCEESWFPKYIVPSQD
	İ	1	LRPYKVNIDPSSEAPGHSCRSRPVESSCSSKFSWDEYEQYKKE
			SCQVEGCTRTYNSSQSIGKHMKTAHPDQYAAFKMQRKSKKGQKA
5362	2	4879	SCOVERCIKTANSSOSTRAMIKTANPOGTAAT MIGKASIKOOMA
	l .	İ	NNLNTPNNGKFVYFLPSPVNSSNPFFTSQTKANGNPACSAQLQH
i	İ	1	VSPPIFPAHLASVSTPLLSSMESVINPNITSQDKNEQGGMLCSQ
Ì			MENLPSTALPAQMEDLTKTVLPLNIDRGSDPFLSLPAESSSIDL
İ	{		FPSPADSGTNSVFSQLENNTNHYSSQIEGNTNSSFLKGGNGENA
	İ	1	VFPSQVNVANNFSSTNAQQSAPEKVKKDRGRGQTGKERKPKHNK
j	•]	1	RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA
	1	}	EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD
		1	PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL
	•		ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH
		1	TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN
1	•	}	GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS
l			ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH
		1	SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT
1	ļ		VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT
1		1	LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ
1			NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL
-			NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHABDQIQEIDEGE QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE
1	}		QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADII VIQPVSE
1		1	MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPB
Į.			MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT
		ì	EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ
1			PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS
}			EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKKPVSQSLEFPTRY
1	1		SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE
- 1			ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL
1	Į		HEMTPEEIESMTASVDVGKFPCDQLECKSSFTTYLNYVVHLEAD
}		1	HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK
l			HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI
1	1		KMPKTKRKKKNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN
j	1		DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKLSKAF
	1		DADSECTSKY V IQI FORIT RGC 13 V V 13 ESWI I RGT RCERCEND
- 1	}	ì	TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSDTCVSESND
	1	1	NSRTTATVSQKEVEKNE*DEMDELTELFITKLINEDSTSVETQA
- 1	1		NTSSNVSNDFQEDNLCQSERQKASNLKRVNKEKNVSQNKKRKVE
,		1	KAEPASAAELSSVRKEEETAVAIQTIEEHPASFDWSSFKPMGFE
1			VSFLKFLEESAVKQKKNTDKDHPNTGNKKGSHSNSRKNIDKTAV
}	1		TSGNHVCPCKESETFVQFANPSQLQCSDNVKIVLDKNLKDCTEL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ì			1 =
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid .	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence		\=possible nucleotide insertion)
			VLKQLQEMKPTVSLKKLEVHSNDPDMSVMKDISIGKATGRGQY
5363	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
İ		ŀ	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
ł	1	i	RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
ł	i	ł	QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
1.	1		PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
1]	ļ	CTIANRCHEGGOSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
Į.	4		··· · · · · · · · · · · · · · · · · ·
		ļ	CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
ì	}	j	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
j	}	,	EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
	1		DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
	ł		KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
			DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
1			DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
	İ		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
!	4	į	GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
1	Ī	1	GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
1	1	[PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1		Ì	SGFRVEYELSEEGDEPOYLVLPSTATSV\NIP\DLLPGRKYIVN
1 .	1	J	, · · · · · · · · · · · · · · · · · · ·
ļ		}	VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
i			PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1	}		KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\ABN
		ļ	TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
ì	1		ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
1	ì	Į.	PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
1		ľ	TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
	1		VSGLTPGVEYVYTIQVLRDGQBRDAP\IVNK\VVTPLSPPTNLH
1 .	•		LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
ĺ	{	ĺ	HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
	l	·	PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
1	1	1	GRMLOSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEOHESTP
l .	1		\LRGROKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1	l l	i .	1 · · · · · · · · · · · · · · · · · · ·
1		1	TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
ł			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
	<u> </u>	· ·	APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
	1		YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
1	1		ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1	{		EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1.	1		DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1		ļ	ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
	İ		QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1	Į.		SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
1	1		ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
	Į	1	DVRSYTITGLOPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
			NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
ł	1	ì	RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
1	}		SGQQPSVGQQMIFEBHGFRRTTPPTTATPIRHRPRPYPPNVGQE
	-		ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
1	Ì		LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
			DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
J)		SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
1			HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1	[ĺ	RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
1			ADREDSRE
5364	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
3304		'03	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
L	L	L	WOLOT OTHER THE TOTAL TAKED TAKED TOTAL AND

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
\	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
(corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
j	sequence		\=possible nucleotide insertion)
			QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
Ì	,		PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
1			CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
ļ			CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
İ			ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
ţ			EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
1			DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
ļ			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
l .			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
			DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
ł		1	DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
)	j	1	DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
1	Į		GDSWEKYVHGVRYOCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
	-		TETPSQPNSHPIQWNAPQPSHISKYLLRWRPKNSVGRWKEATIP
		1	GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
1	j		PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
	1	1	SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
Ī	1	•	VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
	}	<u> </u>	PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
	[ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1	į		KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
ļ		Ì	TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
		ļ	ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
1			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
ì	İ		TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
}	,		VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
			LEAMPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
	1		HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
1	1		PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
1	j		GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
1		ļ	\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
1			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
		j	APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1			YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
İ			ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1			EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1			ELOGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1		[OVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1	1	1	SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
1			DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
			NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1	1	1	RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
1]	KEGATENTAL INDEST DIDOMIOANDERMIDOADANICTOL DOM
1			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
ı			SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
	1.	1	ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
		1	LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
(1	}	DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
1			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
		1	HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
	1	1	RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
			ADREDSRE
5365	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
			PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
1		1	QSKPGCYDNGKHYQINQQWBRTYLGNALVCTCYGGSRGFNCESK
1	1		PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
			CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
			CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
L	<u>. L</u>	<u> </u>	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence	sedgence	\=possible nucleotide insertion)
	7 204 4200		TCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
1			EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
			DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
			GNSNGEPCVLPFTYNGRTFYSCTTEGRODGHLWCSTTSNYEQDQ
			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
1			DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
			DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
			DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
1	į		GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
1			GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
	l .		PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
			SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
1]		PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
	[·	1	ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLOFVN
1	1		ETDSTVLVRWTPPRAQITGYRLTVGLTRRGOPROYNVGPSVSKY
}]		PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
			TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
-			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
	·		LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
1]		HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
1			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEOHESTP
			\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
1			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
	ì		APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
	}		YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
}	}		ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1)		EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1	. [QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
		·	SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
] .			DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
		-	NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
			RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGOE
			ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
1			LTGLTRGATYNI IVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
]]			DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
			HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
			RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
5366	8066	703	ADREDSRE
3300	0000	/03	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
	l		RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
	1		QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
	ſ		PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
		Ì	CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
		}	CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
1 1			ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
			EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
			DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG GNSNGEPCVLPFTYNGRTFYSCTTEGRODGHLWCSTTSNYEQDQ
L			GNSNGEFCVDFF1INGR1F1SC11EGRQDGABWCS113X15QDQ

	,		Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
:OM.	nucleotide	location	Giutamic Acid, Farnenylaianine, Gagiyeine,
.[location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
<u> </u>	bequestee		KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
		ļ	DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
1	Ì	ļ	DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
1	İ	'	
ļ	1		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
ľ			GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
İ		1	TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
i			GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
ł			PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1			SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
ļ			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
1			PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
1		i	ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1		1	KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
1	1	1	TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
i			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
}		1	PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
1			TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
1			LEANPOTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
]	HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
1	{		PPPTDLRFIN/ILGPDTMRVIW\APPPSIDLTNFLVRYSPVKNE
1			GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
ł	ł		\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1		1	TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
1			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
ļ] .		APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
			YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
	1		ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1	ł	ł	EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
Ì			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1			
į.			ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
	1	ł.	QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
	1	ł	SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
	•	1	ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
			DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
1		,	NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1			RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
}	1	1	QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
			SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
1			ALSOTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
({		LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
1			DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
1			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
1		1	HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1		1	
I			RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
L			ADREDSRE
5367	235	3591	KKILNMLCKKNIVIEYLADILYEYLYGFCFSGIKKYLIIHVLRL
ļ	1	I	ILELWMTRLLLEKSVSLQTQYLLLIVKILSWFPGKEMRHHLQIM
1		1	EVMMRKQDS/RIVGNGSEQQLQKELADVLMDPPMDDQPGEKELV
1	1		KRSQLDGEGDGPLSNQLSASSTINPVPLVGLQKPEMSLPVKPGQ
			GDSEASSPFTPVADEDSVVFSKLTYLGCASVNAPRSEVEALRMM
1	1		SILRSQCQISLDVTLSVPNVSEGIVRLLDPQTNTEIANYPIYKI
j			LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCEIQEAVSRI
1			LYSFATAFRRSAKQTPLSATAAPQTPDSDIFTFSVSLEIKEDDG
i			
1	1		KGYFSAVPKDKDRQCFKLRQGIDKKIVIYVQQTTNKELAIERCF
-			GLLLSPGKDVRNSDMHLLDLESMGKSSDGKSYVITGSWNPKSPH
1	ļ		FQVVNEETPKDKVLFMTTAVDLVITEVQEPVRFLLETKVRVCSP
1	1		NERLFWPFSKRSTTENFFLKLKQIKQRERKNNTDTLYEVVCLES
1	1.	1	ESERERRKTTASPSVRLPQSGSQSSVIPSPPEDDEEEDNDEPLL
1	İ		SGSGDVSKECAEKILETWGELLSKWHLNLNVRPKQLSSLVRNGV
1			PEALRGEVWQLLAGCHNNDHLVEKYRILITKESPQDSAITRDIN
L			

CEC	Droddena	Dwadlahad and	
SEQ	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	t .	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
Ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
			RTFPAHDYFKDTGGDGQDSLYKICKAYSVYDEEIGYCOGOSFLA
1	<u> </u>		AVLLLHMPEEQAFSVLVKIMFDYGLRELFKONFEDLHCKFYOLE
1]		RLMQEYIPDLYNHFLDISLEAHMYASQWFLTLFTAKFPLYMVFH
]	j		IIDLLLCEGISVIFNVALGLLKTSKDDLLLTDFEGALKFFRVOL
1	·		PKRYRSEENAKKLMELACNMKISQKKLKKYEKEYHTMREOOAOO
	1		EDPIERFERENRRLQEANMRLEQENDDLAHELVTSKIALRKDLD
į	}		NAEEKADALNKELLMTKQKLIDAEEEKRRLEEESAHLKKMCRRE
)]		LDKAESEIKKNSSIIGDYKQICSQLSERLEKQOTANKVEIEKIR
			QKVDDCERCREFFNKEGRVKGISSTKEVLDEDTDEEKETLKNQL
1			REMELELAQTKL\QLVEAECKIQD\LEHPF*GLPFNE\VQAA\K
			KTWFNRTLSSIKTATGVQGKETC
5368	573	2014	GAAAGAADPRRGSLGGRTMLDFAIFAVTFLLALVGAVLYLYPAS
			RQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVS
			FWFGRRLVVSLGTVDVLKQHINPNKTLD/LF*NHAEVIIKVSIW
1	}		WWQCE*KP\QRKKLYENGVTDSLKSNFALLLKLPEELLDKWLSY
			PETQH\VPLSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHG
			TVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERK
			GRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTW
1			AIWFLTTSEEVQKKLYEEINQVFGNGPVTPEKIEQLRYCQHVLC
			ETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP
1			NTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVT
Ĭ I			TVLLSVLVKRLHLLSVEGQVIETKYELVTSSREEAWITVSKRY
5369	1	6622	PRSLCFSLWAEAAVLADGGLRRRRRLLRGTMSASFVPNGASLED
			CHCNLFCLADLTGIKWKKYVWOGPTSAPILFPVTEEDPILSSFS
			RCLKADVLG/VWRRDQRPERRE\L*IFWGGEDP\VLLTLFTMTY
	ĺ		OKKKMECGRMDFPMNAVLCFSKAVHNLLERCLMNRNFVRIGKWF
1			VKPYEKDEKPINKSEHLSCSFTFFLHGDSNVCTSVEINOHOPVY
i .			LLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK
]	*		LIGEWKQFYPISCCLKEMSEEKQEDMDWEDDSLAAVEVLVAGVR
1			
	i		MIYPACFVLVPQSDIPTPSPVGSTHCSSSCLGVHQVPASTRDPA
1 1			MSSVTLTPPTSPEEVQTVDPQSVQKWVKFSSVSDGFNSDSTSHH
1	,		GGKIPRKLANHVVDRVWQECNMNRAQNKRKYSASSGLCEEATA
	1		AKVASWDFVEATQRTNCSCLRHKNLKSRNAGQQGQAPSLGQQQQ
		•	ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A
]	· ·		SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ
)			PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM
1			EDRIDSLSQSFPPQYQBAVEPTVYVGTAVNLBEDEANIAWKYYK
.			FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK
	t		PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF
į į	1		LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS
			IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT
			PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS
į ĺ			LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE
{ 1			VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY
1 1			LPLIKLPEECIYRQSWTVGKLELLSSGPSMPFIKEGDGSNMDQE
j j			YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP
] [RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP
1			ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK
			GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD
1 .]			IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL
j l			LODOCTNLFSPFGAADODPFPKSGVISNWVRVEERDCCNDCYLA
[LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL
j			RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG
1 1			TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR
1 1	,		1
Į l	1		DIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRLL
			TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV
	ļ		CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA
	1		NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS
			SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ
} ·	Į		QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH
L			AVTYPPAIVVYIIDPFTYENTDESTNSSSVWTLGLLRCFLEMVQ

		_	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence		\=possible nucleotide insertion)
			TLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPQHLKSLAFSAF
İ			TQCRRPLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPP
ł	i		FILAPVKDKQTELGETFGEAGQKYNVLFVGYCLSHDQRWILASC
ł		İ	TDLYGELLETCIINIDVPNRARRKKSSARKFGLQKLWEWCLGLV QMSSLPWRVVIGRIGRIGHGELKDWSCLLSRRNLQSLSKRLKDM
			CRMCGISAADSPSILSACLVAMEPQGSFVIMPDSVSTGSVFGRS
		j	TTLNMQTSQLNTPQDTSCTHILVFPTSASVQVASATYTTENLDL
	1		AFNPNNDGADGMGIFDLLDTGDDLDPDIINILPASPTGSPVHSP
			GSHYPHGGDAGKGQSTDRLLSTBPHEEVPNILQQPLALGYFVST
1]		AKAGPLPDWFWSACPQAQYQCPLFLKASLHLHVPSVQSDELLHS
ļ	}		KHSHPLDSNQTSDVLRFVLEQYNALSWLTCDPATQDRRSCLPIH
	ł		
L		 	FVVLNQLYNFIMNML RWSRKLELRRAAQATESRPPQSQEMHPPTGKEVHALKRLRDSAN
5370	1226	716	ANDVETVQQLLEDGADPCAADDKGRTALHFASCNGNDQIVQLLL
1			DHGADPNQRDGLGNTPLHLAACTNHVPVITTLLRGGARVDALDR
{			AGRTPLHLAKSKLNILQEGHAQCLKAVR/HGGEADHPYAEGVSG
			APRAT*AARCSGVFPSPSRWLGSAPWSRSSCTIWSLPLHEAKCR
			AVRPLSSAAQGSAPSSSSCCTVSTSLALAESLSLFRACTSLPVG
]]	GCISWL
5371	1331	167	IAAMLWKLLLRSQSCRLCSFRKMRSPPKYRPFLACFTYTTDKQS
5371	1331	10,	SKENTRTVEKLYKCSVDIRKIRR*KDGYF*RMKPMLKKLRI/F
1	}		LQELGADETAVASILERCPEAIVCSPTAVNTQRKLWQLVCKNEE
Į.	Į	ł	ELIKLIEGFPESFFTIKDQENQKLNVQFFQELGLKNVVISRLLT
		}	AAPNVFHNPVEKNKOMVRILOESYLDVGGSEANMKVWLLKLLSO
	1		NPFILLNSPTAIKETLEFLQEQGFTSFEILQLLSKLKGFLFQLC
	i	{	PRSIONSISFSKNAFKCTDHDLKQLVLKCPALLYYSVPVLEERM
			QGLLREGISIAQIRETPMVLELTPQIVQYRIRKLNSSGYRIKDG
ļ			HLANLNGSKKEFEANFGKIQAKKVRPLFNPVAPLNVEE
5372	51	857	SPGAQFLWAAPDMPDPLFSAVQGKDEILHKALCFCPWLGKGGME
33.2			PLRLLILLFVTELSGAHNTTVFQGVAGQSLQVSCPYDSMKHWGR
1			RKAWCRQLGEKGPCQRVVSTHNLWLLSFLRRWNGSTAITDDTLG
			GTLTITLRNLQPHDAGLYQCQSLHGSEADTLRKVLVEVLADPLD
			HRDAGDLWFPG\DLRASRMPMWSTASPGASWKEKSPSHPLPSFS
	j		SWPASFSSRF*QPAPSGLQPGMDRSQGHIHPVNWTVAMTQGISS
1			KLCQG
5373	2814	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY
1			QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
1		ļ	TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
1			ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
	i		KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
	ļ	1	DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP
]	j	1	DSSDSEYISDDEQKS*GISQEDIEDKEGCQMDKEFSKYKKKKY TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS
1	ł		PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE
1		1	GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ
		1	GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVBTRSSAQ TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
1	1	1	TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM
1	}	}	AVQRSCGTSSTVQQKEITQSPSTSTITTAVTSIQSSPLVISSGSM STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI
1			STLVSSVNGDLPIGTASADVAADTAKITSKL\MDATKGIM\TET YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQEL\SEMKHN
	1		YNDLSKN\TTWKAQLAEDSQGERTETERLQWDAQQED\SEMANN LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKQWC
1	1	1	LELTMAEMRQSWEQERDRLIAEVKKQHEHEKQQAVDEIKKKQHC ANFKKEAIFYCCWNISYCDYPCQ\QAHWPEH\MKSCTQSATAPQ
	- {		\QEADAE\VNTETLNKSSQGSSSSTQSAPSETASA\SKEKETSA
1			QKADAE VNTETLNKSSQGSSSS 1QSAFSE 1ASA (SKERETSS EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS
1		1	DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
			VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY
5374	2814	346	QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
			TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
1	1		ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
1			KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ
		J	IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
			DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP
1	(1	DOUGHT TODA BOLD OF THE PARTY O

Do beginning nucleotide location corresponding corresponding to first amino acid amino acid amino acid sequence	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Not			f	
location cofreeponding to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence s	1 -			
corresponding to first amino acid amino acid amino acid amino acid sequence and conting the conting to the cont	1		1	
to first endine acid residue of amino acid amino acid sequence seq				
amino acid residue of amino acid sequence Sequence Sequence Residue of amino acid sequence Residue of amino acid sequence Residue of amino acid sequence Residue of Residu	1			
residue of amino acid sequence Sequence				
amino acid sequence Codon, /-possible nucleotide deletion,	{		-	
Sequence	1			
INPUTEREBLEKSTSPASERANPGAYKONASPPERKOPSGRAKES PRIPTKOKKKKORDEN PRIVHLIGLIDGEN (PRIVITALIS GUBLIGGRE GRINKKEPEREPSPERKOVVOKTPSTTYGSHSPPERTYVITESSAN TSAAGATATTSTSSTVTVARAPAATSTEVKORPLIPEKS \ TAP AVORSGOTSSTVOKDE ITOSPSTSTTITUTSTOSSPLVTSKISSM STLVSSVINGDLE ITOSPSTSTTITUTSTOSSPLVTSKISSM STLVSSVINGDLE ITOSPSTSTTITUTSTOSSPLVTSKISSM STLVSSVINGDLE ITOSPSTSTTITUTSTOSSPLVTSKISSM STLVSSVINGDLE ITOSPSTSTTITUTSTOSSPLVTSKISSM STLVSSVINGDLE ITOSPSTSTTITUTSTOSSPLVTSKISSM LELIMABERGSVEGERBERLIABEVKGLEEKGOAUPEKKOWC ANFKERATFYCCWITSSYCDYPCO\QAJHIPBH\MKSCTQSATAPO QUEDALE VISTETITUTSTOSSPLUTSKISSMSSSS EKSKESGSTLDLSOSRETPSSILLOSNOGSBISK\SINKSSMSSS DEKKES\STSDLINGSGETPSSILLOSNOGSBISK\SINKSSMSSS DEKKES\STSDLINGSGETPSSILLOSNOGSBISK\SINKSSMSSS DEKKES\STSDLINGSGETPSSILLOSNOGSBISK\SINKSSMSSS DEKKES\STSDLINGSGETPSSILLOSNOGSBISK\SINKSSMSSS DEKKES\STSDLINGSGETPSSILLOSNOGSBISK\SINKSSMSSS DEKKES\STSDLINGSGETPSSILLOSNOGSBISK\SINKSSMSSS DEKKES\STSDLINGSGETPSSILLOSNOGSBISK\SINKSSMSSS DEKKES\STSDLINGSGETPSSILLOSNOGSBISK\SINKSSMSSS DEKKES\STSDLINGSGETPSSILLOSNOGSBISK\SINKSSMSSS DEKKES\STSDLINGSGETPSSILLOSNOGSBISK\SINKSALLOSNOGSBISK\S	Į.	amino acid	sequence	
### PHOTEXCHAGENERS PTOPULIDADES NEW YOUR GRANKEEPEN GRANKEEPEN GRANKEEPEN BERGOVER WAS TO THE GRANKEEPEN BERGOVER TO THE STANGATATISTS STUTYTAPBANTGSPYKKOPPLEKE YND AVORS GOTSTSTVOKET TO SENST THE THE THE STANGATATISTS STUTYTAPBANTGSPYKKOPPLEKE YND AVORS GOTSTSTVOKET TO SENST THE THE STANGAT THE THE THE STANGAT THE THE THE STANGAT THE THE THE STANGAT THE THE THE STANGAT THE THE THE STANGAT THE THE THE STANGAT THE THE THE STANGAT THE THE THE THE STANGAT THE THE THE STANGAT THE THE THE STANGAT THE THE THE STANGAT THE THE THE STANGAT THE THE THE STANGAT	i	sequence		\=possible nucleotide insertion)
GRNKKEPKEPSPKQDVVGKTPSSTYTGSHSPPETVLTUSSASA TRAAGATATTSTSSTYTVARAPARATSPYKKGPLIPEK TAP AVQRSGCTSSTYQKETTOSPSTSTITLUTSTOSSPLUTSSGSM STLVSSVANGDLEIGTARADAVADILKTSSLMMAN KTMYNTET YNDLSKONTYTWKAGLAEDSQGLEISIEKKJOHLHOGELSEMKEN LELTMARHGSSNSGSPERLAEVERVGKLEKKGOWC ANFKERLFYCONTS YCLYPCO\QAMPBEH MKSCTQSATAPO QUEADAEVYTSTETLAKSSQSSSSTYGABEPTAADAVEKKOWC ANFKERLFYCONTS YCLYPCO\QAMPBEH MKSCTQSATAPO QUEADAEVYTSTETLAKSSQSSSSTYGABEPTAADAVEKKOWC ANFKERLFYCONTS YCLYPCO\QAMPBEH MKSCTQSATAPO QUEADAEVYTSTETLAKSSGSSSSTYGABEPTAADAVEKKOWC ANFKERLFYCONTS YCLYPCO\QAMPBEH MKSCTQSATAPO QUEADAEVYTSTETLAKSSGSSSSTYGABEPTAADAVEKKOWC ANFKERLFYCONTS YCLYPCO\QAMPBEH MKSCTQSATAPO QUEADAEVYTSTETLAKSSGSSSSTYGABEPTAADAVEKKOWC ANFKERLFYTPTOTT YBTOHRSELLAHGKGSBAUTPTACTTK EKKERGSTLDLSGSRTFRSTLLGSRQGSBERNALAHGKERT BEKKERGSTLDLSGSRTFRSTLLGSRQGSBERNALAHGKERT ROAM GRUEAPPSTAADAVENSTAADAVENSSSATAPO REGISTARADAVENSSSATAPO REGISTARADAVENSSSATAPO REGISTARADAVENSSSATAPO REGISTARADAVENSSTAADAVENSSSATAPO REGISTARADAVENSSTAADAVENSSTAADAVENSSSATAPO REGISTARADAVENSSTAADAVENSSTAADAVENSSSATAPO REGISTARADAVENSSTAADAVENSSTAADAVENSSSATAPO REGISTARADAVENSSTAADAVENSSTAADAVENSSTAADAVENSSTAADAVENSSTAADAVENSSTAADAVENSSTAADAVENSSTAADAVENSSTAADAVENSSTAADAVENSSSATADAVENSSTA				TNPVEIKEBLKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS
TSAAGATATTSTSSTVTVTAPAPAATGSPYKKORPLIPKE\TAP AVORSCOTSSTVOORE TICHOSTSTITULTSTOSS STUSSONGOTSTORY OF THE TITULTSTOSS STUSSONGOTSTORY OF THE TITULTSTOSS STUSSONGOTSTORY OF THE TEXTOMILOGEL SERMICH LEITMABRIGSMOGRORI LIBEVEKULIBLEKOONDETTKKKOL ANFKKRAI PYCKORNIS VORDYGO ANHWEN INKSCTOSATAPO \QEADAB\VNTETIMISSOGSSSTOSADSTASA\SKEKETSA EKSKESGSTLIDAGSSETTSSAILGSNOCSSISSTAJA SKEKETSA EKSKESGSTLIDAGSSETTSSAILGSNOCSSISSTYTÄR POTTOKISS SEKKESGSTLIDAGSSETTSSAILGSNOCSSISSTYTÄR POTTOKISS BEKKESGSTLIDAGSSETTSSAILGSNOCSSISSTYTÄR POTTOKISS BEKKESGSTLIDAGSSETTSTATALGSNOCSSISSTYTÄR POTTOKISS BEKKESGSTLIDAGSSETTSTATALGSNOCSSISSTYTÄR POTTOKISS BEKKESGSTLIDAGSSETTSTATALGSNOCSSISSTYTÄR POTTOKISS BEKKESGSTLIDAGSSETTSTATALGSNOCSSISSTYTÄR POTTOKISSA BEKKESGSTLIDAGSSETTSTATALGSNOCSSISSTYL POTTOKISSAILGSNOCSSISSTYL POTTOKISSAILGSNOCSSISSTYL POTTOKISSAILGSNOCSSISSTYL POTTOKISSAILGSNOCSSISSAILGSNOCSSISSTYL POTTOKISSAILGSNOCSSISSA				PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE
TSAAGATATTSTSSTVTVTAPAPAATGSPYKKORPLIPKE\TAP AVORSCOTSSTVOORE TICHOSTSTITULTSTOSS STUSSONGOTSTORY OF THE TITULTSTOSS STUSSONGOTSTORY OF THE TITULTSTOSS STUSSONGOTSTORY OF THE TEXTOMILOGEL SERMICH LEITMABRIGSMOGRORI LIBEVEKULIBLEKOONDETTKKKOL ANFKKRAI PYCKORNIS VORDYGO ANHWEN INKSCTOSATAPO \QEADAB\VNTETIMISSOGSSSTOSADSTASA\SKEKETSA EKSKESGSTLIDAGSSETTSSAILGSNOCSSISSTAJA SKEKETSA EKSKESGSTLIDAGSSETTSSAILGSNOCSSISSTYTÄR POTTOKISS SEKKESGSTLIDAGSSETTSSAILGSNOCSSISSTYTÄR POTTOKISS BEKKESGSTLIDAGSSETTSSAILGSNOCSSISSTYTÄR POTTOKISS BEKKESGSTLIDAGSSETTSTATALGSNOCSSISSTYTÄR POTTOKISS BEKKESGSTLIDAGSSETTSTATALGSNOCSSISSTYTÄR POTTOKISS BEKKESGSTLIDAGSSETTSTATALGSNOCSSISSTYTÄR POTTOKISS BEKKESGSTLIDAGSSETTSTATALGSNOCSSISSTYTÄR POTTOKISSA BEKKESGSTLIDAGSSETTSTATALGSNOCSSISSTYL POTTOKISSAILGSNOCSSISSTYL POTTOKISSAILGSNOCSSISSTYL POTTOKISSAILGSNOCSSISSTYL POTTOKISSAILGSNOCSSISSAILGSNOCSSISSTYL POTTOKISSAILGSNOCSSISSA	ł			GRKNKKEPKEPSPKODVVGKTPPSTTVGSHSPPETPVLTRSSAO
AVORS.GOTS.STVOORE.TTO.SPETSTITLIVETGS.SPLVITS.SSENS.STLVS.SVINGIBLE TGTA.SADVABLAYETIK.\DADA.KSTA\TER \TANDL.SIN\TTWKAQLAEDS.GOLIVETEKK.QNELOGEN.SERNIN LEUTMARRIGGS.MSGORROLLARVKYLGI.ER.KOQUEN.SKKOWC ANFKREAT.FYCCHNTS.YCOVPCO\QAHWERI.\MKS.GTGS.ARGADAQ \QARDAP\NTETHLIKS.SGGGS.STGS.ABSETAS.GREATS.ABSETAS.GEKS.STGS.BETAS.GREATS.ABSETAS.GREATS.ABSETAS.GREATS.ABSETAS.GREATS.ABSETAS.GREATS.ABSETAS.GREATS.ABSETAS.GREATS.ABSETAS.GREATS.ABSETAS.GREATS.GREATS.ABSETAS.GREAT	1	}	1	
STUNSON/NOLIZIENGOLIZIENIA/MIDALKOTINU/ NINESKIN/TYMAKOLEBOGGIR LETEKIO/MURDEL\SERMENI LELTMARMOSMOGERORILAFVIKOLELEROON/DETYKKOMOC ANFKEAT TYCCOKONIS VOLYMOODAHMERIN\MISSCTOSATARO (VORADAR\NYTETLAKSSOGSSSTOSARSETASA \SEKETSA EKSKEGSSTLDLOGSSETTOSARSETASA \SEKETSA EKSKEGSSTLDLOGSSETTOSARSETASA \SEKETSA EKSKEGSSTLDLOGSSETTOSARSETASA \SEKETSA EKSKEGSSTLDLOGSSETTOSARSETASA \SEKETSA EKSKEGSSTLDLOGSSETTOSARSETASA \SEKETSA EKSKEGSSTLDLOGSSETTOSARSETASA \SEKETSA EKSKEGSSTLDLOGSSETTOSARSETASA \SEKETSA BERNEGOGTSVA\OSCAQARGARHKCAHCIRHIF FORWA\LIMITER RCQA\RGL\PLOCTECGRE FRIAP\FLALIRGYUHAATOPWORTACA LCQSSFROWVAU/LULIBAHSANAKOPFACEVORADFWORKAAS SSILRECHSSTROBERFICONCORSI LL\PTWOO\LIKVAHKRYIN\ SRRP \SEROPARVYMOGPROGERSTOTOPHOGGODAVORPF\CCA CCGREFRIK\PULIRSHAACTSGERPHO\CSGRECO\KRFTNIN\ SRRP\SEROPARVYMOGPROGPTOTOPHOGGODAVORPF\CCA CCGREFRIK\PULIRSHAACTSGERPHO\CSGRECO\KRFTNIN\ SRRP\SEROPARVYMOGPTROGPTOTOPHOGGODAVORPF\CCA CCGREFRIK\PULIRSHAACTSGERPHO\CSGRECO\KRFTNIN\ SRRP\SEROPARVYMOGPTROGPTOTOPHOGGODAVORPF\CCA CCGREFRIK\PULIRSHAACTSGERPHO\CSGRECO\KRFTNIN\ SRRP\SEROPARVYMOGPTROGPTOTOPHOGHOAVORPF\CCA CCGREFRIK\PULIRSHAACTSGERPHO\CSGRECO\KRFTNIN\ SRRP\SEROPARVYMOGPTOCORSTOTOPHOGHOAVORPF\CCA CCGREFRIK\PULIRSHAACTSGERPHO\CSGRECO\KRFTNIN\ SRRP\SEROPARVYMOGPTOCORSTOTOPHORADFORPFTCABC GKNOGKYHLVAHSKVIBSGREPFILARKGGRIPLOFROPTOCAP TORAPSOKSANLYBERGTITATATATATATATATATATATATATATATATATATAT				- · · · · · · · · · · · · · · · · · · ·
YNDLSKN/TYMKAQLAEDSQGLRIERKQMLKQQEL/SKKKMC LELTMARRGGSMCRRULIARVKQLGLERKQAUDETKKKKMC ANFKKEATPYCKNTISYCOVPCO\QAHMPBIN\MSCTQSATAGA \QUADARV\MTETHIAKSQGGSSSTQARSETTASA\SKEKETSA EKSKESGSTLDLSGSRETPSSILLGSNQSDHSR\SNKSSMSS DERRGS\TRDIN\TPSTQHRSLLJGGRSSAGTFPLGTSK EKSKESGSTLDLSGSRETPSSILLGSNQSDHSR\SNKSSMSS DERRGS\TRDIN\TPSTQHRSLLJGGRSSAGTFPLGTSK ### HIPLAREEFFMERKREPILAMFRQPRILLSGTSGSPQTTUTGES ### RCQA\RGLPLPCPGGGRFRHAPQPRILLSGTSGSPQTTUTGES ### RCQA\RGLPLPCPGGGRFRHAPQPRILLSGTSGSPQTTUTGES ### RCQA\RGLPLPCPGGGRFRHAPQPRILLSGTSGSPQTTUTGES ### RCQA\RGLPLPCPGGGRFRHAPQPRILLSGTSGSPQTTUTGES ### RCQA\RGLPLPCPGGGRFRHAPQPRILLSGTSGSPQTTUTGES ### RCQA\RGLPLPCPGGGRFRHAPQPRILLSGTSGTATPMPY LCQSSFRGWVALVILILRAHSAAKAGPPACFEMARDAFWRKASA ### SRRP+FRGPPAKVFGGFRFGFPTOTTPPGGGDAVRFP\CCCCCGCRFRHAPQPACTAGTSGTSGTATPMPY LTS\HRRITTHTANGPYPCKSCGRFFHKFNLSHSKHTKSSESS AQAAPGGSQLDLARSAGTAGSTGSTFACTFRAVLLKAGSESCS AQAAPGGSQLDLARSAGTAGSTGSTAGTFHKFNLSHSKHTKSSESS AQAAPGGSQLDLARSAGTAGSTGSTGSTFHAPALAFCHAPPAPPAPPH QDPIRAPPSLYSCDDCGRFRHAPPTAVLLPAEDEAPPAPPH QDPIRAPPSLYSCDDCGRFRHAPPTAVLLPAEDEAPPAPPH QDPIRAPPSLYSCDDCGRFRHAPPTAVLTPAERSKYVCP QDFRAFSQKSHLVAVHAPPTAVGTCAGTSGTSFATAGTFHAPAGSGGGN SABPNAPRGGPYCDCGKAPHKPYLAHPITATPASKYVCP QDFRAFSQKSHLVAVHAPPTAVGTCAGTSGTSFATAGTFHAPAGSGGGN SABPNAPRGGPYCDCGKAPHKPYLAHPITATPASKYVCP QCRRAFSQKSHLVAVHAPTATAKTSKLKGLARFKAVGGATTSPETPD ARTICLARSAGTAGTAGSTGTAGTSGTSGTSTAGTFHAPAGSGGGN SABPNAPRGGPYCDCGKAPHKPYLAAHPITATPASKYVCP QCRRAFSQKSHLVAGGGGGGGRVSNAMQGGALGKHACHAPTSPETPD ASTOVAGASSSLJOPGGSASGELSSSEPSTAQTFLAAPITTPT VLTSPGAVPPLLPSPKSEGGGRAVAVDLBERKLETTTRRPFPTP ASTOVAGASSSLJOPGGSASGELSSSEPSTAQTFLAAPITTPT VLTSPGAVPPLLPSPKSEGGGRAVAVDLBERKLETTRRPFPTP ASTOVAGASSSLJOPGGSASGELSSSEPSTAQTFLAAPITTPTT VLTSPGAVPPLLPSPKSEGGGRAVAVDLBERKETTTRRPFPTPT ASTOVAGASSSLJOPGGSASGELSSSEPSTAQTFLAAPITTPTT VLTSPGAVPPLTATAKTSKLIGHTRAKAGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Ì			<u> </u>
LELTMABRIGSMEGERDELTAPVIKUGLELEKOONVETTIKKON ANFIKKAI TYCCUNTS YCDYPOO, OAHBYBEN (MISKCTOSATAPO \(\) (QEADAR\) VNTETLIMIS SIGGISSESTIGARSETASIA\) SKERTISA EKSKEGISTILDIGGSSETTOSADSETASIA\) SKERTISA EKSKEGISTILDIGGSSETTOSADSETASIA\) SKERTISA EKSKEGISTILDIGGSSETTOSADSETASIA\) SKERTISA EKSKEGISTILDIGGSSETTOSADSETASIA\) SKERTISA EKSKEGISTILDIGGSSELDIGKESSENOTPPLOTIK HIPLAEEEBMLERICRIGPLAMGPAQPALLIGGISSOPPLIGKES RIGHOQOTSVA\) (QSCAQAPGRAINCAHCRIHIP PGWVA\LIMITER RCQA\RGIPLPCERCGRERRIAD PLALIRRYCHAATOROGENILLIGKESSENOTPPLOTIK RCQA\RGIPLPCERCGRERRIAD PLALIRRYCHAATOROGENILLIGKESSENOTPHO\(\) LIVIAHKRYTH SRRP ** ERGPPAKYWGERRIGPPTOTPPGGGGADVARRYKAAS SSILRRCHIPSRERGPRFT CONCORSILLIFUNG\(\) LIVIAHKRYTH SRRP ** ERGPPAKYWGERRIGPPTOTPTOTPFGGGADVARRYKAAS SSILRRCHIPSRERGPRFT CONCORSILLIFUNG\(\) LIVIAHKRYTH SRRP ** ERGPPAKYWGERRIGPPTOTPTOTPFGGADAVRYKAAS SSILRRCHIPSRERGPRFT CONCORSILLIFUNG\(\) LIVIAHKRYTH SRRP ** ERGPPAKYWGERRICHPTUND\(\) LIVIAHKRYTH LTS\(\) HRRITHTIAGRY PICKCORSILLIFUNG\(\) LIVIAHKRYTH SRRP ** ERGPPAKYWGERRICHPTUND\(\) LIVIAHKRYTH QDPIEAPPSLYSCODOCRSFRILLERILAHQKHUP\(\) QDPIEAPPSLYSCODOCRSFRILLERILAHQKHUP\(\) PRICATE PRICATE GKMFGKKTHLVAHSKVISKORGRUTUNYSKTPSGSSKMASSEN ARADARDERGSOLLOGGTFDDEBELHAHQKHUP\(\) SARGVUKREGTTTAKTSKIKAGLAVATLFATGKVYUTLDEAKS KNDOTVOGRKY PTCDECHGIT FVRAGSICOVFEDADTTSRETTOR ARADAVGSKINLINGGRITUNYSKATLFATGKVYUTLDEAKS KNDOTVOGRKY PTCDECHGIT FVRAGSICOVFEDADTTSRETTOR ARADAVGSSILLOFAKSKONGOLOGRITUNGATERISTERPTOR ASTOVAGARSSILDEGGASAGELSSEPSTAGTTELADIT IPTP VLTSPGAVPPLAPSPEKEBGLIGANVOLOGLERIKKÄRKENEKAL EAKERYMEEMADTAALEMATLOKEMAERRAELADIALVA RIMDLISSEKQBIVK\(L) QUKHEKKANQRLEVVRQUERLIKER VDELTTILLELIKKUDALAGEEWVRAUTLDERKIRLERIKVA LAKERYMEEMADTAALEMATLOKARERASELADIALA QETVADYQQTI KKYROLOTALERICHAQUERLIKKENCERSENCSE RPGERGAAGGGISSERGENTALITORNILLERICHSENCSE RPGERGAAGGGISSERGENTALITORNILLERICHSENCSE RPGERGAAGGGISTAALGUVY SILHALGEPBEOCTMULDETNINDELTA KARYYGHUN SILHALGEPBEOCTMULDETNINDELTATURPLIL KARYYGHUN SILHALGEPBEOCTMULDETNINDELTAPROGUER DAPAT	1	1		•
ANFEKERALFYCOMTS YCDYPCQ\QAMPBH\MINSCIQSATAPQ \QORADAP\UNTETNIKSSQGSSSSTQSAPGAFAS\AKKEKETSA EKSKESGSTLDLGGSETPSSTLLGSNQSDISR\SNKSSWSS DEKKGS\TREDH\TPST\GKSLIAGGSBLFR\GKSEKSSSSS DEKKGS\TREDH\TPST\GKSLIAGGSBLFR\GKSEKSSSSS DEKKGS\TREDH\TPST\GKSLIAGGSBLFR\GKSEKSSSSS DEKKGS\TREDH\TPST\GKSLIAGGSBLFR\GKSSLSSSST DEKKGS\TREDH\TPST\GKSLIAGGSBLFR\GKSSSSSST DEKKGS\TREDH\TPST\GKSLIAGGSBLFR\GKSSSSST DEKKGS\TREDH\TPST\GKSLIAGGSBLFR\GKSSSSST DEKKGS\TREDH\TPST\GKSLIAGGSBLFR\GKSSSST DEKKGS\TREDH\TPST\GKSLIAGGSBLFR\GKSSST RGLQGGTSVA\QSGQAAGGRAHECAHGRHFPGWVA\LIMBHTS RCQA\RGLFIAGDFLAGGSALFTWAPLAFWGAATDWGFACH LCQGSFGWVALVLHLRAHSAAGAPFACPKHARDAFWRKAS SILRRCHFSBFPGFPTGTOTFFOGGGADVDFPF\QCA CCGKFFRK\F\ND\ILSHAAGTGSFPHO\CKGAKFTNKFY\ LTS\HRRTHTARQPYPCKEGGRFRHKFPLLSHSKIHKRSGS AQAAPOGGS GDLPAGGGSSAABFTBAVPLKPAQESPPGAPFEHP QDFIEAPSLYSCDDGGSFRLEFFLRAHGRGHTGERPFT\CAEC GKNGKKTHLVAHSKWHISGERPFIAARKCGFRAGGGFGR SAEPNAPRGPFVCPDCGKAFHKFYLAAURFLATPABEKYVCD DCKRAFSGKSML\VSHRRIHTGERPFAAGGGGGN SAEPNAPRGPFVCPDCGKAFHKRYLAAURFLATPABEKYVCD DCKRAFSGKSML\VSHRRIHTGERPFAAGGGGGN SAEPNAPRGPFVCPDCGKAFHKRYLAAURFLATPABEKYVCD DCKRAFSGKSML\VSHRRIHTGERPFAAGGGGTGRVYCDGFSSGKSMAEAS ARPLERGGFGCGGGGGGGGGGGCGVVGCGAFAGGGGGGGGGGGGGG	1	1		
QRADAR\NTPTIANISSOGSSSTQSAFEETASA\SIKKETSA EKSKEGGTLDLGSGNETPSSTLLGSNGCDISK,SMSSMSSS DEKKEGS\TRSDHM\ftpsTQHGSSLLPGKESRAGTPFIGTSK 1116	[
EKSKESGSTLDLGGGRETPSSILLGSNQSDISER,SNKSNSSS DEKKEG \TRESHMYTPSTQMSLLPKGKESSPTGLTSK 5375 2907 1116 HIFLAREEPMLERRCRGFLAMGPAQPRLLSGPSQESPQTLGKES RGLRQQGTSVA\QSGAQAPGRAHRCAHGRHFPGWVA\LMHTR RCQA\RGLFQCGTSVA\QSGAQAPGRAHRCAHGRHFPGWVA\LMHTR RCQA\RGLFQCGTSVA\QSGAQAPGRAHRCAHGRHFPGWVA\LMHTR RCQA\RGLFQCFCGCRFFRKAPAPLAHGRYCKVAARATDWGFACH LCQSFRGWVALVLHLRAHSAAKAGPFACFWAARDAFWRKKAS SSILRRCHFSFRFRGFPTCONGGSILFWGVAWAKRWYN SRPF*BRGFPAVVFWGFPRRGPFTCOTGSEPHO\CSRCGA\RGFTNKPY\ LTS\HRRTTHTARQPYPCKECGRFFRHKPMLISHSKIHKKSEGS AQAAPGGSFQLPAGPGSSAABETFAVVFKLFACHGABYAYC LTS\HRRTTHTARQPYPCKECGRFFRHKPMLISHSKIHKKSEGS AQAAPGGSFQLPAGPGSSAABETFAVVFKLFACHGABYAYC LTS\HRRTTHTARQPYPCKECGRFFRHKPMLISHSKIHKKSEGS AQAAPGGSFGPVCDCGAKFRHKYTLAAHFFLATPAEKFYVCF DCRKAFSQKSRIL\VSHRRITTGERFYACPDCORSFSQKSRNLTH RKSHIRDGAFCALGCGFTDDEERLLHARCKGRFPLFRASKGGRFPTCABC GKMFGKKTHLVAHSEWHGBEFFFLARAKCGRFPLFRASKGGRF SABENAPRFGFYCDCGAKFRHKYTLAAHFFLATPAEKFYVCF DCRKAFSQKSRIL\VSHRRITTGERFYACPDCORSFSQKSRNLTH RKSHIRDGAFCALGCGFTDDEERLLHARCKGUNGTLICH RKSHIRDGAFCALGCGFTDDEERLLHARCKWIDU 5376 4504 591 VSTFSLCUMPAGGGGRGVSNMAGSKRIVYSRTFSGSRMASAS ARRLKVEGGRVYLGKHGKYTAVVAATLFAFTATTREKPTYFD ASTOVAGASSLGPSGSASAGELSSEPSTPAQTPLAAPI1PTP VLTSPGAVPPLPSPSKEBEGLRAQVGLKKKKAPTARTREKPTYRF ASTOVAGASSLGPSGSASAGELSSEPSTPAQTPLAAPI1PTP VLTSPGAVPPLPSPSKEBEGLRAQVGLKKKKAPTARAEDKA KLKELEKHK IQLEQVQSWKSMMGQGALGLKKKKAPTARAEDKA KLKELEKHK IQLEQVQSWKSMMGQGALGLKKKARPARAEDKA KLKELEKHK IQLEQVGSWKSMMGQGALGLKKKARPARAEDKA DAKERWEEMADTADAIBMATLDKEMBAERRABSLQCGVERLKER VDELITTLEEILKBELEGVGABASYQLKKERERETVG DLEANMENNDELGENARFTSLELRRGCLABRAKKBLLCTHMPD SFLRPGGGHOCVILLILMPALICKABLIKAKGVERLERVGVEP DLEANMENNDELGENARFTSLELRRGCLABRAKKBLLCAFMPD SFLRPGGGHOCVILLILMPALICKABLIKAKGVERLERVGVEP ETPFKKKGGSLKARHTSLOLGERUMTSCHVEBLT KAIKYYGHLYSILLARGPECTOMQARHTHYSYSALLCKVEBLT KAIKYYGHLYSILLARGPECTOMQARHTHYSYSALLCKVEBLT KAIKYYGHLYSILLARGPECTOMQARHTHYSYSALLCKSURGLIL APLABREGLLVAALEELLFRAGBOTYGTPSSPYECKAGCKTIL SGARGLKGGRAFTUKTAHAGGGGATTARTSTQALLFRICK CHAPAGAGATARTTSGALLFRAGGCTILLAGGATARTTGOLLET LIQUTHTHVVOITHTSBAKSBGATAVGATTRGSLLFKKL LERNI	ł	ì	i	
DEKRGS VTRSDHM/TPSTQHGRSLIAPGKESRAGTPFLGTISK 1116 HIPLANEERHELERGREGIANGPAGPALISGESPOTTIGKES RGLRQQGTSVA\QSGAQAPGRAHRCAHCRHPPGWVA\LNLHTR RCQA/RGLFLCDECCRFFHADFLALHRQVTRAANTDWGFACH LCQSFRGWAJUHLHRANSARAGPPACHAWARANTDWGFACH LCQSFRGWAJUHLHRANSARAGPPACHAWARANTDWGFACH SRRP+BRGPEAPTICANGRSILPTWOQ/LKVAHKRYHV SRRP+BRGPEAPTICANGRSILPTWOQ/LKVAHKRYHV SRRP+BRGPEAPTICANGRSILPTWOQ/LKVAHKRYHV SRRP+BRGPEAPTICANGRSILPTWOQ/LKVAHKRYHV SRRP+BRGPEAPTICANGRSILPTWOQ/LKVAHKRYHV SRRP+BRGPEAPTICANGRSILPTWOQ/LKVAHKRYHV SRRP+BRGPEAPTICANGRSILPTWOQ/LKVAHKRYHV SRRP+BRGPEAPTICANGRSILPTWOQ/LKVAHKRYHV SRRP+BRGPEAPTICANGRSILPTWOQFACHAGAGPHAPHAGAGPHAPHAGAGPGBPHDQDEAPPHQCACKAGRFRHKPHAGAFPAGAPPHAGAGAGAAAAAAAAAAAAAAAAAAAAA	1			
1116 HIFLAREEPMLERRICROPLAMORAQPELLSGDSGESPOTTAKES RGLRQGOTSVA\GGGAQAGGRIRHCANTEPGWA\LAULHITER RCQA\RGLPLPCPECGREFRHAPFLALHRQVHAAATPDWGFACH LCGGSFRGWVALVHLIRAHSAAKAGFFACFRWARDDFWRKAAS SSILRRCHPSKPRGPRFFICTOGNGGRILLETWDG\CLKVAKKRVHV SRRP*BRGPPAKVFWGPRPRGPFTOTPFGGGGAVRFTNKPY LTS\MRRITHTARQPYPCKECGREFRHKFNLLISHSKHKSFBSS AQAAPGGGSPQLAPAGGGSAAEPTPAAVFGSPPGAPFDRAPSPGGA GRMFGKKTILVAMSFWLSGERPFLARKAGRGHTGERPFTCAGC GKMFGKKTILVAMSFWLSGERPFLARKAGRGHTGERPFTCAGC GKMFGKKTILVAMSFWLSGERPFLARKAGRGHTGERPFTCAGC GKMFGKKTILVAMSFWLSGERPFLARKAGRGHTGERPFTCAGC GKMFGKKTILVAMSFWLSGERPFLARKAGRGHTGERPFTCAGC GKMFGKKTILVAMSFWLSGERPFLARKAGRGHTGERPFTCAGC GKMFGKKTILVAMSFWLSGERPFLARKAGRGHTGERPFTCAGC GKMFGKKTILVAMSFWLSGERPFLARKAGRGHTGERPFTCAGC GKMFGKKTILVAMSFWLSGERPFLARKAGRGHTGERPFTCAGC GKMFGKKTILVAMSFWLSGERPFLARKAGRGHTGERPFTCAGC GKMFGKKTILVAMSFWLSGERPFLARKAGRGHTGERPFTCAGC GKMFGKKTILVAMSFWLSGERPFLARKAGRGHTGERSFGKSMLITH RSHILDGGAGGGGRGRVSMAGSKRHVSERTSGSRNSAEA AFPLRVGSSVEVIGKHGHGTVAVYGATLERKTURKVGVILDEAKG KNOCTVGRKYFTCDEGHGIFVAVYGGILGFGGADTTSEPTDS SAKKUKRGFGTTTATATSKLKGLKPKKAFTTTRKFTTRKFTRK ASTOVAGASSSLGPSGSASAGELSSEPSTPAQTPLAAPIIPT VLTSPGAVPPLSPSYSEESGLAQVRDLEKKLFTLKKTERKFYRP ASTOVAGASSSLGPSGSASAGELSSEPSTPAQTPLAAPIIPT VLTSPGAVPPLSPSYSEESGLAQVRDLEKKLFTLKKTREKFYRP ASTOVAGASSSLGPSKSSTOASSTQLKGLEGGWARLKADLV RMBDLSSSEKGEHVK\LQRIMEKRGGLEVVRQQRERLGELSG AESTIDELKEGVODAGLGAERWENLTORLEKVPLERTETVG DLEAMMEMBLGBNAFTELELLERGLDWAGARVERAGREAL GETVADYQGTIKKYRGLTAHLGDVINELINGCRASVERGQOPP ETFPFKIKRAETKAHAKAIEMSLEKVPLERTETVG DLEAMMEMBLGBNAFTELELLERGLDWAGARVERGKVEVAA OETVADYQGTIKKYRGLTAHLGDVINELINGCRASVERGQOPP ETFPFKIKRAETKAHAKAIEMSLEKVPLERTETVG DLEAMMEMBLGBNAFTELELLERGLDWAGARVERAGREVENAA QETVANYGGTIKKYRGLTAHLGDVINELINGCRASVERGGCP DAGGITANGGAGRATHALDDVINELINGCRASVERGGROWENDIAL KAIKYYGHLYSIHLABGPGVAGATHALDVINELIKKYRGKTERGFGT DAGGITANGGAGGATTIALLLRDLETSCS\DIRGFCKKRRFGET DAGGITANGGAGRAFTELELLERGLPPSKPPPVVLTAAAAQLI APLARMEGILVAALEELAFTGNAAATLERGGAGDTVVVGLILEKKLDS RAGGLKGARGAGGAGGATTIALLLRICREGGGGGGGAGGAGGAGGGGGGGGGGGGGGGGGGGGGGG	1			
RGLEQQOTSVA\QSGQAQAGGRAHCALCREHPGWALALTHURG PACH RQQA\RGLICPQECGER PRIGHPILALHROWINAATDURG PACH LCQQS\PGWVALVLHLRAHSAAKAGPFACPKWARDAFWRRKAAS SSILRRCHPSR\PROFRIFICONGGRSILETURD\(\frac{1}{2}\text{VAKWRWHV}\) SRR\P\RGE\PERG\PROFRIGH\(\text{PROFROT}\) PORGGAVDR\(\text{PROFROT}\) CCG\(\text{RFTMK}\) PILTS\(\text{HRATHSARAGF}\) PORGGAVDR\(\text{PROFROT}\) CCG\(\text{RFTMK}\) PILTS\(\text{HRATHTARGPYPCEGGRF}\) PRIGHQR\(\text{HRAFT}\) GODO\(\text{CGGRF}\) PRIGHQR\(\text{HRAFT}\) GODO\(\text{CGGRF}\) PRIGHQR\(\text{HRAFT}\) GODO\(\text{CGGRF}\) PRIGHQR\(\text{HRAFT}\) GODO\(\text{CGGRF}\) AQAAPGGS\(\text{POLOGYAFTHATPILAAHRPILATBARPYVCG\) DOPIGAPPS\(\text{LVAHSRVHSGERPFRLARKCGRF}\) PRICABEQ\(\text{GCGRF}\) GORK\(\text{RFTMK}\) GORK\(\text{RFTMK}\) PRICABEQ\(\text{LVAHSRVHSGERPFRLARKCGRF}\) GORK\(\text{RFTMCAFT}\) CORK\(\text{RFTMCAFT}\) GORK\(\text{RFTMCAFT}\) CORK\(\text{RFTMCAFT}\) ASTOVAGAS\(\text{SSILGHPAGGGGGRG\(\text{VSTAGGGGGRG\(\text{VSTAGGGGGGRG\(\text{VSTAGGGGGRG\(\text{VSTAGGGGGGRG\(\text{VSTAGGGGGGGAT\) SABVIK\(\text{RFGTDTTAKTSKLRGLKPKKAPTARKTTTR\(\text{RFTMF}\) PRICABEQ\(\text{LSTAKTTTR\(\text{RFTMT}\) ASTOVAGAS\(\text{SSILGHPAGGGGGGAT\(\text{LSTAKTTTR\(\text{RFTMT}\) PRICABEQ\(\text{LSTAKTTTR\(\text{RFTMT}\) ASTOVAGAS\(\text{SSILGHPAGGGGGAT\(\text{LSTAKTTTR\(\text{RFTMT}\) PRICABEQ\(\text{LSTAKTTTR\(\text{RFTMT}\) PRICABEQ\(\text{LSTATTTR\(\text{LSTATTTR\(\text{RFTMT}\) PRICABEQ\(\text{LSTATTTR\(\text{RFTMT}\) PRICABEQ\(LSTATTTR\(\text{LSTATTR\(\text{LSTATTR\(\text{LSTATTR\(\text{	L_	1	<u> </u>	
RCQA/RGLELPC/PECGER PRHAPILALHRQVHAAATPURGEPACH LCQGS/PEGGVALVILHBA/SAARAGPACH/KAADAFWRRACH SSILRRCHPSRPRGPRFICGNCGRSILFTWDQ/LKVAHKRVHV SRRP*BRGPPAKVFWGPRPRGPFTODTPFGGGGDAVDRFY\QCA CCGRRFRHK/PNLIRSHAACTSGRPROD/CSREGG\KRFTMKPY LTS\HRRITHTARQPYCKEGGRRFRHKPNLISHSKIHKRSEGS AQAPGGGSPGDLPAGPQGSAAEPTPAVVEAQPPPGAPPBHD QDPIEAPPSLYSCDDCGRSFRHERFLRAHQRQHTGRRPFTCAGC GKMFGKKTHLVAHSRVHGSERPFLARAKQRPPPGAPPBHD QDPIEAPPSLYSCDDCGRSFRHERFLRAHQRQHTGRRPFTCAGC GKMFGKKTHLVAHSRVHGSERPFLARAKQRPPPGAPPBHD QDPIEAPPSLYSCDDCGRSFRHERFLRAHQRQHTGRRPFTCAGC GKMFGKKTHLVAHSRVHGSERPFLARAKQRPPPGAPPBHD QDPIEAPPSLYSCDDCGRSFRHERFLRAHQRQHTGRRPFTCAGC GKMFGKKTHLVAHSRVHGSERPFLARAKQRPPPGAPPBHD QDPIEAPPSLYSCDDGGRSFRHERFLRAHQRQHTGRRPFTCAGC GKMFGKKTHLVAHSRVHGSERPFLARAKQPPPGAPPBHPD GRAFAGGGRGGRVSMAGASKHVYSRTPSGSRNSABA SABNARRGGPVCPDCGKAFHHYTLAHARRYDTPSGRNSABA ARPLRVGSSVEVIGKGHRGTVAVYGATLERKVGVILDBAKG KNOCTVQGRKYFTCDBGHGIFVAVYGGLIGGAATHSVETTPSGTPDS SASKVLKREGTDTTANTSKLRGLKPKKATRKTVTRKPVTRP ASTOVAGASSSLGPSGSABAGELSSSPSTPAOPPLAAPIIFTP VLTSPGAVPPLPSPSKEBEGLRAVQNDLERTKTTTRKPVTRP ASTOVAGASSSLGPSGSABAGELSSSPSTPAOPPLAAPIIFTP VLTSPGAVPPLPSPSKEBEGLRAVQNDLERTKTTRKTVTRKPVTRP ASTOVAGASSSLGPSGSABAGELSSVEDSTPAOPPLAAPIIFTP VLTSPGAVPPLPSPSKEBEGLRAVGNUTERTKTTTRKFVTRR ASTOVAGASSSLGPSGSABAGELSSVEDTPAOPPLAAPIIFTP VLTSPGAVPPLPSPSKEBEGLRAVGNUTERTKTTTRKFVTRF ASTOVAGASSSLGPSGSABAGELSSVEDTPAOPPLAAPIIFTP VLTSPGAVPPLPSSSVEDEGLRAVGNUTERTKTTTRKFVTRF ASTOVAGASSSLGPSGSABAGELSSVEDTPAOPPLAAPIIFTP VLTSPGAVPPLPSSSVEDEGLRAVGNUTERTTTRKTTTRKFVTRF ASTOVAGASSSLGPSGSABAGELSSVEDTRAKTTTRKFTRKFTRF VBLITTDLEILLKAEISEKSSDGASSYQLKQLBEQGVBALKER VBLITTDLEILLKAEISEKSSDGASSYQLKQLBEQGVBALKER VBLITTDLEILLKAEISEKSSDGASSYQLKQLBEQGVBALKER VBLITTDLEILLKAEISEKSSDGASSYQLKQLBEQGVBALKER VBLITTDLEILLKAEISEKSSDGASSYQLKQLGBEGGARAKABAL BARSTIDBLKEQVODABAGARVERAGERAUBLUTANDEG GRAFDGAGGATTLAHARDATALLERLAKTHTLAHARDATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	5375	2907	1116	
LCGGSFRGWALVLHILRAHSAAKAGPPACPMARDAFWRRKAAS SSILRRCHPSRPRGPRPFICGNGRSILPTWDQ/LKVAHKRVHV SRR** SRGPFAKVFWGPRPRGPTOTPFGGGDAVDRPF\QCA CCGRFRHK\PNILRSHAACTSGERPHO/CSRGQ\KRFTNKPY LTS\HRRITHTARQPYPCKECGRFRHEPNILSHSKIHKRSEGS AQAAPGGGSPQLPAGPGGSSALBTPAVVLKPAGEPPGAPPEHP QDPIEAPPSLYSCDDCGRSFRLEFILARQKHTGRPFTCAEC GKMFGKKTHLVAHSRVISGRPPPLARKCGRFFLPBASGSGGN SAEPNAPRGPPVCPDCGKAFRHKPYLAHRPIATPBASGSGGNN SAEPNAPRGPPVCPDCGKAFRHKPYLAHRPIATPBASGSGGNN SAEPNAPRGPPVCPDCGKAFRHKPYLAHRPIATPBASGSGGNN SAEPNAPRGPPVCPDCGKAFRHKPYLAHRPIATPBASGSGGNN SAEPNAPRGPPVCPDCGKAFRHKPYLAHRPIATPBASGSGGNN SAEPNAPRGPPVCPDCGKAFRHKPYLAHRPIATPBASGSGGNN SAEPNAPRGPPVCPDCGKAFRHKPYLAHRPIATPBASGSGGNN SAEPNAPRGPPVCPDCGKAFRHYPYLAPPLOCDRSFSQKSNLITH RKSHIRDGAFCCALCGCTPDDEERLAHQKKHNU STSTELCHAPAGGGGGGRGVNNMAGSKRWYSRTPSGSRNSAEAS ARPLRVSSRVEVIGKGHRGTVARVGATLFATGKRWGVILDBAKG KNDGTVOGKKYFTCDEGHGIFVNGGIQVFEDGADTTSFETDDS SASKVLKRGGTDTTAKTSKLRGLKPKKAPTARATTTRRRKPTRP ASTGVAGASSSLGPSGSAASGELSSEPSTPAQTPLAAPIIPTP VLTSPGAVPPLSPSPSREBEGLRAQVRDLEEKLETTRIKRAEDKA KLKELEKHHIQLEGVGSWKSKMGGQADLCRRLKEARKAEAL EAKERTWEMMATTAAD LATHATLLEKHERESLOGGEVEALKER VDELTTDLEILKAGUDAALCAERWEMITDRNILLEEKVRELRRETVG DLEAMNEMNDELQENARETELELRGLOBVARGKRERESLOGEELAK ABSSTIDBLKEQUDAALCAERWEMITDRNILLEEKVRELRETVG DLEAMNEMNDELQENARETELELRGLOBVARGVRCAGRERCEELSC AESTIDBLKEQUDAALCAERWEMITDRNILLEEKVRELRETVG DLEAMNEMNDELQENARETELELRGLOBVARGVRCAGRERCEELSC SPLERGGGGGDECVLVLLHUMPRLICKAELIRKQAGEKVELSEGCS RPGLRGAAGGQLSFPAATGLVY\SIMPAAGHRYHRYYCHALSQCR ELD\YYKVGSLYPPEMSAHRESLIDFLILKDQLDETNVEPLIT KAIKYYOHLYSIHLAEQPEDCTMQLADHIKFTGSALDCMSVEVG RIRAFLQGGGBATDIALLLRDLETSCS\DTRIPYSTCHAAALARACLI APLAEMEGGLLVAALEELAFKASEQIYGTPSSSYPCLRQGCNIL KAIKYYOHLYSILLERDLETSCS\DTRIPYSTCHAAALARACLI APLAEMEGGLLVAALEELAFKASEQIYGTPSSSYPCLRQGCNIL LISMMNYLUTMAGGGEGEDAAFPSSPTSPVVELRAAALRAETDA EGIGLKLEDRSTVIKELKKSLEKTETTSCALABFOQGCNILL STMNYLUTMAGGGEGETTALLGRUKKEFFETMDALQADIOL EAEKAELKORLNSGSKRTIEGLGFPPSGTATLVSGLAGERQG GATPQAAGSVPGPGLVKDSPLLLQGISAMCHINGLQDHENSILL KGAQMKASLASLPPLTVARLSHEGGGELPAGALYKKTSQLLET LNQLSTHTHVVDITTSTSPAAKSPSAQLMEQUAGLKSLSDTVEKL KUS	1	1		RGLRQQGTSVA\QSGAQAPGRAHRCAHCRRHFPGWVA\LWLHTR
LCGGSFRGWALVLHLRAHSAAKAGPPACPMARDAFWRRKAAS SSILRRCHPSRPRGRPRPI CGNGRS I LPTWDQ/LKVAHKRVHV SRR** SRGP PAKVEWGRPRRGPTOTD PFGGGDAVDRPF\QCA CCGRFRHK\PNLIRSHACTSGERPHO/CSRGG\KRFTNKPY LTS\HRRITHTARGPYPCKECGRFRHEPNLLSHSKIHKRSEGS AQAAPGGSPQLPAGPGSSALETPAVVLKPAGEPPFGAPPEHPP QDPIEAPPSLYSCDDCGRSFRLEFIRANGNGHGERPTCAEC GKMFGKKTHLVAHSRVISGRPPPLARKCGRFLPPBASGSGGN SAEPNAPRGPPVCPDCGKAFRHKPYLAHRPLATPBEKPYVCP DCKAFSQNSNL\VSHRRIHTGERPYACPLOCORSFSGKSNLTH RKSHIRDGAFCCALCGCTPDDEERLAHQKKHDY 5376 4504 591 VSTFSLCLIMPAGGGGGGKVSNMAGSKRWVSRTPSGSRNSAEAS ARPLRVSSRVEVIGKGHRGTVAYVGATLFATGKWGVILDEAKG KNDGTVGGKKYTTCDGHGIFVROSICJVFBGADDTISFETDDS SASKVLKRGGTDTTAKTSKLRGLKPKKAPTARKTTTRRFKPTRP ASTGVAGASSSLGPSGSASAGELSSEPSTPAQTPLAAPIIPTP VLTSPGGVPPLSSPSKBEBGLRRQVRDLEEKLETTRLKRAEDKA KLKELEKHRIQLEQVGSWKSKWGQQADLCRRKKARKAEAL EAKERTWBEMDATAAD LATNALTLEKRAERESLQQEVEALKER VDELTTDLSILKAEIEBKGSDGASSYQLKQLEEGNARIKDALV RRMDLSSSSKGBHVK\CKIMEKKAQDEVGGGERCYGELSG AESTIDBLKEQVDAALGAERWEMLTDRNLLEEKVRELRETVG DLEAMNEMNDBLQENARETELELRQLDWAGNRFLGELSG AESTIDBLKEQVDAALGAERWEMLTDRNLLEEKVRELRETVG DLEAMNEMDBLQENARETELELRQLDWAGNRFRQKRVEDA QETVADYQQTIKKRQLTARLDDVRRELTINQGEAVERQQCPPP ETTPFKIKRAETKAHAKAISIMEERLERLIRQQEKFELSENCSE RPGLRGAGGGLSFPAJGLVY\SIMPAAGHRYHRY*CHALSQCR LD\YYKVGSLYPPEMSAHERSLIDFILEHQQLBETNSPLT KAIKYYQHLYSIHLAEQPEDCTWQLADHIKFTQSALDCMSVEVG RLRAFLQGGGATDIALLLRDLETSCS\DIRQFKKRRRMGT DAGGIPAALAFQCQVSDTLLLGRELTRQCDEKSCNIL KAIKYYQHLYSIHLAEQPEDCTWQLADHIKFTQSALDCMSVEVG RLRAFLQGGGATDIALLLRDLETSCS\DIRQFKKRRRMGT DAGGIPAALAFQCQVSDTLLLGRELTRAQAGKEELSENCSE RPGLRGAGGGLSFPAJGLVY\SIMPAAGHRYHRY*CHALSQCR RLRAFLQGGGATDIALLLRDLETSCS\DIRQFKKRRRMGT DAGGIPAALAFQCQVSDTLLLCRELTRACQAGKEELSERCSE RPGLRGAAGGQLSFPAJGLVY\SIMPAAGHRYHRY*CHALSQCCNIL KAIKYYQHLYSIHLAEQPEDCTWQLADHIKFTQSALDCMSVEVG RLRAFLQGGGATDIALLCRUKKEEFFETDMLAQADIQLD EARKAELKORLNSQSKRTIEGLGFPPPSGTATLVSGLAGERQG GATPQQAFGSVPGPGLVKDSPLLLLQGLSANGHLHISQLQHENSIL KGAQMKASLASLPPHVAKLSHEGGGELFGAAGALYKKTSQLLET LNQLSTHTHVVDITTSTBAAKSPSAQLMCVQALGKSLSDTVYKL KUPTSCAAGFGGRRRLLVTTOTGLHGKKEEFFETDMLAQADTVYM KVFTSCAAGFGGRRRLUVTTOTGLHGKREEGSV*VHEWRO	1			RCQA/RGLPLPCPECGRRFRHAPFLALHRQVHAAATPDWGFACH
SSILRRCHPSRPRGPRPICGNGGRSILPTMOD/LKVARKRVHVY SRRP+ERGPPAKVFWGPPPRGPTGDTPMCPGGDAVDRPF\QCA CCGKRFRHK\PNLIRSHAACTSGERPHO/CSRCG\KKFTKKPY LTS\HRRITHTARQPYPCKSCGGRFRHKPNLLSHSKIHKRSEGS AQAAPGESPQLPAACPGESAAETTPAVPLKPAGEPPGAPPEHP QDPIEAPPSLYSCDCGRSFRLERFLRAHGGHTGERPFTCAEC GKNPGKKTLLVAHSRVHGSGRPPELARGCGRFLPRASCSGGN SAEPNAPRPGPFVCPDCGKAFRHKPYLAAHRPIATPAEKFYVCP DCKKAFSGKSNI\VSHRRIHTGERFYACPDCDRSFSGKSNLITH KSHIRGSAFCCALGGTPDDEERLAHGKCHDV 5376 4504 591 VSTTSLCLWPAGGGGGGVSNWAGSKRWYSRTPSGSNNAITH KSHIRGSAFCCALGGTPDDEERLAHGKCHDV SAKSKUKREGTDTTAKTSKLRGLKPKKAPTARTKTVSILDEAKG KNDOTVCGRKYFTCDECHGIFVVGSCICVFEDGADTTSPETDS SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTVTTRPKPTRP ASTGVAGASSSLGPSGSSASGELSSEESTPAGTPLAAPIIPTF VLITSPGAVPPLPSPSKEEGLRAQVRDLEEKLETLKKRAEDKA KLKSLEKRHKIGLEGVGWKSKMGGGADLCRRIKKEARKAEAL EAKRYMEEMADTADAIEMATLDKEMASEERSELOGEVBALKER VDELTTDLILIKAELERKSGGGASSOLLCKEQMARKALDLV MRGDLSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEGVDAALGAEEMVEMITDENLILEEKVRELERTVG DLEMMERMBOLIGENBAETELLERGJGCASSCYCQPEPP ETTSPKIKREPTKAHRAKIEMBLEGNAGAVERAGANEWBLAGCR QETVADYQQTIKKVRGUTAHLQDVRELTNQCEASVERQQQPPP ETTSPKIKREPTKAHRAKIEMBLEGNGAAVGANEMBLITARMPD SFLRPGGDBCCVLVLLLMPRLICKBELIRKVGLGSVERCQGPPP ETTSPKIKREPTKAHRAKIEMBLEGNGAAVGANEMBLITARMPD SFLRPGGDBCCVLVLLLMPRLICKBELIRKVGLGSVERCGGGG LD\VYKKVGSLYPEMSAHERSLDFLIELLHKOQLDETVNVEPLT KAIKYYOHLYSIHLAEQPEDCIMQLADHIKFTGSALDCMSVEVG RLAPALGGGGGARTDIALLLBUETSG LDRGYCKKIRRNPGT DAPGIPAALAPGPQVSDTLLLGCKHLTWVAVLQEVAAAAAQLI ISTMNK\LVTAMQSGEDAERPPSPPP\VELRAALRAETDA EGIGLKLERRETVIKELKKSLKUKGELSEANVRUTLLEKKLDG AANDABERIELVGYRLEGGGGATTOLAGLBDIKFTGSALDCMSVEVG GAPGGAGSVEPGLUKOSDFLLLGGIAFSFETSMDALGADDIQG GAPGGAGSVEPGLUKOSDFLLLGGIAFSFETSMDALGADDIQG EARKAELKGRLNSGSKRTIEGLGGPPPSGTATLVSGIAGERQG GAPGGAGSVEPGGLUKOSDFLLLGGIAFSSFETCHALGADDIQG CAPEGAPSVEPGTUTTFTFFFFSSAFFRAKERGCDDTTVYM KVYTSCAAGFGGRRTLUKLSHEGGESGEGFF*VHEVGAEGES* VMCDMWCGUTITTSCAARSPSAFLIKGEGSLGENDTVYM KVYTSCAAGFGGRRTLUKLKREATSKRRAESLGFETSMDALGABELGT SWPCKEVUTSCAAGFGGRRTLUTTGCGLHGLKSLLIS SWPCYGGWGGGGTTTGCCESGERGFF*VHEVGAEGES* VMCDMWCGGUTITSCCESGERGGFF*VHEVGAEGES* V	1	1 .]	
SRR* BEGFPAKVFWGRPRGPTGDTPFGGGGAUDRFF\QCA CCKSKFRKK\PNLIRSHAACTSGERPHQ/CSRECG\KRFTNKPY LTS\HRRITHTARGPYPCK&CGRRFHKPNLLSHSKIHKRESGS AQAAPGGGSPQLPAGFQESAAEPTPAVPLKFAQEPPFGAPEHP QDPIEAPPSLYSCDDCGSFSFLEFILRHQRQHTGERPFTCAEC GKWFGKKTHLVAHSRVISGRPPHLARKCGRFLPPBASQSGGRN SAEPNAPRFGPFVCPCCKAFRHKPYLAHRPLATPEAPPYCCPL DCRKAFSQKSNL\VSHRRIHTGERFYACPDCDRSFSQKSNLITH RKSHIRDGAFCCALCGTFPDDEBRLLAHQKKHDV S376 4504 591 VSTFSLCLWPAGGGGGGRVSNMQSKRVYSFTPSGSRMSAEAS ARPLRVSSRVEVIGKGRRGTVAVGATLFATGKWGVILDEAKG KNDGTVQGRKYFTCDEGHGIFVRQSQLQVFEDGADTTSPETPDS SASKVLKREGTDTTAKTSKLRGLKFKKAPTARKTTTRRFKFTRP ASTOVAGASSSLGPSGSASAGELSSEESTAPTLAAPITTTRRFKFTRP ASTOVAGASSSLGPSGSASAGELSSEESTAPTLAAPITTTRRFKFTRP ASTOVAGASSSLGPSGSASAGELSSEESTAPTLAAPITTTRRFKFTRP ASTOVAGASSSLGPSGSASAGELSSEESTAPTLAAPITTTRRFKFTRP ASTOVAGASSSLGPSGSASAGELSSEESTAPTLAAPITTTRRFKFTRP ASTOVAGASSSLGPSGSASAGELSSEESTAPTLAAPITTTRRFKFTRP ASTOVAGASSSLGPSGSASAGELSSEESTAPTLAAPITTTRRFKFTRP ASTOVAGASSSLGPSGSASAGELSSEESTAPTLAAPITTTP VLTSPGAVPPLPSPSKEEBELRAQUALEEKLETLELKRAEDKA KLKELEKHKIQLEOVQEKKKKAPTARKTTTRRFKFTRP ASTOVAGASSSLGPSGASAGGLSSEESTAPTLAAPITTPRFKTRE ASTOVAGASSSLGPSGASASGLSSEESTAPTLAAPITTPRFKTRRFKTVG ASTOVAGASSSLGPSGASASGELSSEESTAPTLAAPITTPRFKTREETVG ASTOVAGASSSLGPSGASASGELSSEESTAPTLAAPITTPRFKTREETVG ASTOVAGASSSLGPSGASASGELSSEESTAPTLAAPITTPRFKTREETVG ASTOVAGASSSLGPSGASASGELSSEESTAPTLAAPITTPRFKTRATTTRRFKTRRF ASTOVAGASSSLGPSGASASGELSSEESTAPTLAAPITTPRFKTRAETHAPT ASTOVAGASSSLGPSGASASGELSSEESTAPTLAAPITTPRFKTRAETHAPT ASTOVAGASSSLGPSGASASGELSSEESTAPTLAAPITTPRFKTRAETHAPT ASTOVAGASSSLGPSGASAGGELSTAPTPRAALTATTTRRFKTTRRFKTTRRFKTTRRFKTTRRFKTTTRRFKTTRRFKTTTRRFKTTRRFKTTRRFKTTRRFKTTTRRFKTTRRFKTTTRRFKTTRRFKTTTRRFKTTRRFKTTTTRRFKTTTR	ı	}		1
CCGRFFRHX PNLIRSHACTSGERPHO/CSREGGKRFTMKPY LTS\HRITHTARQPYPCKECGRFFRHKPNLISHSKHKKRSGS AQAAPGGSPQLPAGPGSSABETPJAVPKRQGEPPPGAPPEHP QDPIEAPPSLYSCDDCGSSFRLERFLRAHGQRHTGRFFTCAEC GKNFGKKTLIVAHSRUKBGSRPFRLAKGGRFPBASGGGRN SABPNAPRGPPSUVCDCGKAFRHKPYLAAHPIATPAEKPYVCP DCRAFSGKSIN_VSHRIHTGERPFYCDDCBRSFSQKSGINLITH RKSHIRDGAFCALCGQTFDDEBERLAHQKKHDV 5376 4504 591 VSTTSLCLWPAGGGGRGRVSNWAGSKRIVYSRTFSGSKNSAEA ARPLRVGSRVEVIGKGRRGTVAYVGATLFATGKNVGVILDEBKG KNDGTVCGRKYFTCDEHGIFVRQSQLQVFEDGADTTSFETDS SASKVLKRGSTDTTAKTSKLRGLIKPKAPTARKTTTRRFKPTRP ASTGVAGASSSLGPSGSASAGELSSEESTPAQTPLAAPIIPTP VLITSPGAVPPLFSPSKEBGLARQVRLDEBKLETRLKRAEDKA KLKELEKHRIQLEQVGEKKSWCGGOADLCRRLKEARKAEAL EAKERYMEEMADTADAIEMATLDKEMAEERASELQEVEALKEAL EAKERYMEEMADTADAIEMATLDKEMAEERASELQEVEALKEAL EAKERYMEEMADTADAIEMATLDKEMAEERASELQEVEALKEAL PRINCLSSEKGBHVK\LQKLMEKKNGDLEVVGQGRRLCDELSG AESTIDELKEQVDAALGAEEMVEMLIDDRINLEEKVRELRETVG DLEANMENNDBLQENRAETTLELERQLDMAGARVREAGKRVEAA QETVADYQQTIKKVRQUTAALIDDVRRELTNGCBSVERQQOPPF ETTSFIKIKFAFTKAHARAIEMELGROKEVAGANEHMSLITAFMPD SFLRPGGDDLGVLVJLLIMPRLICKAELIRKKOAGSKFELSENCSE RPGLRGAAGGGUSPAGTGLVYSLHAHGYRIYRIYS'CHALSGCR LD\VYKKVGSLYPEMSAHERSLDFLIELLKHQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQADHIKTYGJALDCMSVEVG RLARFIGGGGATDTALLIELEKKESEGSPSPECLGSSENCGCE RARFLGGGGATDTALLIELEKKESEETSSPECKSEE RPGLRGGAGGGATDTALLIELEKKESEETSSPECKSEE RPGLRGGAGGGATDTALLIELLEKTURVAVUQUEVAAAAAQLI APLAEMEGLIVAALEELEKAFASGSITYSSPECKGSCNIL ISTMIK\LVTAMQEGEYDAERPSKPPP\VELRAAARACITDA EGIGLIKLBERSTVIKELKKSLKKSLEKTSEETSMDALGADIDQL EAKKAELKQRLNSQSKRTIEGLRGPPPSGYPPVVELRAAALRAEITDA EGIGLIKLBERSTVIKELKKSLEKKSEETETMDALCADDIDQL EAKKAELKQRLNSQSKRTIEGLRGPPPSGYBPPTGATATVSGIAGERQG GATGQGASVDGFGLUVADSPLLLKGESSPPECLAGALTYKTSGLAEEQG GATGQGASVDGFGLUVADSPLLLKGKSLEKTPETET LNQLSTHTHVUTTRTSPAAKSPSAQLMEVAAQLATGLEGEGGE GATGGGASVDGFGLUVADSPLLAGKSLEDDTVYM KVITSCAAGFGGRRILUTUTGCGLHGLHSRLIS URGDSTHTPUTUTTTTSPAAKSPSAQLMEVAAGLGSGEDQTVYMM KVITSCAAGFGGRRILUTUTGCGLHGLHSRLIS SSWPGYDGWGGQUTFTPROHKWEBQP 5378 2009 664 OASGTTLRFLEDDLQLKKREATSRINKELKFCBELVIMTSCLPAL	1	1	ł	·
LISHRITHTAROPYPCKEGGREFRHKENLISHSKIHKRSEGS AQAAPGGSPQLPAGPGESAAPTPAVPLKHAQEPPDGAPPEHD QDPIEAPPSLYSCDDCGRSFRLERFIRAHQRGHTGERFFTCAEC GKNFGKKTHLVAHSRVHSGERPFRLARKCGRFLPRASGSGGRN SABENAPRFGPPVCDCGKARFHLYALARFITATPAEKPYVCP DCRKAFSQKSNLVSHRRIHTGERPYACPDCDSFSGKSNLITH RKSHIRDGAFCCAICGGTFDDERLLAHQKKHDV 5376 4504 591 VSTTSLCLMPAGGGGGRGVSNMAGSKRHYVSRTPSGSRMSAEAS ARPLRVGSRVEVIGKGHRGTVAYVGATLFATKWVGVILDEAKG KNDGTVGGRKYFTLOEBGGIFVGGVGVPEGADTTSFETPDS SASKVLKREGTDTTAKTSKLRGLKPKKAPPARKTTTRRPKPTRP ASTGVAGASSSLGPSGSASAGELSSSEPFTPAGTLAAPIIPTP VLTSPGGAVPPLEPSPSKEEGLRAQVRDLEEKLETLRKREDKA KLKELERHKIGLEQVGEWKSKMGRQQADLGRRIKEARKARAL EAKBRYMEMADTADA IEMATLEAMEERASSLOGVEALKER VDELTTDLEILKAEIBEKGSDGASSSVOLKQLEEQNARLKDALV RMDLSSSKKGHVVLLQKAMEKKNGELSVVQQRERLGELSQ AESTIDELKEQVDAALGAERWVEMLTRNUNLEEKVRELRETVG DLEAMMEMMIDBLQENARSTELELREQLDMAGARVREAQKRYWBA QCETVADVQQTIKKVRQLTAHLQDVAHCHTORVLAUERVBACK CETVADVQQTIKKVRQLTAHLQDVAHCHTORVLAUERVBACK CETVADVQQTIKKVRQLTAHLQDVAHLTNOQCASVRQQDEPPD ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFIRPGGDHIDCVLVLLIMPRICTGAELIERQGEKFELSENGEE RPGLRGAAGGLUSFAALGLAVSLAUHLTRVORABVERQQDPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQARRHMSLLTAFMPD SFIRPGGDHIDCVLVLLIMPRICTGAELIERQGEKFELSENGEE RPGLRGAAGGLUSFAALGLAVILTKVORABVERQQDPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQARRHMSLLTAFMPD SFIRPGGDHIDCVLVLLIMPRICTGAELIERQGEKTELSENGEE RPGLRGAAGGLUSFAALGLAVILTGVALGEVAAAAAQLI KAIKYVGHLYSHLABAPGDCTTMJAHLTRYGASLDCMSVEVG RLRAFLQGQCATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DARGIPAALAFQGVGDTLIDCKRHITWVVALQEVAAAAAQLI APLAEMEGGLIVAALEELAFKASBGITGSTSSSPYECLRGSCNIL ISTMNKLUTMAQGCGEYDAERPPSKPPPVERFACAGGCTTLEGEGGG GAIFGGAPGSVEPGGLVKDSFLLLQGISAMRHISGLQHENSIL ISTMNKLUTMAQGCGYDAERPPSKPPPVLERGAGCTLEGGCGC GAIFGGAPGSVEPGGLVKDSFLLLQGISAMRHISGLQHENSIL KGAQMKASLASLPPHIVAKLSHEGGGSEFSAVNATLLEEKLDS AAKDADERIEKVYGTREETGALLVKSKEFETMDALQADIDQL EAEKABLKQRLKNSQSKRTIEGLRGPPSGIATVKTSOLLET LNQLSTHTHVVOITTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KOEVUKETVSQRPGGATVFTFFSSAFLRAKEQQDDTVYMG KVTFSCAAGFGGRHLULTGGLUGLHSKLIS SYNGYYDGWWGQYIPIFFRGMEBED 5378 2009 664 ODFKKRVLPARGGGGRG	1	1	}	
AQAAPGGSSQLPAGPGSSAAEPTPAVPLKPAQEPPPGAPPEHD QDPIEAPPSLYSCDDCGRSFRLERFLRANQRHTGERPFTCAEC GKNFGKKTHLVANSKVHSGREPFRLARKCGRFLPPAGSGGRM SABPNAPRGPFVCPDCCKAFRHKPYLAAHRPIATPAEKPYVCP DCRKAFSQKSNLVSHRRHTGERPACPCDCRSFSQSSNLITH RKSHLRQGAFCCAICGCTFDDERELLAHQKKHDV 5376 4504 591 VSTFSLCLWPAGGGGRGRVSNMAQSKRHVYSBTPSGSRMSAEAS ARPLRVGSRVEVIGKGHRGTVAYVGATLFATCKWVGVILDEAKG KNDGTVCGRKYFTCDEGIGIFVRQSQLOVFEDGADTTSPETPDS SASKVLKREGTDTTAKTSKLRGLKPKKAPPARKTTRRFKPTRF ASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLAAPIIPTF VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKELTLRLKRABDKA KLKELERHKIQLEGVGEWKSKMGQADLCAFRIKERARKARAL EAKRRYMERMADTADAIEMATLJKEMMEERABSLQGEVEALKER VDELTTDLEILKAEIEEKGSDGAASSYCLKQLEEQNARKLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSG AESTIDBLKEQVDAALGAEEMVENLITDRNINLEEKVRELRETVG DLEAMMEMDELGEMARTETLELREADHAGARVREARA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFOFKIKFAETKAIKALIEMELRQHEVAQARKHSLLTARMPD SSIRPGGDHDCVLVLLLMPRILGKLIRKQAGKTVEAS QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFOFKIKFAETKAIKALIEMELRQHEVAQARARHSLLTARMPD SFIRPGGDHDCVLVLLLMPRILGKLIRKQAGKREFELSENCSS RPGLRGAAGGGLSFAAIGLVY\SIMPAAGHRYHRY*CHALSQCR LDVYKKVGSLYPEMSAHERSLDFLIELIRKQQDKFELSENCSS RPGLRGAAGGGLSFAAIGLIVY\SIMPAAGHRYHRY*CHALSQCR LDVYKKVGSLYPEMSAHERSLDFLIELIRKQQDKFELSENCSS RPGLRGAAGGGUSFAAIGLIVY\SIMPAAGHRYHRY*CHALSQCR LDVYKKVGSLYPEMSAHERSLDFLIELIRKQQCKVALAAAQLI KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGQGCATDTALLLIRDLETSCS\DIRGCKKIRRRMPGT DAGGIPAALAFGGYGDYDTLLDCKRHUVVAVALQEVAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAAQBGEYDAERPPSKPPVVELRAAARAEITDA EGIGLKLEDRETVI KELKKSLKKIKGBLESAAVRAITLEKKDD AAKDADER IEKVQTTLLEETQALLRKKKKFEFETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLGGAPPSGTATLVSGIAGEEQQR GAIFGQAPGSVEGPGLVXGBFLLLQGISAMGHAILLEKKLD AAKDADER IEKVQTRLEETQALLRKKEKGFLEETMDALQADIDQL EAEKAELKQRLNSQSKTTIEGGEGEGFGFAHALTTSQLLET LNQLSTHTHVVOITTSTSAAKSPAGLMGVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFFSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRUNLTGQLHQHINSLIL KGQMKASLASLPPHVAKLSHEGGSELPAAGALYTKTSQLLET VMGDPWRLVHTQLKTKKPGGTLKAKFYLHTGSTKFAARISCTK SS*MPGYYDGWMGGQYI	1	1		
ODPIEAPPSLYSCDDCGRSFRLERFLRAHGRORTGERSPTCAEC GKNPGKKTHLVAHSRVHSGERPFRLARKGGRRFLPRASQSGGRN SABENAPRROPPVCEDCGKARRHKPYLAAHREIATPAEKPYVCP DCRKAFSQKSNL\VSHRRIHTGERPYACEDCDRSFSQKSNLITH RKSHIRGAFCCALGQYFDDEBELAHGKKHUV 5376 4504 591 VSTFSLCLWPAGGGGRGRVSNMAQSKRHVYSRTPSGSRMSAEAS ARPLRVGSRVEVIGKGHRGTVAYVGATLFATKKWGVILDEBAG KNDGTVGGRKYFTCDEGGGIFVRGSQIQVBEDGADTTSPETPDS SASKVLKRBGTDTTAKTSKLBGLKPKKAPTARKTTTRPFKPTRP ASTOVAGASSSLOPGSGASAGGLSSPETPAQTPLAPPITPT VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQDMKSKMGEQQADLGRAKKERAREAAL EAKERYMEEMADTADAIEMTLUKAMEERABSLOGVEVALKER VDELTTDLEILKAEIERGSGGAASGSVOLKOLEEGNARLKDALV RRDDLSSEKQBHVAVLOKLMEKKMERABSLOGVEVALKER VDELTTDLEILKAEIERGSDGAASSVOLKOLEEGNARLKDALV RRDDLSSEKQBHVAVLOKLMEKKMERINQGASVERQQAPP ETTFFKIKFAETKAIKALIEMELRGOLDVAGGARVREAQKRVEAA QETVADVQOTIKKYRGLTAHLQDUAGLEVVQQQREALKER OETFFKIKFAETKAIKALIEMELRGOLDVAGGARVREAQKRVEAA QETVADVQOTIKKYRGLTAHLQDUAGLEVVQQQREAPLQEELSG AESTIDELGEQUDAALGABEMVENLTORANDRAWCHAA SFLREGGGAGGGLSFAAIGLYY\SLMPAAGHRYHRY*CHALSQCK LD\VYKKVGSLYPEMSAHERSLDPLIELLHKOQLDETVINVEPLT KAIKYYGHLSYHLLARGPEDCTMGAHIKFTGSALDCMSVEVG RLARAFLQGGGATDLALLLRDLETSCS\DIRGCKKIRRNMPGT DAPGIPAALAPGQGATDLALLLRDLETSCS\DIRGCKKIRRNMPGT DAPGIPAALAPGQQVSTLALLELAFKASEQIYGTPSSSPYECKRGGCNIL ISTMNX\LVTAMQEGEYDAERPPSKPPVVELERAALRAEITDA EGGLLKLEDRETVI KELKKSLKKRGBLSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFETMDALQADIDQL EAEKABLKGRLKNGSKRTIBCLRGPPPSGTATUSGTAUSGTAGGEGGG GATGGAPGSVEGPGLVKDSPLLLQGISAMRHISCHENDTWKL KGAQMKASLASLPPHTVARKLSHEGGGSELPAGALYRKTSQLLET LNQLSTHTHVVDITTSPSAAXSPAALRSOETTVAGK KVTFSCAAGFGGRHKULTGGGLHGLMSALIS 5377 762 1106 DVPKKRVLPAEAGGGGTISCGGGGG FFYHBVRQAGGGS* /WGGPMVRLVHTQLKTKRSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGGWGGQYTPIFRGRWEBQP 5378 2009 664 OASGTTLRFEPEDPGLKRREATSRNRALKPRGRUVLWTSCLPAL		1		
GKNPCKKTHLVAHSRVISGERPPRLARKCORFFLPRASQSGGRN SABPNAPRFOFVCPDCGKAFFHKYLAAHRPIATPAEKPYVCP DCRKAFSQKSNL\VSHRRIHTGERYYACPDCDRSFSGKSNLITH RKSHIRDGAPCCAICGQTFDDEERLIAHGKKHDV 5376 4504 591 VSTFSLCLWPAGGGGRGRVSNMAQSKHVYSRTPSGSRMSAEAS ARPLRVGSRVEVIGKGHRGTVAYVGATLFATSKWGVILDEAKG KNDCTVGGRKYFTCDEGHGIFVRQSQIQVFBGADTTSPETPDS SASKVLKREGTDTTAKTSLIKGIKPKKAPTARKTTRRPKPTRP ASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLAAPIIPTP VLITSPBAVAVPPLPSPSKEBEGLRAQVRDLEEKLETLRKAEDKA KLKELEKHKIQLEQVQEWKSKWAYGQQADLQRRIKFARKBALK EAKERYMEMADTADAIEMATLDKEMAEERABSLQOEVEALKER VDELTTDLEILKAEIBEKGSGASYQLKQLEEGONARKUDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNIALIEEKVERLERTVG GETVADVQQTIKKYRQLTAHLQDVRELTUNQGASVERQQQPPP ETTDFKIKFAETKAHAKAIEMELRQMWAQARRHMSLLTAFMPD OETVADVQQTIKKYRQLTAHLQDVRELTUNQGASVERQQQPPP ETTDFKIKFAETKAHAKAIEMELRQMEVAQARRHMSLLTAFMPD SFLRPGGDHICVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGUVY\SLMPAAGHRYHKY*CHALSQCK LD\VYKKVGSLYPBMSAHERSLIFLIELHKUQLDETVNVEPL KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFFLQGGGATDIALLLRDLETSCS\DIRGFCKKIRRMPGT DAPGIPALAFPGVOSTOLILDETSCS\DIRGFCKKIRRMPGT DAPGIPALAFPGVOSTOLILDETSCS\DIRGFCKKIRRMPGT DAPGIPALAFPGVOSTOLILDETSCS\DIRGFCKKIRRMPGT JAPLAENEGLUVAALEELAFKASEQIYGTPSSPYECLRGSCNIL ISTMK\LVTMAQEGEYDARRPPSSPYPCLRGSCNIL ISTMK\LVTMAQEGEYDARRPPSSPYPCLRGSCNIL ISTMK\LVTMAQEGEYDARRPPSPPPSGIATUVGGTAGEGQQ GAITGGAPGSVPGPGUVKDSLILQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSKEGEGSSENPAALTRILSGLAET LNQLSTHTHVUTTTRTPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRRGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTTSCAAGFGQRHRLVUTQRQLHQLHSRLIS 5377 762 1106 DVPCKRVIDARGGQYVTFIFRGMKWEEQP 5378 2009 664 QASGTTLRFLPDDLPQLKREAFRRRALKFRGRUVLWTSCLPAL		1		
SABENAPRGPFVCPDCGKAPRHKPYLAAHRPIATPAEKPYVCP DCRKAFSQKSNLIVA DCRKAFSQKSNLIVA S91 VSTESICLWPAGGGGGRGVSNAPQSKRHVYSRTPSGSRMSABAS ARPLRVGSRVEVIGKGHRGTVAYVGATLFATGKWVGVILDEAKG KNDGTVCGRKYFTCDEGHGIFVGSQIQVFBIGADTTSPETPDS SASKVLKREGTDTTAKTSKLRGLKPKKARPTARKTTRTPKFTPP ASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLAAPIIPTP VUTSPGAVPPLPSPSKEBGLRAQVRDLEEKLETLRKRAEDKA KLKELEKHKIQLEQVQBWKSKMQEQQADLQRRLKEARKRAEAL EAKRRYMENADTADAIEMATLDKBMAERRABSLQGEVGALKER VDELTTDLEILKAEIBEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVGQCRERLQEELSQ AESTIDELKEQVDAALGAEBWHMITDRNALIEEKVRELRETVG DLEAMMEMNDBLQBNARETELBLRSQLDWGARKKWAQA QETVADYQQTIKKYRQLTAHLQDVVRELTNQQEASVERQQQPPP ETFDFKKKFAETKAHAKAIEMELRQMEVAQANRIMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIKQAQKFFELSENGSE RPGLRGAAGGQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFILELHKQLDDETVNVEPLT KAIKYYGHLYSIHLARQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGQGAFDIALLLRDLGSCS\DIEDKFCKKTRRMPGT DAPGIPAALAFGPQVSDTLLLDCRCKKKTRRMPGT DAPGIPAALAFGPQVSDTLLDCRKKHTWVAVLQEVAAAAQLI APLAENEGLLVAALEELAFKASEQIYGFTSSSPYECLRGSCNIL ISTMNK\LVTMAGGGFYDAERPSPPFVVSIKAAALRABITDL GEGLGKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFETMDALQADIDQL EAEKAELKGRLNGSKRTIEGERPPSGIATLVSGLAEGQG GAIPGQAPGSVPOPGLVKDSPLLLQOISAMLHISQLDETNIKEL LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRRGATVPTDFATFFSSAFLRAKEGQQDDTVYMG KVTFSCAAGFGQRHLVLTTQEQLHQLHSRLIS 1005HTHTWVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRRGATVPTDFATFFSSAFLRAKEGQQDDTVYMG KVTFSCAAGFGQRHRLVLTTQECHHGLHSRLIS SSYNBGYDGWGGGYVFIFFRGMKWEGQP 5378 2009 664 QASGTTLRFLPDDLFQLKREATSRNRALKFRGRLVLMTSCLPAL	{	[1 ~
DCRKAFSQKSML\VSHRRIHTGERPYACPDCDRSFSQKSNLITH RKSHIRDGAFCCAlCGQTFDDEERLLAHQKKHDV 5376 4504 591 VSTFSLCLWPAGGGGGROSWMAGSKHVYSRTPSGSRMSAEAS ARPLRVGSRVEVIGKGRGTVAYVGATLFATGKNVGVILDEAKG KNDGTVQGRKYFTCDEGHGIFVATQSQIQVFEDGADTTSPETPDS SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTTTRPKPTRP ASTGVAGASSSLGPSGSASAGELSSSEPSTPAOTPLAAPIIPTT VLTSPGAVPPLPSPSKEEEGERGAQVRDLEEKLETLRLKAREDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKEAKEAL EAKERYMEEMADTADAIEMATLDKEMAEERAESLQGEVEALKER VDELITTDLEILKAEIEBKGSGAASSYQLKQLEEQNARLKHDALV RMRDLSSSEKQEHVK\LQKLMEKKNQBLEVVRQQREBLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNINLEEKVRELRETVG DLEAMMEMNDELGENARETELELREQLDMAGARVREAQREVEAA QETVADVQQTIKKYRQLTAHLQDVNTRELTMQDEASVERQQQPPP ETFDFKIKFAFAKAHAKIEMELGNEVAQANRIMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGSQLSFAAIGLVY\SLMMAGARKYHSY*CHALSQCK LD\VYKKVGSLYPBMSAHERSLDFLIELLREQDLDTWAPLTFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGSQLSFAAIGLVY\SLMMAGARKYHSY*CHALSQCK LD\VYKKVGSLYPBMSAHERSLDFLIELLREQDLDTWAPLTFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGSQLSFAAIGLVY\SLMMAGARKYHSY*CHALSQCK LD\VYKKVGSLYPBMSAHERSLDFLIELLREQDLDTWEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLRADLETSCS\DIRQFCKKIRRRMPGT DAPGIPAALAFGPQVSSTILLDCRRHTWVAVLQEVAAAAQLI APLAENEGLLVAALEELAFKASEGIYGTFSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPPVVELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLITLEKKLDS AAKDADERIEKVQTRLEETQALLRKKKKFFEETMDALQADIDQL EAEKKALKQRLNSQSKRTIERGPPSGLATLVSGIGAGEGQQ GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVVDTRTSTBAAKSPBQLMEGVYQLKSLSDTVVEKL KDEVLKSTVSGRPGATVPTDFATFFSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRRHLVUTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQUTIFIFRGMREEGP 5378 2009 664 QASGTTURFLPDDLYKKKEBGTSKNRALKFGGRLVLMTSCLPAL	}	1 .	ł	(
RKSHIRGAFCCAICGQTFDDERLLAHQKKHDV 5376 4504 591 VSTTSLCLWPAGGGGRGVSNMAQSKRHVYSRTPSGSRMSAEAS ARPLRVGSRVEVIGKGHRGTVAYVGATLFATGKKVGVILDEAKG KNDGTVQGRKYFTCDEGHGIFVAYVGATLFATGKKVGVILDEAKG KNDGTVQGRKYFTCDEGHGIFVAYVGATLFATGKKVGVILDEAKG KNDGTVQGRKYFTCDEGHGIFVAYVGATLFATGKKVGVILDEAKG KNDGTVQGRKYFTCDEGHGIFVAYVGATLFATGKKVGVILDEAKG KNDGTVQGRKYFTCDEGHGIFVAYVGATLFATGKKVGVILDEAKG ASTOVAGASSSLGPSGSASAGELSSSFSTPAGTPLAAPIIPTF VLTSPGAVPPLPSFSKEEGGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEGVVGEWKSKMQEQQADLQRRLKEARKEAKEAL EAKERYMEEMADTADAIEMATLDKEMAEERABSLQCEVEALKER VDELTTDLEILKABIBEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\QCUMEQCRAPLQGELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVJ DLEAMMEMNDELQENARETELELREQLDMAGARVREAQKRVEAA QETVADVQQTIKKYRQUTAHLQVRACHKVQCASVERQQOPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFIRPGGDHDCVLVLLLMPRLICKGLIRRQAQBKFELSENCSE RPGLRGAAGBGLFSAAIGUVSJAMPAGHRYNKY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELHKDQLDETVNVEPLT KAIKYYQHLYSIHLARQPEDCTMQLADHIKFTQSALDCMSVEVQ RLRAFFLQGGGGRATDIALILADLETSCS\DIRPGYCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRRHLTWVAVLQEVAAAAAQLI APLAENEGLLVAALBELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEVDARPPSKPPP\VELRAAALRABITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLITLLEKKLDS AAKDADER IEKVQTRLEETQALLARKKEKFEETMDALQADIDQL EAEKAELKQRLINSQSKRIIEGLRCPPPSGTATLVSGIAGEEQQR GAIFGQAPGSVFGFGLVKDSPLLLQGISAWRLHISQLQHENSIL KGQMKASLASLPPLHVVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSFAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKSTVSQRPGATVPTDFATFFSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGORRLVLTOFGQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAGEKGQITISCGESEGFEGYFYHEVRQAEGES* /WGDNVRLVHTQLKTKKPSGTLKAKKYLHTGSTKFAARISCTK SS*WPGYDGWGGQYIFIFPGDERGELTGALFTVLTGTKFAARISCTK SS*WPGYDGWGGQYIFIFPDDPQLKRREATSRNRALKFRGRLVLMTSCLPAL	· ·		7	1
S376 S91 VSTFSLCLWPAGGGGRGRVSNMAQSKRHVYSRTPSGSRMSAEAS ARPLRVGSRVEVIGKGHGGTVAYUGALFATGKNVGVILDEAKG KNDGTVGGRKYFTCDEGHGFFFORGOTQVFEDGADTTSPETPDD SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTTTRPKPTRP ASTGVAGASSSLGPSGSASAGELSSSESSTPAGTPLAAPIIPTT VLTSPGAVPPLPBFSKEEGEGRAQVRDLEEKLETLRLKKAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKEAKEAL EAKERYMEEMADTADAIEMATLIKEMAEERAESLQGEVEALKER VDELTTOLETILKAEIEBEKGSDGAASSTQLKQLEEQNARLKHOALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDBLKEQVDAALGAEEMVEALITDRNLNLEEKVEELEETVG DLEAMMENNDELQENARETELELERQLDMAGARVREAQKEVEAL QETVADVQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFOFKIKFAETKAHAKAIEMELRQHEVAQANRHMSLLTAFMPPD SFLKPGGDHDCVLVLLLMPRICKAELIKRQGEKFELSENGSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELHLHKOQLDETVNVEPLT KAIKYYGHLVSIHLAEQPEDCTMQLADHIKFTGSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGQQVESTILLDCRKHLTWVVAVLQEVAAAAAQLI APLAENBGLLVAALBELAFKASEGIYGTPSSPYECLRGSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPPVVELRAAALRAEITDA EGGGLKLEDRETVIKELKKSLKIKGEELSEANNVELTLEKKLDS GEGGLKLEDRETVIKELKKSLKIKGEELSEANNVELTLEKKLDS GANADBRIEKVOTRLEETQALIKKKKEFETETMDAIQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIFGQAPGSVPGPGLVKOSPLLLGGISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGGSLEPAGALYRTKSCLLET LNQLSTHTVVVITRTSFAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRAGATVPTDFATFFSSAFLRAEEQQDDTVYMG KVTFSCAAGFGGRRINLVLTGGLGHGHSRISIS 5377 762 1106 DVPCKRVLPAEAQEKGQITLSCGESGEEG\F*YHEVRQAEGES* /WGGPNVRLVHTQLKTKKPSGTLKAKKYLHTGSTKFAARISCTK SSWPQYDGWGQYIFIFTGGLGHGHSRISIS	1	Ì	[DCRKAFSQKSNL\VSHRRIHTGERPYACPDCDRSFSQKSNLITH
ARPLRVGSRVEVIGKGHRGTVAYVGATLFATGKWVGVILDEAKG KNDGTVQGRKYFTCDEGKGIFVTQSQIQVFEDGADTTSPETPDS SASKVLKREGTDTTAKTS KLRGLKPKKAPTARKTTTRPRPTRP ASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLAAPIIPTP VLTSPGAVPPLPSPSKBEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKKKIQLEQVQEW KSKWQEQQADLQRRLKERAKKARLEL EAKERYMEEMADTADAIEMATLDKKMAEERASSLQGEVEALKER VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQWARLKDALV RMRDLSSSEKQEHVK\LQKAMEKKNQELSVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEMVEMLTDRNINLEEKVRELRETVG DLEAMNEMNDBLQENARETELELRBQLDMAGARVREAQKRVEAA QETVADVQQTIKKYRQLTAHLQDVRRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQAKRHMSLLTAFMPD SFLRPGGDHDCVLVLLMPRLICKAELIRKQAQSKFELSENCSE RPGLRGAAGGGLSFAAIGLVYSLHPAAGHRYHRY*CHALSQCR LD\YYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLABQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRGFCKKIRRMPGT DAGGIPAALARGPQVSDTLILDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVVALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQSGEYDAERPPSKPPP\VELRAAALRAEITDA GGLGLKLEDRETVIKELKKSLKIKGEBLSEANVRLITLLEKKLDS AAKDADERIEKVQTTLEERLGDFPPSGIATLVSGIAGEBQQR GAIFGQAPGSVPGPGLVKDSPLLLQGISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALVRKTSQLLET LNQLSTHTHVVDITRTSFAAKSPSAQLMEQVAQLKSLSSTVEKL KDEVLKETVSQRPGATVPTDFATTFSSAFLRAKEGQDDTVYMG KVTFSCAAGFGORHRLVLTQGGLHGNALIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGEGGEGG\F*YHEVRQAEGES* /WGDNVRLVUTQLKTKKRPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQVYLTLGRGRWEEQP 5378 2009 664 QASGTTLRPLPDLDEDLRKRRATSRNRALKPRGRLVLMTSCLPAL	Į.	1		RKSHIRDGAFCCAICGQTFDDEERLLAHQKKHDV
KNDGTVQGRKYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDS SASKVIKREGTDTTAKTSKIRGLKPKKAPTARKTTTRRPKPTRP ASTOVAGASSLGPGSGSAGGELSSEPSPAQTPLAPIIPTP VLTSPGAVPPLPSPSKEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEGVQEWKSKYGEGQADLQRRLKEARKBAKEAL EAKRRYWEMBADTADAIERABSLOGVERLKKERKBAKEAL EAKRRYWEMBADTADAIERABSLOGVERLKKERKBAKEAL ODELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKGQVDAALGAEWVEMTJORNINLEEKVERLERTVG DLEAMNEMNDELQENARETELELRBQLDMAGARVREAQKRVEAA QETVADVQQTIKKYRQLTAHLQDVNRELTINQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMBLRQMEVAQANRHMSLLTAFMPD SFIRPGGDHDCVLVLLLMPRLLCKAELIRKQAQEKFELSENCSE RPGLRGAAGGGLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELHKDQLDETVNVEPLT KAIKYYOHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLRDLETSCS\DIRGPCKKIRRRMPGT DAPGIPAALAPGPQVSDTLLLCRKHLTWVAVLQEVAAAAQLI APHAENSGLLVAALBELAFKASGQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRABITDA EGLGLKLEDRETVIKKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEVQTRLEETQALLRKKEKFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIFGQAPGSVPPGGLVVRDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGGGSELPAGALYKKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFFSSAFLRAKEEQDDTVYMG KVTPSCAAGFGORNHLVLTQECLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEG\F*YHEVRQAEGES* /WGDPNVRLVHTQLKTKKRPSGTLKAKFYLHTGSTKFAARISCTK SS*WGCYGGGGQYTLSTGRGWEEQP 5378 2009 664 QASGTTLRPLPDDFQLKRREATSRNRALKPRGRLVLMTSCLPAL	5376	4504	591	VSTFSLCLWPAGGGGRGRVSNMAQSKRHVYSRTPSGSRMSAEAS
SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTTTRRPKPTRP ASTOVAGASSIGPSGSASAGELSSSEPSTPAQTILAPI1PTP VLTSPGAVPPLPSPSKEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKEAKEAL EAKERYMEEMADTADAIEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEKGSGGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEMVEMITDRILLEKVRELETVG DLEAMINEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADVQQTIKKYRQLITAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFILRPGGDHDCVLVLLLMRRLICKAELIRKQAQEKFELSENCSE RPGLIRGAGEQUSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLARQPEDCTIMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQBATDIALLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRSPPSSGIATLVSGIAGEEQQR GAIFGQAPGSVPGPGLVKOSPLLLQISAMLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSFAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEQDDDTVYMG KVTFSCAAGFGQRHLIVLTQCEUQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /MFCPNWRLVHTQLKTKKPSGTLKAKKYLHTGSTKFAARISCTK S*MPGVDGWGGQVIFIFFRGMRMEBQP 5378 2009 664 QASGTTLRPLPDDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	į	l		ARPLRVGSRVEVIGKGHRGTVAYVGATLFATGKWVGVILDEAKG
SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTTTRRPKPTRP ASTOVAGASSIGPSGSASAGELSSSEPSTPAQTILAPI1PTP VLTSPGAVPPLPSPSKEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKEAKEAL EAKERYMEEMADTADAIEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEKGSGGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEMVEMITDRILLEKVRELETVG DLEAMINEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADVQQTIKKYRQLITAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFILRPGGDHDCVLVLLLMRRLICKAELIRKQAQEKFELSENCSE RPGLIRGAGEQUSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLARQPEDCTIMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQBATDIALLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRSPPSSGIATLVSGIAGEEQQR GAIFGQAPGSVPGPGLVKOSPLLLQISAMLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSFAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEQDDDTVYMG KVTFSCAAGFGQRHLIVLTQCEUQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /MFCPNWRLVHTQLKTKKPSGTLKAKKYLHTGSTKFAARISCTK S*MPGVDGWGGQVIFIFFRGMRMEBQP 5378 2009 664 QASGTTLRPLPDDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	ł	1		KNDGTVOGRKYFTCDEGHGIFVROSOIOVFEDGADTTSPETPDS
ASTGVAGASSSLGPSGSASAGELSSEPSTPAQTPLAAPIIPTF VLTSPGAVPPLESPSKEEGLRAQVRDLEEKLETLRLKKAEDKA KLKELEKKKIQLEQVOEWSKMCBQQADLQRRLKERAKEAL EAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVEALKER VDELITDLEIILKAEIBEKGSDGAASSYQLKQLEEQNARKKDALV RMRDLSSSEKQEHVKLQKLMEKKNQELEVVRQQRERLQEELSY AESTIDELKEQVDAALGAEEMVEMLITDRNINLEEKVRELRETVG DLEAMNEMNDBLQENARETELELRBQLDMAGGRVERAQREVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFOFKIKFAETKAHAKAIEMERQMEVAQANRHMSLLTAFMPD SFILRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\YYKKUGSLYPEMSAHERSLDFLIELLHKDQLDETUNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGQVGSUTDLDCRHLTWVVAVLQEVAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMKK\LVTAMQEGEYDAERPPSKPPP\VBLRAAALRAEITDA EGLGLKLEDRETVIKELKSLKIKGBELSEANVENLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRINSQSKRTIEGLRGPPPSGTATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQIMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGGRHRLVLTQGCHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEGG\F*YHEVRQAEGES* /MFGPNVRLVHTQLKTKKPSGTLKKKFYLHTGSTKFAARISCTK SS*MPGYBORWGGQVIFIFRGMRXEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	· ·	1	Į	
VLTSPGAVPPLPSPSKEEGLRAQVRDLEEKLETLRLKRAEDKA KLKBLEKHRIQLEQVQEWKSKMQEQQADLQRRLKEARKBAKEAL EAKERYMEEMADTADAIEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLINLEEKVRELRETVG DLEAMNENNDBLQENARBTELELRBQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMLRQMEVAQANRIMSLLTAFMPD SFLRPGGDDCVLVLLMMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETUNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGGEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMKK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGIGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIFGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSISDTVEKL KDEVLKETVSQRPGATVVDTDFATFPSSAFLRKEEQQDDTVYMG KVTFSCAAGFGQRHRLVITGEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*MPGYDGWWGGQYLFIFFGGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	1	1		
KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKEALE EAKRRYMEMADTADAIEMATLDKEMAEERABSLQQEVEALKER VDELITDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNENNDBLQENARETELELRRQLDMAGARVREAQKRVERAA QETVADYQQTIKKYRQUTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELHKUQDLETVNVEPLT KAIKYYQHLYSHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLRDLETSCS\DIRQFCKKIRRRMPGT DAPGIPAALAPGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGTATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQUISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSFAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQUTLSCGESGEEG F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK S*WPGYDGWWGGQYIFIFRGMRWEBQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	ł			1
EAKERYMEEMADTADAIEMATLDKEMAEERABSLQQEVEALKER VDELTTDLEILKAEIEBKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGABEMVEMLITDRNIANLEEKVRERLERTVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELINNQQBASVERQQPPP ETFOFKIKFABTKAHAKATEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SIMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCIMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTMVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTFSSSPYECLRQSCNIL ISTNKK\LVTAMQGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIFGQAPGSVPOFGLVKDSPLLLQQISAMRHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITTRTSFAAKSPSAQLMEQVAQLKSLSDTVEKL KGEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQUTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKAFYYLHTGSTKFAARISCTK SS*WFGYDGWWGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	J.		·	
VDELTTDLEILKAEIEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQBELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMDBELQENARETELELRBQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVILLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGBYDAERPPSRPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLBETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGTATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYKKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVIKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEURQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	ļ	:		
RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEKVRELRETVG DLEAMNEMNDELQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLYY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMEGBYDAERPPSKPPPVVELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTOEQLHCHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEGFF*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDCWWGGQYFIFFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	ł	}	ł	1 ·
AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDELQENARETELEELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRNPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTBSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPPVVELRAAALRAEITDA EGLGKLEDRETVIKELKKSLKIKGEELSEANVRUTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIEGQAPGSVPGPGLVKDSPLLLQUISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITTRTSPAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGORHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEC *YHEVRQAEGES* /WPGPNORLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	1	,		l "" , " , " , " , " , " , " , " , " , "
DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFABTKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLRDLETSCS\DIRQPCKKIRRMPGT DAPGIPAALAPGPQVSDTLLDCRKHLTWVVAVLQEVAAAAQLI APLABNEGLVAALEELAFKASEQIVGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLBETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEGQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGGRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	,			
QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAPGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRABITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRIVLMTSCLPAL		İ	l	
ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SIMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVVNEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGSYDAERPPSKPPP\VELRAAALRAEITDA EGLGKKLEDRETVIKELKKSLKIKGEELSEANVRITLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFESTMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIFGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVIKETVSQRRGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				
SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTFSSSPYECLRQSCNIL ISTMMK\LVTAMQEGETDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEGG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				
RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLERDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMIK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLITLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIPRGMRWEBQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	I			ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD
LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL]	J		SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE
LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	1	l		RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR
KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	l	1		1
RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAPGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	1) .		1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -
DAPGIPAALAPGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGORHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	l			
APLAENEGLLVAALEELAFKASEQIYGTFSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	}		i	,
ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	ì	}		DADGTDAALARGDOVSDYLTDCDKRITAMVVAVITOKVAAAAACIT
EGLGLKLEDRETVI KELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADER I EKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL]			
AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL
EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA
GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS
KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL
LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR
KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR
KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL
KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS 5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET
5377 762 1106 DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL				APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL
/WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS+WPGYDGWWGGQYIFIFRGMRWEEQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL		·		APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG
SS+WPGYDGWWGGQYIFIFRGMRWEBQP 5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	5377	762	1106	APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS
5378 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL	5377	762	1106	APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES*
	5377	762	1106	APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK
RF1ATPKL5AMPH1DNDVKLDFKDVLLRPKRSTLKSRSEVDLTR				APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP
				APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS DVPCKRVLPAEAQEKGQITLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGWWGGQYIFIFRGMRWEEQP QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	\=possible nucleotide insertion)
	sequence		SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD
	}	{	VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
	[1	Abower and the second of the s
]	\	KHYSLVQWQEFAGQNPDCLBHLAASSGTGSSDFEQLEQILEAIP
	1	1	QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
	1	10	EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
	Í	1	HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
	ì	i	ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
		1	PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ
	(VNPIFSEAC
		<u> </u>	QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL
5379	2009	664	OWOCITIES OF WORLD PROVIDE DESCRIPTION OF THE PROPERTY OF THE
•	1	Í	RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR
	1		SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD
	1		VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
•	1	1	KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
	}	}	OVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
			EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
	! .		HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
	,	1	ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
			PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ
		1	1
		<u> </u>	VNPIFSEAC
5380	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
	ł		SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME
	Į	1	SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
ł	i	1	SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
}	1	1 .	RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
	ì	·	YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
Į.	1	Í	RGPI/EQVYQEIA/ILKKLDHPNVV/KLVEVL/DDPNEDHLYMV
]	1	1	KGAI /EOA I OETA / ITRUTTURA A / VETA E A PARA DE MEDITEMENT
1	1	ı	F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII
1	1	ı	H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
			FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM
	l .]	CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI
ł	1	1	KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV
· ·	1	1	ILVKTMIRKRSFGNPFEGSRRBERSLSAPGNLLTKKPTRECESL
[1	1	SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR
ì	ł	}	*PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL
1			PDLVGAPGSHFCFLNIALLRYNSHTM
			PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
5381	2	2050	PSKAGGAEKGKAAAAKSPGGSAAGWECPSVDDAAGACINSSCVS
1			SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME
			SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
1		1	SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
[RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
ł		į.	YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
J	1	j	RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV
1			F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII
i			H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
1			H\KDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNIVGTPA
1			FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM
1	1		CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI
1			KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV
1			ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL
Į.	1	1	SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR
1	1 .		*PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL
1	1	Í	PDLVGAPGSHFCFLNIALLRYNSHTM.
L		_	GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS
5382	1536	203	GARGSQQDAPALQEAEVKGPERAQPAKGKITKAKDFKDWDVDGS
Ī		(VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE
		ļ	LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG
1			YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD
1	i	1	DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH
1			RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL
	1		KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV
1	1	1	RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH
1	1	1	KOPHOPAKLGARGLPKWPQ\VSFAMTIQIDDPRILEKLAPPNEH
ĺ	ľ	[WRQVYRLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDLAAPLP

Deginning nucleotide location corresponding to first amino acid amino acid residue of amino acid sequence provided to first amino acid	SEQ	Predicted	Predicted end	
No: nucleotide	1 -			Amino acid segment containing signal peptide
corresponding to first amino acid amino acid residue of amino acid residue of amino acid amino acid sequence se			· ·	(A=Alanine, U=Cysteine, D=Aspartic Acid, E=
Cotresponding	l wo:	l e e e e e e e e e e e e e e e e e e e	1	Grucamic Acid, r=rnenylalanine, G=Glycine,
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid sequence s]			
amino acid residue of amino acid sequence seq	1			
meino acid sequence ##TYPYDOPHAIN, Y=TYPYDOPHAIN, Y=DYDOPHAIN, S=Dtop Coden, /=possible nucleotide deletion, Popering psystempter insertion ### PERFORP psystempter insertion ### PERFORP psystempter psychonycytyperptyperyper ### PERFORP psystempter psychologytyperptyperyper ### PERFORP psystempter psychologytyperptyper ### PERFORP psystempter psychologytyperptyp	1		N .	
amino acid sequence	1			
Sequence				w=Tryptopnan, Y=Tyrosine, X=Unknown, *=Stop
PELEGGP PSSWEEDWRAKI PLAWROCLYKLYEADPVLFGYPXP RNLLRD 5383 45 5250 VERLIGCENSKRYPRINLISKOMPWRRJGG IS FGWYSARELKKLIS VESTITREYLDGLINDRAWGYTURLERADAS KYCYTOVOPEN CGGHLGHI ELIPLTYVYPLLIFOKLYLLLRGGCIAKOMINTCPRAYI HLLLCQLPVLEWGLAGOVYELREN ILSPELEBANDPSSBE IREIL BOYTTEIVOSINLIAS GGARIVKNYCESISKI TALFWKAMMAKKC PHCKTGSVYREIBHSKLITTPPAWINTRAGKOSEPJETEEL BOYTTEIVOSINLIAS GGARIVKNYCESISKI TALFWKAMMAKKC PHCKTGSVYREIBHSKLITTPPAWINTRAGKOSEPJETEEL BOYTTEIVOSINLIAS GGARIVKNYCESISKI TALFWKAMMAKKC PHCKTGSVYREIBHSKLITTPPAWINTRAGKOSEPJETEEL BOYTTEIVOSINLIAS GGARIVKNYCESISKI TALFWKAMMAKKC PHCKTGSVYREIBHSKLITTPPAWINTRAGKOSEPJETEEL BOYTTEIVOSINLIAS GGARIVKNYCESISKI TALFWKAMMAKKC PHCKTGSVYREIBHSKLITTPPAWINTRAGKOSEPJETEEL BOYTTEIVOSINLIAS GGARIVKNYCESISKI TALFWKAMMAKKC PHCKTGSVYREIBHSKLITTPPAWINTRAGKOMEN TOKK SILDKINTSI HELGENIN TOKKTON TOKKTON SILDKINTSI HELGENIN TOKKTON TOKKTON GERVAKGLITPATGAPKOCHTIVCTEN TOKKTON TOKKTON OPENVAKGLITPATGAPKOCHTIVCTEN TOKKTON OPENVAKGARANACHTON OPENVAKGLITPATGAPKOCHTIVCTEN TOKKTON OPENVAKGLITPATGAPKOCHTIVCTEN TOKKTON OPENVAKGLITPATGAPKOCHTIVCTEN TOKKTON OPENVAKGLITPATGAPKOCHTIVCTEN TOKKTON OPENVAKGLITPATGAPKOCHTIVCTEN TOKKTON OPENVAKGLITPATGAPKOCHTIVCTEN TOKKTON OPENVAKGLITPATGAPKOCHTIVCTEN TOKKTON OPENVAKGLITPATGAPKOCHTIVCTEN TOKKTON OPENVAKGLITPATATATATATATATATATATATATATATATATATATA			sequence	
5383 45 5250 VERLICKENSKRTWRRILTSKNMBWRRIGG ISFOMYSABELKKILS VESITHREYLIDSLANDFANGLYDLLALGPADSKRUCSTCVODESN VESITHREYLIDSLANDFANGLYDLLALGPADSKRUCSTCVODESN HILLOQLEVLBUGGLAUVERLERSLISTERSCHAMMARKE EQYTTEIVONNLISSCGAHVENVOSSKILTLEFKENADPSABETREEL EQYTTEIVONNLISSCGAHVENVOSSKILTLEFKENADPSABETREEL EQYTTEIVONNLISSCGAHVENVOSSKILTLEFKENADPSABETREEL EQYTTEIVONNLISSCGAHVENVOSSKILTLEFKENADPSABETREEL EQYTEIVONNLISSCARLISTANTSKENLISTERDENDESSEPLEER IGKRUTHEN EN STANDEN EN STANDEN JEKKLALMAGGKULPENSARENLISTANTSKENDOMERSEPN PSVPFLDELVVDPBRRSEDVSHLOMMTNOOTVILQAVMKDUVL, IRKLALMAGGKULPENSARENLISTANTSKENDOMERSEPN SALDKLANTSELGOMETNOOTVILQAVMKDVIL, IRKLALMAGGKULPENSARENLISTANTSKENTENDOM SLIDKLINSTEELGOMETNOOTVILQAVMKDVIL REKURLANGGKULPENSARENLISTANTSKENTENDOM GREAVAKOLLTDRAGPROCTSTEUTVILTSELGTENVERTLITYP OPVTPRINGELGOVI INGRIVERGASTUTENDESTALTSPETLOP GREAVAKOLLTDRAGPROCTSTEUTVILTSELGTENVERTLITYP OPVTPRINGELGOVI VINGROVERSKOLLTANTSELGTEN TENDET RESOLUTERSELLOVILDSENSARI VINGROSPALISTANTSKENT GREAVANCALTURESCHATTOKAVATARENDEDBINALFPORS ELGREAVAVLATTOKOVALTERSKOLLTON TENDETSCHAMP RESOLUTERSELLOVILDSENSARI VINGROSPALISTANTSKENTENDOM ESOLUTIOLAR ELEVATION TENDETSCHAMP ELGREAVALLETENDOMERSELLOVILDSENSARI VINGROSPALISTANT MOTSCLLICKTERSTEUTVILTSELGOMETSKANT TOKKORSHIPPTILGE COPONYRALMEDERAS VIDERCHANDESSANTOLUTERSTETT OCHOONING TENDET COPONYRALMEDERAS VIDERCHANDESSANTOLUTERSTETT COPONYRALMEDERAS VIDERCHANDESSANTOLUTERSTETT COPONYRALMEDERAS VIDERCHANDESSANTOLUTERSTETT MOTSCHAMPEN TOLUTERS COPONYRALKEESSANTANT TOLUTERSTETT OCHOONING TENDET ERSTANDAM TENDETSCHAMPEN TOLUTERSTETT TOLUTERSTETT COPONYRALMEDERAS VIDERCHANDESSANTOLUTERSTETT MOTSCHAMPEN TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTERSTETT RESIDENCE TOLUTER		sequence	<u> </u>	
S383 S250 VERLICENSKRIPMENLISKINPERIKLGI SFORMSZEERUKZ	1	i	1	
VKSITMPRYLLDSIGNPEANGLYDLALGREADSKEVCSTCYQUES CGGHLGHIELDLYTWYNILDSIGNLYCHLICHGSCLUNGHTCPRAVI HLLLCQLRVLEVGALQAVYELBRILLGRIELERIADPSASSITERS CGGHLGHIELDLYTVYNILDSIGNLYCHSKAKLLANPKARNNARC PHCKTGRSVYRKEHNSILITTFPAMWHRTAGOKDSEPLGIEBER ATTTETVONNILLGSGGAHVRKYCESKSKLILAPKARNNARC PHCKTGRSVYRKEHNSILITTFPAMWHRTAGOKDSEPLGIEBER IGKRGVITPTSARERLISALMKNEGFLAVITGOKDSEPLGIEBER PSVPFLDPLVVPPSRSEPVSRLGDOMFTNOGTVNLQAVKKUVL IRKLALMAGOKOLDE EVENTPTTDERKOGLIATDSFILSTUPGO SLIDKLYSHINIRLGSHVNIVFDSSMDCLMMOKYPGIRQILEKER GLFRKHMGKRVDVARASVICEDHYNTNIBGISPHSTLDRO SLIDKLYSHINIRLGSHVNIVFDSSMDCLMMOKYPGIRQILEKER GLFRKHMGKRVDVARASVICEDHYNTNIBGISPHSTLDRO SLIDKLYSHINIRLGSHVNIVFDSSMDCLMMOKYPGIRQILEKER GLFRKHMGKRVDVARASVICEDPLASHININGSSTALSAVOV OREAVAKGLITPATAEPKCYSTKIVCTRIVKOGTULLINGCPTLH RPSIQAHRARILDEEKVLRHYANCKANNADPFGDENNAHTOR CPTTREHYMELVYRGLTDKVGRVVELLSPSILKPPPLMTKKKVV TLLINITEDHILGGKANTTOKAWWKTPRSYPGFNPDSWC ESQVI IRBOBLLCGVLDKARAYGSSATGLVHCCYST YGGSTSSKOW TLLINITEDHILGGKANTTOKAWWKTPRSYPGFNPDSWC ESQVI IRBOBLLCGVLDKARAYGSSATGLVHCCYST YGGSTSSKOW TLLINITEDHILGGKANTTOKAWWKTPRSYPGFNPDSWC ESQVI IRBOBLLCGVLDKARAYGSSATGLVHCCYST YGGSTSSKOW TLLINITEDHILGGKANTTOKAWWKTPRSYPGFNPDSWC ESQVI IRBOBLLCGVLDKARAYGSSATGLVHCCYST YGGSTSGKAW KREWNYSNNIKAGAMPGGALBOPPRINTLLWRGANGKASTVDT MOISCILLGJELGERSTPLMASGKSIDPCFRYSPTPRAGGFVTG RPLTGITKPPSTFPTAMSGCKSIDPCFRYSPTPRAGGFVTG RPLTGITKPPSTFPTAMSGCKSIDPCFRYSPTPRAGGFVTG RPLTGITKPPSTFPTAMSGCKSIDPCFRYSPTPRAGGFVTG RPLTGITKPPSTFPTAMSGCKSIDPCFRYSPTPRAGGFVTG RPLTGITKPPSTFPTAMSGCKSIDPCFRYSPTPRAGGFVTG RPLTGITKPPSTFPTAMSGCKSIDPCFRYSPTPRAGGFVTG RPLTGITKPPSTFPTAMSGCKSIDPCFRYSPTPRAGGFVTG RPLTGITKPPTTAMSCKSIDPCFRYSPTPRAGGFVTG RPLTGITKPPTTAMSCKSIDPCFRYSPTTTAMSGCHDRTLLL SNYKYLLMSCHLHAULSSENDSSVORGHNOSHENDRICHTHLE RQAFLGYSGCKTALARGVKSLKYGLCRVCLGEVLKKIDV SNYKYLMSCHLHAULSSENDSSVORGHNOSHENTALL RAMTYGTAMAGGFTAMATGCHARACTARACTARACTARACTARACTARACTARACTARA	F363	 		
CSGHLGHIELPITTYNTPLIEPEKIYLLIKEGSCINGTMITCPERNYL HLLLCQLRVLEUSCHAQAVYELBEILGRFIEERINDSASSIRREI BQYTTSIVONNLLGSGGAHVRNVCESKSKLIAIFHKAHNNAKE PHCKTGRSVVRKRHNSKLITTPAMVHRTAGOKSEPIGITERQ IGKRGYLTPTSABERLSALMKNEGFELNYLFSGMDDGMESFRF PSVPFEDPLVVPPSSRPPVSRLDGMETMGAVMKDVVL IRKLALMAGOKOLPERVATPTTDERGGSLIAIDESHGSTLEKG SLIDKLYSINIRLGSHVATVEDSSRMVLMMOKYPGAVKDVVL IRKLALMAGOKOLPERVATPTTDERGGSLIAIDESHGSTLEKG GLPRKHMMGRRVDVAARSVICDMYINTNETGIPVVRAKENDVY QPVTPRNVQLIKGAVITOPMYDRASMVLHMOKSTALSAVDPY QPVTPRNVQLIKGAVITOPMYDRASMVLHMOKSTALSAVDPY QRAVAKOLLTPATCAPKPGTKIVCRAVKGOTILLINROPTHIA RPSIGOHRARI LIBERKVLRIKHNAKCANNAPDPGAMATIPGS CFPTERHYMBLIVYRGLTDKVGRVKLLGPSILKRPPIHATGKVYV TLLINIIPEDHIPLMLGGGAKITTGKAWVKETTREYPIHATGKVYV TLLINIIPEDHIPLMLGGGAKITTGKAWVKETTREYPIHATGKVYV TLLINIIPEDHIPLMLGGGAKITTGKAWVKETTREYPIHATGKVYV TLLINIIPEDHIPLMLGGAKITTGKAWVKETTREYPIHATGKVYV TLLINIIPEDHIPLMLGGAKITTGKAWVKETTREYPIHATGKVYV TLLINIIPEDHIPLMLGGAKITTGKAWVKETTREYPIHATGKYVY TLLINIIPEDHIPLMLGGAKITTGKAWVKETTREYPIHATGKYVY TLLINIIPEDHIPLMLGGAKITTGKAWVKETTREYPIHATGKYVY TLLINIIPEDHIPLMLGGAKITTGKAWVKETTREYPIHATGKYVY TLLINIIPEDHIPLMLGGAKITTGKAWVKETTREYPIHATGKYVY TLLINIIPEDHIPLMLGGAKITTGKAWVKETTREYPIHATGKYVY TLLINIIPEDHIPLMLGGAKITTGKAWVKETTREYPIHATGKYVY TLLINIIPEDHIPLMLGGAKITTGKAWVKETTREYPIHATGKYVY TLLINIIPEDHIPLMLGGAKITTGKAWVKETTREYPIHATGKYVY TLLINIIPEDHIPLMLGGAKITTGKAWVKETTREYTHATGKYNAM KREWPHYSMISHLAKAMAPPOLAUTAVKTSTRAYCHIPLMLKGCHAMATGKA KREWPHYSMISHLAKAMAPPOLAUTAVKTSTRAYCHIPLMLKGCHAMATGKA KREWPHYSMISHLAKAMAPPOLAUTAVKTSTRAYCHIPLMLKGCHAMATA SNIPETYMKSGHLHUKULGSGAKAMAHAMAPPOLAUTAVKTSTRAYCHIPLMLKGCHAMATA SNIPETYMKSGHLHUKULGSGAMAPPOPOLAUKAMAPPOLAUTAVKTSTRAYCHIPLMLKGCHAMAPPOLAUTAVKTSTRAYCHAMAPPOLAUTAVKTSTRAYCHAMAPPOLAUTAVATKGTTHAA KREMPARAYCHAMAPPOLAUTAVATKGTTAWAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	5383	45	5250	
HILLICQUEVIEWSALQAVYELERILGRELERIADPSASTITERS POTTETIONNILGSGGAHYMYCERSKENLIAHRAMNARAC PHCKTGRSVYRKEHNSILITTEPAMVHERJAQKDSEPLALIERS PHCKTGRSVYRKEHNSILITTEPAMVHERJAQKDSEPLALIERS JGKRGVLPPTSABERLSALAKHREFFINVIPSENDDOMBSERFN PSVPFLDFLVVPPSSSRVSLGDOMFTMOQTVILQAVMKUVL IRKILALMAQGOKUPESVAPTPTBERSOSILATBASTSTURO SLIDKLYHINIRLQSHVNIVFDSEMDKIMDDAYBSFTHEO SLIDKLYHINIRLGSHVNIVFDSEMDKIMDAYFGIRQILEKKE GLFKHMMGRRVDTARASVICPDMTINTNISIGIMVAFAKTIVT QPVTFWAVQELKQVIR INGRAVERDSKWVILEDSSTALSAVDMT GRRAVAKQILITPATGAFKYCGTKIVCRIVKNGDILLINRQPTH RPSIGAHRARILEFEKVILEHYAKCAKNAPGEDENAHFPQS ELGRAPAVLACTOQQ'LIVPKDGQFLAGLIQDHWYGGASHTTRG CPFTREHMBLVYRGIDKLORGAVGANGTOGOBENAHFPQS ELGRAPAVLACTOQQ'LIVPKDGQFLAGLIQDHWYGGASHTTRG CFTREHMBLVYRGIDKLORGAVGANG'LICCCTE'YGGTSGKV LTCLARLEFAYLQLYRGFTLAYEDILVYRKADVKRQNI'ESTSTA' TLLINI'I EBBH FUNLSGKAKITGKAWVKBTPRSVPGFMPDBW ESQVI'I RRGGILLGQUILDAHYGGSAVGIVHCCT'EY'GGTSGKV LTCLARLEFAYLQLYRGFTLAYEDILVYRKADVKRQNI'ESTSTA' CGPQAVRAALIHEPRASYTBEVKGMODAHLGKUORDINIDLKK KERVINIYSINSINKACMPFGLHRQYPENTLQIMVQGGAKGSTVITY MQISCILJQI'ELEGGSTPJMASGSLUPCPE'PFPRAGGYVTC RFLTGIKPPFFFHCMAGREGLUPTAVKTSRGGVLQGCI'IKHL GLWYQDLI'VRDSDGSVVQFLVEGGDOLDIPRTGFPRAGGYVTC RFLTGIKPPFFFFHCMAGREGLUPTAVKTSRGGVLQGCI'IKHL GLWYQDLI'VRDSDGSVVQFLVEGDOLDIPRTGFPPAGGYVTC RFLTGIKPPFFFFHCMAGREGLUPTAVKTSRGGVLQGCI'IKHL RGAPLSYSQKI'QGAVKALLUSERSKIPCFPEVFFPAGGYVTC RFLTGIKCYDLI'NGVAKALCEBGGDAVALCHCI'IKHL RGAPLSYSQKI'QGAVKALLUSERSKIPCFPEVFFPAGGYVTC RFLTGIKROPSTOMULATFHPAGGGGMAVTLGI'PLUETLAVAX ANIXTPMSVPUHNYKALKAVKALKKOLOPULCHKI'NO ELDESSRKYQKKAAACPDPSLSVPPTPAGGSWVTLGI'PLUETLAVAX ANIXTPMSVPUHNYKALKAVKALKKOLOPULCHKI'NO ESCCMERGOKTOVYOLRAPARTATOLORGINGRGRG RQGGDEBGGGH'VTANKARAPARTATOLORGINGRGG RQGGDEBGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1.			
BOYTTEIUONNLLGSOGAHVRNVCESKSKLIALFMKANNINAER PHCKTGRSVVRKRNSKLITTEPMANDHRTAGOGEBEPLGIERG HCKTGRSVVRKRNSKLITTEPMANDHRTAGOGEBEPLGIERG HCKTGRSVVRKRNSKLITTEPSSKPVSKLIGDAWHRTAGOGEBEPLGIERG HCKTGRSVVRKSPSKPVSKLIGDOMTHOGTVNLGAWKDOVL IRKLLALMAGOGUL PEVARPTTDERKOSLIALDESHISTLUG SLIDKLYSTHINLGAVNIVTOPSKRKLAMDKY POTROLLEKKE GLPRKHMMGRRVDVARASUTCDMYINTINETGI PMVTATKLITUP OPVTPRNVQLKOVALNIGPTVLORGAMVLHODENGALSAVDAT ORGAVAKOLLTPATCAPKJOGTKI VCRAVKGOTILLINOPTHE RPSIGOHRAAL LIPBEKVLIRLHANCKANAADPOGEMANTPOG ELGRAZAVULACTDOQVI VPKOQOPLAGLI ODIMVSGASHTIRG CEPTERHYMBLUVYRGITDKVGRVKLLGPSILKPPPLATGKOVY TLLINI PPEDHIPIMLGGGAKITOKAMVKETTRESYGFRPDSMC ESQVI I REDGELGOVIDKOHVGROVALLGPSILKPPPLATGKOVY TLLINI PPEDHIPIMLGGGAKITOKAMVKETTRESYGFRPDSMC ESQVI I REDGELGOVIDKOHVGROVALLGPSILKPPPLATGKOVY LICHARLFTAYLIQLIKOFTLUKYRGOVKORGILESSTH CORQAVRAALMIPERAS TDEVRCKODAHLGKORGDENNI DLKK KERVHYSNISI KIKAMP FOLHARDY PSHILGIKORGININI DLK KERVHYSNISI KIKAMP FOLHARDY PSHILGIKORGAKSTVANT MQI SICILIGGI ELEGRSTPHASGKSLD-CFEPYEFTPRAGGFVTY RFLTGI KPBEFFFHOMAGREGLUTVATVITSRSGVI TISHLE GLIVOYDLIVURDSDSSVVQFLYGEDGLIDI ENTOFLOPROFPTILLA SNIYEVIMKSCHLHEVSLERADEKKALHFRAIKKONGKHNYTLIKA RGAPLSYSGKI QEAVKALLKISSKRRIGK JAPRIDS (FRILEMAN) SNIYEVIMKSCHLHEVSLERADEKKALHFRAIKKONGKHNYTLIKA RGAPLSYSGKI QEAVKALLKISSKRRIGK JAPRIDS (FRILEMAN) ANIKTPMMSVPVLNTIKKALKRVKSLKKOLTRVCLGEVLQKIDVO SCHEEKQNKVOVOLIN POLHARYYOOKKULPETTKVOUL YSQBMAAQTEKSYEKSELSIDRIKTILLOLI KOMGRELGEPGEAVA ANIKTPMMSVPVLNTIKKALKRVKSLKKOLTRVCLGEVLQKIDVO ESCHEEKQNKVOVOLIN POLHARYYOOKKULPETTKVOUL SECHEEKQNKVOVOLIN POLHARYYOOKKULPETTRVDI RFFKLLMESI KKKINKASAPRIVATERATORDILINAGELGESSE EGEBGEBGENDEBMGERNEHRIGARKTUGODEVOLIGHT GETE RFFKLLMESI KKKINKASAPRIVATERATORDILINAGELGESSE EGEBGERGENDEBMGERNEHRIGARKTUGODEVOLIGHT GETE RFFKLLMESI KKKINKASAPRIVATERATORDILINAGELIGESSE EGEBGERGENDEBMGERNEHRIGARKTUGODEVOLIGHT GETE RFFKLLMESI KKKINKASAPRIVATERATORDILINAGELIGHENG SOGGRAFTVALLAPOTORDARKENGANTORDILINGENGENGENDER SPERSENGENDEBMGERNEHRIGARKTUGODEVOLIGHT GETE RFFKLLMESI KKKINKASAPRIVATERATORDILINAGELIGHENGA ANDATORDAR GETERAT	1	[1	li di di di di di di di di di di di di di
PHICKTORS VVEKEHNSKLTTTP PANUHETIGGKDSEPLGIEERA IGKRGKILTTSREHHSLALMKRGFFILNILFSGWODDGMESREN PSVFFLDELVVPPSKSRPVSRLGDØMFTNOGTVILGAVKKUVU. IRKLALMANGORGU FPEWATTTDEKUGSLINERJESTTPGG SLIDKLYNIBTRIQSHVNIVPDSEMBUMDRYPGTRUTYB GLFRHMMGKRAVTYARASVI-DPMYNITNEIGHVPRIKTLTPH GLFRHMMGKRAVTYARASVI-DPMYNITNEIGHVPRIKTLTPH GLFRHMMGKRAVTYARASVI-DPMYNITNEIGHLINROPTHH RESIGAHRARI LDERKULLHYANCKAYNADPDGDEMNAHPPQS ELGRAVAKLATDAVIDLYDKOGQPLAGLIQDHWYSGAMTTRG CFFTREHMBLVYRGLTDKYGQPLAGLIQDHWYSGAMTTRG CFFTREHMBLVYRGLTDKYGQPLAGLIQDHWYSGAMTTRG CFFTREHMBLVYRGLTDKYGGVLAGLIQUHWYSGAMTTRG CFFTREHMBLVYRGLTDKYGGVLAGLIQUHWYSGAMTTRG CFFTREHMBLVYRGLTDKYGGVLAGLIQUHWYSGAMTTRG CFFTREHMBLVYRGLTDKYGGVLAGLIQUHWYSGAMTTRG CFFTREHMBLVYRGLTDKYGGSAMICHTGKYVESTYGGTSGKV LTCLARLFTAYLQLKRGFTLGVBDLILVKPKADVKRGRIEESTH CGPQAVRAALNEBEASYDEVSKKMOPAHLGGDFNIDLKK EESVHYSNEINNACHPFGLHRGFFBSTLQIMVQSGAKGSTVNT MQISCLIAGUI ELEGRSTPLMASKSLDCTEPTPAGGFVTG REFLTGIKPPBFFFHCMAGREGLUDTAVKTSRSGVLORGI IRHE GLUVYDLITVBDGSVVQPLYGBGGLDI BRYDTLGRWFPSCHYTHAGGVTG REFLTGIKPPBFFFHCMAGREGLUDTAVKTSRSGVLORGI IRHE GLUVYDLITVBDGSVVQPLYGBGGLDI BRYDTLGRWFPSCHYDG REFLTGIKPPBFFHCMAGREGLUDTAVKTSRSGVLORGI IRHE GLUVYDLITVBDGSVVQPLYGBGGLDI BRYDTLGRWFPSCHYDG REFLTGIKPPBFFHCMAGREGLUDTAVKTSRSGVLORGI IRHE GLUVYDLITVBDGSVVQPLYGBGGLDI BRYDTLGRWFPSCHYDLGRWFPSCHYDLAGVYGA REFLTSSKSFLOGAWARLUESSENNORG, REPNATUR ELDESSRKYQKKAAACPDPSLSVWRPDIYFASVSETFSTVDD YSQSMAAQTTEKSVERSGLISLBRINGN/REPNATUR ELDESSRKYQKKAAACPDPSLSVWRPDIYFASVSETFSTVDD YSQSMAATEKSVERSGLISLBRINGN/REPNATURA LAAGSIGEPSTOMTLATTFIPAGRGEMIVTLGIPRREHLAVAS ANIKTHMSVPUVLNTKKALKRYKSLKKQITEWGLUKJKTUV ESPCMBERGNFFOVOLRFORFSTRATHAGREGELGKTUKLTURA ANITYGIEAALEVULTKALKKYKSLKKQITEWGLUKJKTUV ESPCMBERGNFFOVOLRFORFSTRATHAGREGELGKTUKLTURA ANITYGIEAALEVULTKKALKKYKSLKKQITEWGLUKJKTUK ERSEMCOUTVLIPINGNICHTSTFOFLANGELGSBUKKTURAGSEE EERGGEBUDBDMGBERNPRISGARKTORGEGERULKTITOV PSRPDAAPTTHPGFGAPGA SAMERKVOAVRGHFFFTFTIDDYQTT TERSIMCOUTVLIPINGTRINGHDELFKTRATHAGREGE EGRGGEBTOMTLOGGFWANGTRINGHTHSTFOTTB-A VKIKSNISLLVFTSISNSSDLQOMTFTSTFOFLADHHVITIKFPLTTB-A VKIKSNISLLVFTOVARNHGIKGAVKK/LC	į		•	
IGKRGYLTPTSAREHLSALMWRGSFINITSGMONDGWERSPRY PSVPFIDELVYPSSRRPVSGLODMFTNGCTVILLGAWKDVUL IRKILALMAGOGOKLPEVATPTDESKGSLILIDESPISTLEGG SLIDKLYNIN IRTIGSHVAITUSEMDKIMMEDPITOTLEKKE GLFRKHMMGKRVDYAARSVICPDMYINTNEIGIPMVFATKLTIP QPVTFWNVQELRQAVINGPWHEGASWUNNEGSRTALSAUDMT GRAVAKGLITPATGARFQSTRIVUCHWKOMIDILLLRAQPTIH RPSIQAHRARILEEKVURLHVANCKAYNADPDGDEWAHPPOS ELGRABAVILLITATAGRAPGTRIVUCHWKOMIDILLLRAQPTIH RPSIQAHRARILEEKVURLHVANCKAYNADPDGDEWAHPPOS ELGRABAVILLITATUSHVANCKAYNADPDGDEWAHPPOS ELGRABAVILLITATUSHVANCKAYNADPDGDEWAHPPOS ESQVIIRBGELLGGVLUKAHYGGSAYGLWICCYEIVGGTSGKV TLLINIIPEDHIPLBLAGGKAKTGKAWKEREPOHPDSMC ESQVIIRBGELLGGVLUKAHYGGSAYGLWICCYEIVGGTSGKV LITCLARLFTAYLQLWRGFTLGGDILLVKPPLWTGKQVVS TLLINIIPEDHILGKAKATGKAWKEREPOHPDSMC ESQVIIRBGELLGGVLUKAHYGGSAYGLWICCYEIVGGTSGKV LITCLARLFTAYLQLWRGFTLGGDILVKRYDGLJKGKOGNINIILKK KERVHYSMSILINKACMPFGLHKGPFBWITLGHKGRGREFWT GOPQAVRAALMLPEAAS YDEVRKKWODAHLGKOQRDFNIILKK KERVHYSMSILINKACMPFGLHKOPFFBUTLAGKOGKGSTVUN WOISCLLGGIELGGRSTPLMASGKSLCFFPYEFFPRAGGRYCT RPLTGIKPPBFFFFCMAGREGUDTDAVKTSBGVLQRCVICHIELLE GLUVQYDULTVUDDGGSVVQFLXGBGGLJFRWGPLAGKOFFFL RRADFLSYSQKIQBAVKALKLESENRIGR/RFWGLAGKOFFFL RRADFLSYSQKIQBAVKALKLESENRIGR/RFWGLAGKOFFFL RRADFLSYSQKIQBAVKALKLESENRIGR/RFWGLAGKOFFL RRADFLSYSQKIQBAVKALKLESENRIGR/RFWGLAKOMSSLOFFFL RRADFLSYSQKIQBAVKALKLESENRIGR/RFWGSLGEFGBAVS LLAAGSIGBSSTOMTLANTFHIPAGRGEMNVILGIPRETEXVDS YSGWAAQTEKKSIKSLISLBLARTLQLK KWQSLCEFGGBAVS LLAAGSIGBSSTOMTLANTFHIPAGRGEMNVILGIPRETEXVDS YSGWAAQTEKKSIKSLSLBLARTLQLAKVGSLKCGLTRAVSS ANIKTPMMSVPVUNTNIKKALREVKSLKGLITATYQGKCLAPBGILTRYBTT RFFKLLMBSIKKKNAKSASFRANVINTRAATQRGDLONGGLGBSRG GOGGDEBEGHIVODABAGEGDADASDAKKKEKQGESVUNTSBEER ERREGERDDDEMOGERNIPREGARARTYGOEGEGLAKTOV ESSCCMEERQNKFOVYGURFGFFLEHAYYOGRKCLAPBGILTRYBTT THERETLANDS PSRPADAPETHQFGAAGA SAMBERVQAVRETHPPIDOVOY TESSLMCQUTVKLIPMIN TOPHSSLVVILAHAAAVTATGGITRG LLAETTINKWEKKELULATEGINLDELEKYAEVULDUKGGENSGA GOGGDEBEGHT VORDARAVTAGGTEPAAT TILKGDKGDGFMGDGERGHTMPSGLAKVALVADUHBUKKNITIM SPTRRPKTL*LARGPKYPWKGSTCTHELKJAVAVTSADDYTTTF SGHLLKARDD AVKRIRMSLLVERVILOKAGGTGTATHLAUTANTSADDYTTTF SGH	1		1	
PSVPFIDELVVPPSRSRPVSRLGDOMPTNOGTVNLQAVMKUVUL IRKLALMANGORUL PEWATPTTDEEKDSLISPISTLEGE SLIDKLYNIHIRIGSRVMIVEDSEMBUKMODKYPGIRGILEKKE GLFRHPMMGKRVDYAARSVICPDMYINTNEIGIPMYPSTRLITYP QPVTPWNVQELRQAVINGPWHEGASWINDEGSRTALSADDMY GREAVAKQLLTPATGAFKPGSTKIVCKHVKNODILLLINGPTHI RPSIQAHRAR ILBEEKVURLHVANCKAYNADPOGDEMANHPOG ELGRABAVULACTDQQYLVPKROGPLAGLIQDHWYSGAMTTRG CPFTREHTMELVTSGITDKVGSWKLLBSPILLFPPLMTGKQVVS FLILINI IPEDHIPINLAGKAKTTOKAWVKETPRSVPGNPPDSMC ESQVITREBELLGGVLDKAHYGSSAYGLWCFIYGGSTSKV LTCLARLFTAYLQLVRGFTLSVEDLLVKPKADVKRORIIESSTH CGPQAVRALINLPERAS YDEVRKWODAHLGDFNIDLKF GESVHNYSNEINNACMPFGLHRGFPENTLQLWQSGKGSTVNT MOISCLLGGIELGGRSTPLMASGKSLPCFEPYEFTPAGGFYTO RPITGIKPPBFFFHCMAGREGLVDTAVKTSRSGVLGRCIIELSSTH GLWGYDLTVRDSDCSVVQFLYSGBGLDIFKTQFLQKFQFFTA SNIVENIMSQHLHEVLSRADPKKALHHFRAIKWGSKHENTLLR RGAPLSYSQKIQBAVKALKLESENNAGR/RPMDS/G/RHLRMY ELDESSRKVQKAAACPDSISVWRDTYFRASFELTENTLAGNA ANIKTPMSVPVLNTKKALKRVSLKKOLTRVCLGSEVLGKIDV SGSKAAAGTEKSYEKSBLSLDRLRTLLQL\KWQSSLGEGGBAV LLAAGSIGBSFSTOMTLNTFHFARGRENNVTICHREILLINAS ANIKTPMSVPVLNTKKALKRVSLKKOLTRVCLGSEVLGKIDV ESPCHEEKQNFCVVQLAFPGJHAYYOGKCLAPBDLIRTMET RFFKLLMSIKKKNNKASAFRVNTRBATQRDLDNAGELGSRG EQGEDESSEGHTUDABABGDAAPDAKREKQEBEVDYESEEE ERGEGENDDEDMQERNNPHREGARKTQGVEERGHIFFHINT TRESSLWQCVTVKLPJAKHTPGSSLVVSLARGVITSGHIRGHNAGH BERNELVENSKLUNLPJAKHTPGSSLVVSLARGVITSGHIRGHNAGH LLAETTINKREKKELVLAHTEGIHLPELEKVASEULDLERLINSDDH AIANTYGIFBARVULSHKIEDVFANVGTSFYPTINT TIKGBKERDPGMGLPGYMREGROOFGPGPGGSKKMEMSPG GGGGRLFTVT-T1-GPPGSCFCLISLEYPRHALDGCFDMAT GGPAPALRGT LLAETTINKREKKELVLAHTEGITHLPELEKVASULDLERLINSDDH AIANTYGIFBARVULSHKIEDVFANVGTSFYPTINT TIKGBKERDPGMGLPGYMREGROOFGPGPGGSKKMEMSFG APQCKRFPASVORKTALHSGEDDTLIJERRFVNILDGCFDMT GGPYKLJARRGT SRNSSPLQOMTFETSFYPTINT TIKGBKERDPGMGLPGYMREGROOFGPGGSKKMEMSFG APCOKRFPASVORKTALHSGEDDTLIJERRFVNILDGCFDMT GGPKAYKLAPDVBGGTGFFELKGAKLALVENGUSHKKNKTHM SPTFRRFKTL-LERGPKYPWKSTTRRNKLDHHVI IKPPLTTEF-A VKKIENNSLLVFTVDVXANHOJKGAVKK/LODUSHKKNKTHM SPTFRRFKTL-LERGPKYPWKSTTRRNKLDHHVI IKPPLTTEF-A VKKIENNSLLVFTVDVXANHOJKGAVKK/LODUSHKKNKTHM SPTFRRFKTL-LERGPKYPWKSTTRRNKLDHHVI IKPPL	1			1
IRKLLALHAGOGOKLPERVATETTDESKOSILAIDRSFLISTLEGG SLIDKLYNIN TRICOSHNAULVEDSEMDKLAMDKYPGTOROLLEKKE GLFRKHMMGKRVDYARASVICEPDMYINTNISIGIPMVERTKLITYP QPVTPENVOGLEGOAVINDEPVHEGASWITINDIGIPMVERTKLITYP QPVTPENVOGLEGOAVINDEPVHEGASWITINDIGIPMVERTKLITYP QPVTPENVOGLEGOAVINDEPVHEGASWITINDIGIPMVERTKLITYP QPVTPENVOGLEGOAVINDEPVHEGASWITINDIGIPMVERTKLITYP QPVTPENVOGLEGOAVINDEPVHEGASWITINGIPMVERTKLITYP QPVTPENVOGLEGOAVINDEPVHEGASWITINGIPMVERTKLITYP QPVTPENVOGLEGOAVINDEPHAGASVILOPHAGAMATION CFPTREHMMELVYRGITDKVGRVKLLDSSILKEPPLWTGKQVVS TLLINI IPDEDIIPLALSGKAKTOKANVKERSYSPENPDSMC ESQVII REGELLOGVLUKRAHYOSSAYGLWICCTEITYGGTSGKV LTCLARLFTRYLQLVKGFTLIGABLILVYRGANKRORIIESSTH CGPQAVRAALMLESASVDEVRGKWQDAHLGGDORDFNIDLKE KERVINYSNSILNIKACHPFGHAGTEGDTVARVKRORIIESSTH GGPQAVRAALMLESASVDEVRGKWQDAHLGGDORDFNIDLKE KERVINYSNSILNIKACHPFGHAGTPFTHYLDVASGKAKSTVNT MQISCLIGGIELGGRSTPLMASGKSLOCFEPYETPTPAGGSVTG RPHTGIKPPBEFFHCMAGREGUADTAVKTSRSGVLORGITEKST GLVVQYDLTVRDDGSSVVOPLVGSDGLDIFKTQFLOPKOFPFLA SNVEVIMKSQHLHEVLSRADPKALHHERALSSTVLORGKYGKTIESSTH RGAPLSYGKLOBAVKALALCESSINNINGKARPHOSHORITAK GLAVGYGULTVADDGSSVVOPLVGSDGLDIFKTQFLOPKOFPFLA SNVEVIMKSQHLHEVLSRADPKALHHERALSSVENDTTTETSVD YSQBMAAQTEKSYEKSELSLDRLRTLLQL\KNGRSLCEEGGAVS LLAAGSIGBPSTQMTLATFFIFAGRGEBNVTLLIFRETLAWAS ANIKTPMSVPVYUNTKKALKKVELSKALTITVYQSKCLAPEDILLRAWS LLAAGSIGBPSTQMTLATFFIFAGRGEBNVTLLIFRETLAWAS ANIKTPMSVPVYUNTKKALKKVELSKALTITVYQSKCLAPEDILLRAWS EGGEDEBEGHTVDARABEGODADASDAKRCEKGESSVVYESEBEE ERREGESENDDDEWNYNTRATAGROBLORGHGKNSELGANKY ESPKEMEGRINDEMOSENNYNTRATAGROBLORGHGKNSELGANKY ESPKEMEGRINDEMOSENNYNTRATAGROBLORGHGKNSELGANKY FPSRPTANNYNTRATAGROBLORGHGKNSTANDYSBEER ERREGESENDDEMOSENNYNTRATAGRAHAVIYATKGITTEC LLMETTINKKEKKELVLANTEGIHAPELFKYABVULDLERRYSMOH ALANTYGIFARAVILFAKTRYBSSLVQAWGTHTPTDYTTYT TILKGDKODPOMOLOCHYMGREGOCOFPOGGSKGDKEMSIGG APCARPIARISTENSSPLQOMTFETSFOPLKGATHLGSHDELR SPRENCVYVLNJEMIGTGYMGREGOCOFPOGGSKGDKEMSIGG APCARPIARISTENSSPLQOMTFETSFOPLKGATHLGSHDELR SPERMYNSULDATHVYWGRATHGITYCHYNLISHDVANTHLIQ SCHKARYVLARDDY SPFERMYNTYLFARAGFYPARAKAKALLKARVLKDVHSHKKNITHN SPTFRRPKTL*LRROPKYPWKSTP	[The state of the s
SLIDKLYNIWTRLOSHVALVEDSEMDKLMMMKYPGTROLIEKKE GLERKHMMGKPUYAARSVICEDMYINTEGERYALSAUDMY OPTPWHVOELROAVINGENVERDASMVINEDGERYALSAUDMY ORAVAKQLLTPATGAPKPQTKIVCHVKNOEDILLLINRQPTLH RPSIQAHRARILPEREVIRLHYANCCANYADPEDGEMAAHPQS ELGRABAVULACTDQYLUYENGGGLAGLIQDHHVSGAMTTRO CFFTREHMMELVYRGLIDKUKGWALSIESILKPPFLWTGKQVVS TLLINIIPEDHIPLMISGKAKITOKAWVKEPTPRSVPGRYPDSMC ESQVIIREGEBLLGGULDKAHVGSARGILGDHHVSGAMTTRO CFFTREHMELVYRGLIDKUKGWAVKEPTPRSVPGRYPDSMC ESQVIIREGEBLLGGULDKAHVGSARGILGKDGROPPNIDLKE KEEVHYSNEINKACMPFGLHRQPPENTLQLMVQSGAKSTVNT MQISCILGGIELGERSTPUMAGSKSLICPTFTPRAGGFVNT MQISCILGGIELGERSTPHAAGSKSLICPTFTPRAGGFVNT MQISCILGGIELGERSTPHAAGSKSLICPTFTPRAGGFVNT RPLTGIKPPEFPFRAGGRUNGSGAKSTVNT MQISCILGGIELGERSTPHAAGSKSLICPTFTPRAGGFVNT RGAFLSYSQKIQEAVKALKLESENRIGK, RRUDS /G KILKPHILL GLVVQYDLTVRDSDGSVVQFLXGEDGLDIPTTQFLQKPFFPTA SNINEVIMKSQHLEVLSRADPKAGLHIPFATKIKWQSKHPNTLLR RGAFLSYSQKIQEAVKALKLESENRIGK, RRUDS /G KILKPHILL RGAFLSYSQKIQEAVKALKLESENRIGK, RRUDS /G KILKPHILL RGAFLSYSQKIQEAVKALKLESENRIGK, RRUDS /G KILKPHILL RGAFLSYSQKIQEAVKALKLESENRIGK, RRUDS /G KILKPHILL RGAFLSYSQKIQEAVKALKLESENRIGK, RRUDS /G KILKPHILL RGAFLSYSQKIQEAVGAKALKLESENRIGK, RRUDS /G KILKPHILL RGAFLSYSQKIQEAVGAKALKLESENRIGK, RRUDS /G KILKPHILL RGAFLSYSQKIQEAVGAKALKLESENRIGK, RRUDS /G KILKPHILL RGAFLSYSQKIQEAVGAKALKLESENRIGK, RRUDS /G KILKPHILL RGAFLSYSQKIQEAGHTLARAUR /G KILKPHILL RGAFLSYSQKIQEAGHTLARAUR /G KILKPHILL RGAFLSYSQKIQEAGHTLARAUR /G KILKPHILL RGAFLSYSQKIQATA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA /G KILKPHILL RSCHAMA	[
GLFRKIMMOKEVDYARRSVICEDMYINTBEIGIPMYPATKLITY QPVTPHNVOGERQAVIAGDENVHORASMVINEDGSFRALSAUDMY QREAVAKQLLTPATGAPKPQGTKIVCRHVKNGDILLINRQPTLH RPSIQAHRAR ILDEBEVURLHYRNCKAYNADPODDBWAHPPOSS ELGRAEAVILACTOQQYLVPKOGQILAGILQIDHHVSGASMTIRG CFFTRHYMELVYRGLTDKVGRVKLLSPSILKPPEJMYGKQVPS TLLINIIDEDHIPLINSGKANITOKAWVETPRSVPGRPIPSM ESQVIIREGELLGGVLDKAHYGSSAYGLVHCCYEIYGGETSGKV LTCLARLFPATALQLYRGFILGYBILVKPETPRSVPGRPIPSM ESQVIIREGELLGGVLDKAHYGSSAYGLVHCCYEIYGGETSGKV LTCLARLFPATALQLYRGFILGYBILVKPAVRGRIIESTH CGPQAVRAALMLPRAASYDEVRGKWODAHLGKDORDFNIDLKK KERVINIYSMEINKACMPFOLHROPPENTICJMYOGGAKGSTVNT MQISCLLGQIELGGRSTPLMASGKSLDCFEPYEFTPRAGGFVTG RFLTGIKPPBFFFHCMAGREGLUDTAVKTSRSGYLDGCINHLE GGLVVQYDLTVABDOGSVVQPLYGEGDGLIDFKTDFLOFKOFFFLA SNYEVIMKSQHLHEVLSRADPKKALHHFRAIKWQSKHPNTLER RGAFLSYSGKIQBAVKALKESSRNINGKNDS/G/RNLHMY ELDEBSRKYQKKAAACPDPSLSVWRPDIYPASVSTETEKVDD YSQSMAQTUEKSYEKSELSDLRRITLLGLAKWQSKHPNTLER RGAFLSYSGKIQBAVKALKESSRNINGKNDS/G/RNLHMY ELDEBSRKYQKKAAACPDPSLSVWRPDIYPASVSTETEKVDD YSQSMAQTUEKSYEKSELSDLRRITLLGLAKWQSKHPNTLER RGAFLSYSGKIQBAVKALKALKSSLRKQLTEVCLGEVLOKATUO YSQSMAQTUEKSYEKSELSDLRRITLGLAKWQSKHPNTLER RFKLIMSSIKKRNINGASAFRNNNTRATGRDLDNAGSLCREGBAVG LLAAOSIGBPSTOMTLNTFHPAGRGMVVTIGIPRIBLIAWAS ANIKTPMMSVPULNTKKALKAVKSLKKQLTEVCLGEVLOKATUO ESFCMEEKQNKFQVYQLRFQFLBAPIYQORKCREPDILRFMBT RFFKLIMSSIKKRNINGASAFRNNNTRATGRDLDNAGBLGRSNS EQBGDBEERGHIVDARABEGDADASDARKGEERVYPSBEEE ERREGEBDDDDMQGERRYPHREGARKTQCDDEBVGI/H*GGBP PSRPPDAADFETHPQCAGAFGA LEAMBERVQAVREIHPFIDVQYD TEBSLIMCQVTVKLPLIMKINFDMSSLVSLAHGAUIYARGITRC LLMETTINKRKEKELULNITEGINLDELFIKYAVAVLGLADAVHCF EGYYKPLARFGITRSNSDLAQAMTEGINDLEPHYNDLATHAGHTACH ALANTYGIEBALBVILKKEILDVPAVYGLADPBRHLSCHAMAGS SPSACLVVGKVVRGGTGILFELKQDER SPSACLVVGKVVRGGTGILFELKQDER SPSACLVVGKVVRGGTGILFELKQDER SPSACLVVGKVVRGGTGILFELKQDER SPSACLVVGKVVRGGTGILFELKQDER SPSACLVVGKVVRGGTGILFELKGRAGALKALKKAVLKOVHSHKKNKHM SPTFRRPKTI*LERGPKYPMKSTPRRNILDHHVILKPLITE*A VKKIENNSLLVFTVDVKAMRHQIKQAVKK/LCDIDVAKVMTLIQ SDGERKAVVRLAPDVALVVAKRIGITGILTYLYMHILINGKENLCAGALLSSY LVVANLGLAPPSVWAKRARQILGANVAKIGILTYVJSMILIDA SDGERKAVVRLAPDVALVVAK	1			7
QPTTPWNVQELRQAVINGENVENGEMULILLANGPTLM QREAVAKQLLTPARGAPREVGTK LVCRHVGD LLLLANGPTLM RPSIQAHRAR ILPEEKVLRLHYANCKAYNADFDGDEMNAHPQS ELGRAEAVULACTDQYLVPKDGGPLAGLIQDHWSGSMYTRG CPFTREHWRHLVYRGLTDKVGRVELLSSEJ LKPFPLWTGKQVVS TLLINIIPDDHI PINLSGKAKITOKAWVEFPRSVPGFNPDSMC ESQVIIRBEGELLGGVLDKAHVGSANGIUKGNDFFNHIDLKS ESQVIIRBEGELLGGVLDKAHVGSANGIUKGNDFFNHIDLKS KEEVNHYSNEINKACMPFGLHRQFPENTLQLMVQSGAKGSTVNT MQISCLLGQIELGEGRSTPLMASGKSLPCTEPYEFTPAGGFVTS RPHTGIKKPEFFFCHAGREGLUDTAVKTSSGYLGGLICHLE GLVVQYDLTVRDSDGSVVQFLYGBDGLDIPKTGFLQGFVFST RPHTGIKKPEFFFCHAGREGLUDTAVKTSSGYLGRCIICHLE GLVVQYDLTVRDSDGSVVQFLYGBDGLDIPKTGFLQGFVFST RPHTGIKKPEFFFCHAGREGLUDTAVKTSSGYLGRCIICHLE GLVVQYDLTVRDSDGSVVQFLYGBDGLDIPKTGFLQGFFFSA SNNEVIMKSQHIHEVLUSRAPKKALHIFFAIKKWGSKIPNTLLAR RGAPLSYSGKIGEAVKALKLESSNRNIGK/RPMDS/GRMLEHWIS ELDESBRRKYQKKAAACPDSLSVWRDTHAS/GKFLKWGSKIPNTLLAR RGAPLSYSGKIGEAVKALKLESSNRNIGK/RPMDS/GRMLEHWY ELLEBESBRRKYQKKAAACPDSLSVWRDTHAS/GKFLKWGSKIPNTLIRAR RGAPLSYSGKIGEAVKALKLESSNRNIGK/RPMDS/GRMLEHWY ELLEBESBRRKYQKAAACPDSLSVWRDTHAS/GKFLKVGKGEGLGFDGAVG LLAAGSIGEFSTQMTLNTFHARGMWVTLGIPREREILMVAS ANIKTPMWSPVLNTKKALKAKVSLEKGLIVEVCLGGFVLQKIDVQ ESSCMEEKQNKFQVYQLRFQFLEPATYQCBKCCRPEDLIRMETT RFFKLLMESI KKKNNKASAFANVNTRATQLDANGGLGRSRR EQGODEBEGGGIVDABABEGGDADASDAKRKKGEBEVIJSEEE EERRGGENDEDMOERRIPHERGARKTOGDENGLINGCHGRSRR EGRGDEBEDEDMOERRIPHERGARKTOGDENGLINGCHGRSRR EGRGDEBEGGRIVDABABEGDADASDAKRKKGEBEVIJSEEE EERRGGENDEDMOERRIPHERGARKTOGDENGLINGCHGNSR EGRGGVFLFWLTJMKINFHMSGLVVSLAHGBAVITAKGTITEC LLMETTINKMEKELVLINTEGINDELTWGLAHGBAVITAKGTITEC LLMETTINKMEKELVLINTEGINDELTWGLATGLANDAYTGHTAKGTTEC LLMETTINKMEKELVLINTEGINDELTWGLATGLANDAYTGHTAKGTTEC LLMETTINKMEKELVLINTEGINDELTWGLATGLANDAYTGHTAKGTTEC SPSACLVVGKVVRGGTGLFELKQDLR SGCGRAFFYLVILT-LT-GPGPGSCYLLIS-LYGERPHALDETRFYINI ALANTYGIEAALBVITEKSILVOPAVVGIAVDFHGLINDAKGAVILVAQPS ERSIMOSGSVMLDLAYGRVWVRLFRQRENAIYSNDDDTYITT SGGLIKARDD 5386 326 799 LMVPRTKERGFAPPKARAKARALKAKKAVLKUVHSHKKKNKIHM SPPFRRPKTL-LLRQPKYPWKSTPRNNLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKGAVKK/LCDIDVAKVNTLIQ				
CREAVAKQLITPATQAPKPCGTFIK IVCHHVISHOLILLINGPITLI RPSIGAHRAR LIPBERVILLEHYANICKAYNADPODDEMCHIPPOS ELGRAEAYVLACTDQQYLVPKDQQPLAGLIQDHMVSGASMTTRG CPTTREHTMELVTRGLTDKVGRVULLSPSILKPPEJMTGKQVVS TLLINIIIPEDHIPINISGKANITGKAWWSTPRSVPGRNPDSMC ESQVIIREGELLGGVLDKAHTGSSAYGLVHCCYEIYGGETSGKV LTCLARLFTAYLQLYRGFTLGVSBILVKEPBAYRGRYIPSSMC ESQVIIREGELLGGVLDKAHTGSSAYGLVHCCYEIYGGETSGKV LTCLARLFTAYLQLYRGFTLGVSBILVKEPBAYRGRYIPSSMC ESQVIIREGELLGGVLDKAHTGSSAYGLVHCCYEIYGGETSGKV LTCLARLFTAYLQLYRGFTLGVSBILVKEPBAYRGRYDPSMC ESQVIIREGELLGGVLDKAHTGSSAYGLVHCCYEIYGGETSGKV LTCLARLFTAYLQLYRGFTLGVSBILDHAYCQUSGAKGSTVNT MOISCLIGGIELGGSTPLMASGKSLPCCFBYBFTPRAGGFVTG RPLTGIKPBFFFFCMAGREGLVDTAVKTSRGYLQRCIIKHLE GLWQYDLITVRDSDGSVVQFLXGSBLDCTBTPLGLQLYBKYGFFFLA SNYBVIMKSGHLBEVLSRADPKKALHHFRAIKKWGSKBPNTLGR RGAFLSYSGKYGENVARLKLESSENRIGK, DSVG/SKRAMENT ELDBESRRKYQKKAAACPDPSLSVWRPDIYPASVSTTETKVDD YSGBMAQTIEKSYBKEBLSDRLRTLLGLAJKROGSKBPNTLGRUMPY ELDBESRRKYQKKAAACPDPSLSVWRPDIYPASVSTTETKVDD YSGBMAQTIEKSYBKEBLSDRLRTLLGLAJKROGSKLCFGEGAVG LLAAGSIGBFSTOMTLNTFHPAGRGEMVTLGTPRIREITLMVAS ANIKTPMMSVPVLNITKKALKRWSLKKGVLJKCGLGBVLQKLDVQ ESSCMBEKGNFQVVQLRRGJEBRATYQCHAYCGBEVGLFBDLIRMBT RPFKLLMESIKKKNNKASAFRNVNTRATATORLOGGRONSH EQGODEBERGGITODARABEGDAASDAKRKKGGEEVDYBSEBE ERREGGENDDEDMQGERRYPHBEGARKTGEODEBVGLJN-HGGDFV PSRPPDAAPETHPQGAGAGA LSAMBERVQARREHPFTDDVQTD TESSLWCQVTVKLPLMKINFPMSSLVVSLAHGBAVITAKGTTRC LLMETTNNKHKEKLULNITEGITNLDELFKYABVLDLBRIJSNDTH ALNIYGTEAALBVTEKEIKDVPAVVGIAVOPBHISLUADYMCF EGGYNGLJBRGTENSSSLOLQOMFFTS FOPLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSGGRLFTVL-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1				1
RPSIGAHRARILPSEKVIRLHYANGKANNADPOSEMMAHPPOS ELGRAEAVUACTOGQ/LVPKGOGPLAGLIODHMYGGAMTRO CPFTREHYMELVYRGLTDKVGRVKLLSPSILKPPPLWTGKQVVS TLLINIIPPBLIPLLSGKAKTGAWKETPRSVPGRNPDSMC ESQVIIREGELLCGVLDKAHYGSSAYGLVECCYEIYGGETTSGKV LTCLARLFFTAYLQLYRGFTLSVEDILVKPRADVKRGRIIEESTH CGPQAVRAALNIPPBAS YDEVGKRWGGKIGKGCGVETSGKV LTCLARLFFTAYLQLYRGFTLSVEDILVKPRADVKRGRIIEESTH CGPQAVRAALNIPPBAS YDEVGKRWGGKIGKGCRGTVATT MOISCLLGGIELGGSTPLMASGKSLDFBYFFTPRAGGYTG RFLTGIKPPEFFFHCMAGREGLUDTAVKTSRSGYLQRCIIKHLE GLWQYDLTVRDSDGSVVQFLKGBGLDIPKTQFLQFKQFFFLA SNYEVIMKSQHLHEVLSRAPPKKALHHFRAIKKWGSKHBFYLLR RGAFLSYSGKIQEAVKALKLESENNRGF, KPWDS /G /RMLRMMY ELDEESRRYQKKAAGCPDPSISVENTHERAIKKWGSKHBFYLLR RGAFLSYSGKIQEAVKALKLESENNRGF, KPWDS /G /RMLRMMY ELDEESRRYQKKAAGCPDPSISVENTHAGKSLSFTLAVDS YSQSMAAQTEKSYSKSELSIDRIRTLIQL\KWGRSICEPGEAVG LLAAOSIGEFSTQMITLATHFPAGAGENTYLGFPRSTETKVDD YSQSMAAQTEKSYSKSELSIDRIRTLIQL\KWGRSICEPGEAVG LLAAOSIGEFSTQMITLATHFPAGAGENTALGFPEDILRFMET RFFKLLMESIKKNNKASAFRAVNTRATGFDLDMAGGLGRSRG RQSGDEEEGGIIVDARABEGDAAGAKKREKGESUPYSSEES ERRGGENDDEMMGEERNPERGARKTALLGREDDLERMET RFFKLLMESIKKNNKASAFRAVNTRAGLDAMAGCRSRG RQSGDEEEGGIIVDARABEGDAAGAKKREKGESUPYSSEES ERRGGENDDEMMGEERSPHPRGGARKTALHGAVITAKGTTRC LLMETTINKNEKELVLNTEGINLPELFKYAEVLOLRRLYSNDIH AIANTYGIEAALRVIEKEIKDVFAVYGIAVOPHHISIVADYMCF EGYYKPLMFFGISNNSSPLQQMTFETSFQFLKXQATMIGSIDELR SPSACLVVGKVVRGGTGLEFELKQPLR GYGGRAPLRGITYPLVL-LGPGSCPCILSFQFLR SPSACLVVGKVVRGGTGLEFELKQPLR GGRAPLRGITYPSSCPCILSFY PGRPHALPETRPYINI TILKGDKGDPGPMGLPGYMGRSGPGGSGSGKGEMGSEMGSPG APCOKRFPAFSVGRKTALHSGEDFQTILFERVFVNILDGCPDMAT GGRAPLRGITYFTSLAVHSWYKTSTYNHLDHNIKSKAVLLYAGOS ERSIMOSGSVMLDLAYGDRVWVRFKRQRENAIYSNDPDTYTTF SGGLIKKAEDD 5386 326 799 LWYPRTKKRAPAPPKAEAKAKALKAKKLKAKKAVKDVHSHKKKKHM SPPTFRPFTIT-LIRRQFKYPWRSTTGRRKLDHHVILKPPLTTE*A VKKIENNSLLVFTVDVXANKHGIKCHKUNSHKKNKHM SPPTFRPFTIT-LIRRQFKYPWRSTTGRRKLDHHVILKPPLTTE*A VKKIENNSLLVFTVDVXANKHGIKCHCUTUKNKICHTLQ SDGERKAVVRLADDYDALVVATKIGIT 4WPATKKEAPAPPKAEAKAKALKKAKCHCHUNSHKKKKCHLD SDGERKAVVRLADDYDALVVATKIGIT 5386 22117 FVVAASGGCWFULGERRAGSLLSAYGTFAMFGWULFGRWATA	1			1 · · · · · · · · · · · · · · · · · · ·
ELGRAEATVILACTIOQYLVERUGQELAGLIQDEMYSGASMITTEG CPFTREHYMELVYRQLTDKVGRVKLLSPSILKPPPLWTGKQVVS TLLINIIPEDHIPLINLSGKAKTTGKAWKRETFRSYPGFNPDSMC ESQVIIREGELLCGVLDKAHYGSSAYGLVTCCTYITGGETSGKV LTCLARLPATAIQLYRGFTIGWEDILWFRADVKRGTIESTH CGPQAVRAALAIDERASTDEVRKWODAHLGKDGRDFANTDLKF KERVINLYSMEINKAOMPGGLHRQFPSGDFANTDLKF KERVINLYSMEINKAOMPGGLHRQFPSTLAWGSGASGTWTI MQISCLLGQIELEGRSTPLMASGKSLPCFEPYEFTPRAGGFVTG RFLTGIKPPEFFFRCMAGREGLUDTAVKTERSGYTQRCIIKHLE GLVVQYDLJVRDSDGSVVQPLVGSEDGLDIRKTGPLQFWGFPFLA SNYEVIMKSQHLHEVLSRADPKKALHHFRAIKKWGSHIPNTLIR RGAFLSYSKOLGAVKALKLESSENRAGKPSDS/GKRLMMY ELDEESRRKYQKKAAACPDPSLSVWRPDIYPASVSSTFETKVDD YSQBWAAQTEKSYEKSELSDRLRTLLQL\KWQRSLGEPGEAVG LLAAGSIGEPSTQMTLNTFHFAGRGEMNVTLGIPRLEREILMVAS ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVQGKUDVQ ESSCMEEKRNKFQVYQLRFOFLHAFYQGEKCLEPUGLIRMBT RFFKLLMSSIKKKNKASAFRSVNTRRATGRDLDMAGSLGRSRG RQGGDEEEGGHIVDABARBEGDADADAGKRKGOBEUPYSESEE EERRGEENDDEDMQEERNPHREGARKTQQDEEVGL/GH*GGPV PSRPPDAAPETHPQFGAFGA\SAMMRRVQAVREIHPFIDDYQG TERSLMCOUTYKLPLWKINFDMSSLVVSLAHGRVIYARKGITEC LLMETTNNKNEKEUVLNTSGINLPELFKYAEVLDDRRLYSNDIH ALANTYGIEAALRVIEREIKDVPAVYGDFRLSUNDYNGF EGYVRPLRRFGIESNSSPLQQMTFFTSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTCLPELKQPLR 5384 196 886 QSGGGEPTVL*1-**GPFGSCFCILSL**PGRPHALPEIRFYTNI TILKGDKGDFGPMGLFGYMGRRGFGGSFGFGSFGKGKGEMGSFG APCQKFFFAFSVGKKTALHSGEBFGTLINFVVFLLGGCFDMAT GQFAAPLRGIYFFSLAVHSWNYKETYVHIMHNCKEAVILVAQPS ERSIMQSQSVMLDLAYGGRVWVRLFKRGRENDIYSNFFTTFFT SGGLIKABDD 5386 326 799 LWYPETKREAPAPPKEAKAKAL\KAKKAVLKDVHSHKKNKHM SPTFRRPKTL**LRRQPKYWKSTTRRKLDHHVIKFPLTTE**A VKXIENNSLLVFTVDVXANKHGIKGAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LWYPETKREAPAPPKEARAKKAL\KAKKAVLKDVHSHKKNKHM SPTFRRPKTL**LLRRQPKYPWKSTTRRKLDHHVIKFPLTTE**A VKXIENNSLLVFTVDVXANKHGIKGAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGGWVLGERRAGSLLSASYGTFAMPGWVLFGRRMATA SDDLVPFGFFLLVVRLWMIGILTLYMMIRGKLDCAGGALLSSY LIVUHLLLAVICTVSAINCVSMRGTTCRPGFRKSMSKLLYTLL ALFFPENWVAASGCAGAVKGAGGGGAALLSSY LIVUHLLLAVICTVSAINCVSMRGTTCRPGFRKSMSKLLYTR	ł			T T
CPPTREHYMELVYRGLIDKORUKULSPSILKPPPLWTGKQVVS TLLINII IPDDHIPLINLGKAKITIGKAWKEPRSVPGNPDSMC ESQVIIROGELLCGVLDKAHYGSSAYGLVRCCYEIYGGETSGKV LTCLARLFTAYLQLYRGFTLGVEDILVKPRADVKRQRIIESSTH CGPQAVRAALNLPBASA YDEVGKKWQDAHLGKURQRIFMIDLKF KERVNHYSMEINKACMPFGLHRQFPENTLCLMVGSGAKGSTVNT MQISCLIGGIELGGSTPJMASGKSLGVPTSVFTRRAGGVTG RFLTGIKPPEFFFFRMAGRSGLUDTAVKTSRSGVTQKCIIKHLE GLVVQYDLTVRDSDGSVVQFLYGBODLDIPKTQFLQPKQFPFLA SNIVEVIMKSQHLHEVLSRADPKKALHHFRIKKWGSKHPNTLLR RGAFLSYSGKIQEAVKALKLESENBNGR/RFMDS/G/KMLRMY ELDEESRRYQKKABACPDPSLSVWRPDIYFASVSSTETETKVDD YSQBWAAQTEKSYEKSELSLDELRILLQL\KWGRSLCEPGEAVG LLAAQSIGEPSTQMITLATFHFAGRGKPUTGIPRETTKVDD YSQBWAAQTEKSYEKSELSLDELRILLQL\KWGRSLCEPGEAVG LLAAQSIGEPSTQMITLATFHFAGRGKPUTGIPRETTKVDD YSQBWAAQTEKSYEKSELSLDELRILLQL\KWGRSLCEPGEAVG LLAAQSIGEPSTQMITLATFHFAGRGKPUTGIPRETTKVDD YSQBWAAQTEKSYEKSELSLDELRILLQL\KWGRSLCEPGEAVG LLAAQSIGEPSTQMITLATFHFAGRGKPUTGIPRETTKVDD YSQBWAAQTEKSYEKSELSLDELRILLQL\KWGRSLCEPGEAVG LLAAQSIGEPSTQMITLATFHFAGRGKPUTGIPPRETTKVDD YSQBWAAQTEKSYEKSELSLDELRILLQL\KWGRSLCEPGEAVG LAAQSIGEPSTQMITLATHFHAGAGALAACHAGALYAAMACHAGALYAAMACHAGALYAAMACHAGALYAAMACHAGALYAAMACHAGALYAAMACHAGALYAAMACHAGALYAAMACHAGALYAAMACHAGALAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		1	}	_ =
TLLINI I PEDHI PINLSGKARITGKAWVKETPRSVPGENDSMC ESQVI I REGELLGGVLDKAHYGSSAYGLVHCCYEI YGGETSGKV LTCLARLFTAYLQLVRGFTIGVEDILVKEKADVKRQRI IEESTH CGPQAVRAALNLPEAAS YDEVRGKWQDAHLGKDQRDFNMIDLEF KEEVNHYSME INKACMPFGLHRGFTHTQLMVOSGARGSTVNT MQISCLLGQI ELEGRSTPLMASGKSLDCFEPVEPTPRAGGFYTG RPTIG LKPPEFFFFHOMAGREGLUTYKTSGRGYLQRGI IKHLE GLVVQYDLTVRDSDGSVVQFLYGEDGLDIPKTQFLQPKQFPFFLA SNYEVIMKSQHLHEVLSRADPKKALHIFFALKKMQSKHPNTLLR RGAFLEYSGK (LGAVKALKLESERNERGR/RPMDS/G/RMLRMWY ELDEESRRKYGKAAACPDPSLSVWRPDTYFASVSETTETKVDD YSGBWAAQTEKSYEKSELSLSDLRICHLOL KWRGSLCEPGEAVG LLAAQSIGBPSTOMTLNTFHFAGRGEMNVTLGI PRLREILMVAS ANIKTPHMSVPVLNTKRALDLA YQQGKCLAPEDILAFMET RFFKLLMESI KKKNNKASAFRNVNTRRATQRGKLDVAGELGRSRG ESCRDEEEGGHI VDAAPETHPAGRGEMNVTLGI PRLREILMVAS ANIKTPHMSVPVLNTKRALDAYAYQGKCLAPEDILAFMET RFFKLLMESI KKKNNKASAFRNVNTRRATQRGDEVUS,GH-GGGBV PSRPPDAAPETHPQPGAPGA\CAMERKOGEEDVYSSEEE EEREGGENDDEDMQEERNPHREGARKTOSQDEEVUS,GH-GGGBV PSRPPDAAPETHPQPGAPGA\CAMERKOGEEDVYSSEEE EEREGGENDDEDMQEERNPHREGARKTOSQDEEVUS,GH-GGGBV PSRPPDAAPETHPQFGAPGA\CAMERKOGEEDVYSSEE EEREGGENDDEDMGETSTPHEGGARKTOSQDEVUS,GH-GGBV PSRPPDAAPETHPQFGAPGA\CAMERKOGEDVYSSEE EEREGGENDDEDMGETSTPHEGGARKTOSQDEVUS,GH-GGBV PSRPPDAAPETHPQFGAPGACATUSTATATATATATATATATATATATATATATATATATA				
ESQVITREGELLGGULDRAHYGSSAYGLWECCYETYGGETSGKY LTCLARLFTAYLQLYRGFTLGYBDILVYPKADVKRORITESTH CGRQAVRAALNLPEAAS YDEVRGKWQDAHLGGDGDRYMIDLKF KEEVNHYSMEINKACMPFGLHRQFPENTLJUNVQSGAKGSTUVT MQ1SCLLGGIELEGERSTPLMASGKSLDCFEPVEFFPRAGGFVTG RFLTGIKPBEFFFHCMAGREGLUDTAVKTSRSGYLQRCIIKHLE GLVVQYDLTVRDDGSVVQFLYGEDGLDIPKTQFLQRKQFFPLA SNYEVIMKSQHLHEFLSSADPKKALHHFRAIKKWQSKHPNTLLR RGAFLSYSGKIQEAVKALKLESENRNGR/RPMDS/G/RMLRMMY ELDESERKTYQKKAAACPDPSLSVWRPDTYFASVSETFTKVDD YSQBWAAAQTEKSYEKSELSLDRLETLLQL\KWQRSLCEPGEAVG LLAAQSIGBPSTQMTLNTFHFAGRGEMNVTLGIPRLEEILMVAS ANIKTPMMSVPVLNTKKALKAVKSLKKQLTRVCLGEVLQKIDVQ ESSCMEEKQNKRQVVQLRFQFLPHAYYQQSKLPEDILHFPMT RFFKLIMESIKKKNKNASAFRNVHTRATQRDLDNAGELGRSRG EQEGDEEEGHIVDAABAEEGADASDAKRKEKQEEVDYESEEE EERGERIDDEDMQEERNPRREGARKTQQDDEBVGL/GH-GGFV PSRFPDAAPETHPQPGAPGA\EAMBRRVQAVREHPPIDDYQTD TEBSLMCQVTVKLPLMKINFPMSSLVVSLAHAQNIYATKGITRC LLMETTNNNNKELLVLNTEGINLPELFKXAEVLJAURHSINDH AIANTYGIEAALRVIEKSIKOVFAVYGLAVDPRHLSLVADYMCF EGVYKPLNRFGIRSNSSPLQQMTFETSYPLXQATMLGSHIDELR SPSACLVVGKVVRGSTGLIPELKQER 5384 196 886 QSGQRLPTVL-L**GPPPSCCTLISLF\PGRPHALPEIRFYINI TILKGDKGDGPGMGLDGYMGREGPOGPOGSKORGMGGFG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWYXETTVHIMINQKEAVILVAQPS ERSIMGSQSWINDLAYGDRWWRLFKRQENAIYSNDFDTYITF SGHLIKAEDD LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKRNKIHM SPTFRPRKTL*LRRQPKYPWKSTPRRNKLDHVIIKFPLTTE*A VKXIENNSLLVFTVDVRANHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAVYNLAPDYDALVVAATIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKRNKIHM SPTFRPRKTL*LRRQPKYPWKSTPRRNKLDHVIIKFPLTTE*A VKXIENNSLLVFTVDVRANHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVAATIGIT 5387 2 2117 FVVAASGGGWFVLGERRAGSLLSSASGFTAMPGWVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LTVLMILLAVVICTVSAIMCVSWRGTICNFGPRKSMLLLYTIL AAFFPERWASLGAARVADGVVCQUFANGTICNFGPRKSMSKLLLYTIL AAFFPERWASLGAARVADGVVCQUFANGTICNFGPRKSMSKLLLYTIL AAFFPERWASLGAARVADGVVCQUFANGTICNFGPRKSMSKLLLYTIL				-
LTCLARLFTAYLQLVRGFTLGVEDILVKPKADVKRQRIIESTH CGPQAVRAALNLPEAASYDEVRGKWQDAHIGKDQRDFNMTDLKF KEEVNHYSNEINKACMPPGLHRGFPENTLQLMVQSGAKGSTVAT MQISCLLGQIELEGRSTPLMASGKSLPCFEPYEFFPRAGGFYVG RFLTGIKPEFFFFMAGREGLUDVKTSRGSTVLGCIIKHLE GLVVQYDLTVRDSDGSVVQFLYGEDGLDIPKTQFLQPKQFPFLA SNYEVIMKSQHLHEVLSRADPKKALHIFFAIKWGSKHPNTLLR RGAFLEYSGKIQEAVKALKLESERNRGR/RPMDS/GYMLKRMY ELDESGRRYQKKAAACPDPSLSVWRPDIYPRASVSETTETKVDD YSQBWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEFGEAVG LLAAQSIGBFSTQWTLATTFHFAGRGMNVTLGIPRLAEILMVAS ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRCLGEVLQKIDVQ ESSCMEEKQNNKFQVYQLEFFGELPHAYQQBKCLRPEDILFFMET RFFKLLMESIKKKNNKASAPRNVNTRRATQRDLDMAGELGRSRG EQGGDBEEEGHIVDABAEEGDADASDAKKKEGEEVDYESSEE EEREGERDDEEMGERNPHECARTGQDEEVGL\GH-GGPV PSRPPDAAPETTHPQFGAPGA\EAMERRVQAVRETHPPIDDYQD TEBSLMCQVTVKLPHAKINPMSSTGQDEEVGL\GH-GGPV PSRPPDAAPETTHPQFGAPGA\EAMERRVQAVRETHPPIDDYQD TEBSLMCQVTVKLPHAKINPMSSTGQDEEVGL\GH-GGPV PSRPPDAAPETTHPQFGAPGA\EAMERRVQAVRETHPPIDDYQD TEBSLMCQVTVKLPHAKINPMSVLSLAHGAUIYAHKGITEC LLMETTNNKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH AIANTYGIEBALRVLEKBIKDVFAVVGIAVDPRHLSLVADYMGF EGYVKPLNRFGIERNSSFLQQMTFSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQDER SGCGGRLPTVL*L*GPPGSCFCILSLF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGYMGREGPGGSGRGKGEMGSFGF APCQKEFFAFSVGRKTALHSGEDFGTLLFERFYNNLGGCFDMAT GGPAAPLRGIYFFSLHVHSNNYKETHMINGKGAVLKVLYADGS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGGLLKAEDD SGCERKATVRLAPDYDALVVATKIGIT SJCERKRAVVRLAPDYDALVVATKIGIT SJCERKRAVVRLAPDYDALVVATKIGIT SJCERKRAVVRLAPDYDALVVATKIGIT SYPFRRPKTL*LRRQPKYPWKSTPRNKLDHHVIKFPLTTE*A VKKIENNSLLVFTVDVKANRHQIKQAVKK/LCDIDVAKVNTLIQ SJCERKRAVVRLAPDYDALVVATKIGIT SJCERKRAVVRLAPDYDALVVATKIGIT SJCERKRAVVRLAPDYDALVVATKIGIT SJCERKRAVVRLAPDYDALVVATKIGIT SJCERKRAVVRLAPDYDALVVATKIGIT SJCERKRAVVRLAPDYDALVVATKIGIT SJCERKRAVVRLAPDYDALVVATKIGIT SJCERKRAVVRLAPDYDALVVATKIGIT SJCERKRAVVRLAPDYDALVVATKIGIT SJCERKRAVVRLAPDYDALVVATKIGIT AVKIENNSLLVFTVDVKRANRGIKCDHVIKFPLTTE*A VKKIENNSLLVFTVDVKRANRGIKCDHVVIKFPLTTE*A VKKIENNSLLVFTVDVKRANRGICTCNPGPRKSMSKLLYTRL AVFFIERMVASLGARAVADGVVCQUFVGITANGGILTSVNSHILIAN SDDLVFPGFFELV				ł i
CGPQAVRAALNIPEAASYDEVRGKWQDAHLGKDQRDFNMTDLKF KEEVNHYSNBINKACMPFGHRQFPENTLQLMVQGGAKGSTVNT MQISCLLGQIELEGRSTPLMASGKSLPCFBFYBFTPRAGGFVTG RFITGIKPPBFFFHCMAGREGLUDTAVKTSSGTLQRCIIKHLE GLVVQVDLTVRDSDGSVVQFLYGBGDLDIPKTQFLQFKPFPTLLR SNYBVIMKSQHLHEVL;SRADPKKALHHPRAIKKWQSKHPNTLLR RQAPLSYSQKIQEAVKALKLESENRNNGR/RPWDS/G/RMLRMWY ELDEESRRKYQKKAAACPDPSLSVWRPDIYPASVSETFETKVDD YSQBWAAQTEKSYEKSELSLDRLRTLLQL/KWQRSLCEPGEAVG LLAAQSIGBPSTQMTLNTFHPAGGEMNVTLGIPRIREHLMVAS ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ ESSCMEEKQNKTQVVQLBPQFLDHAYYQQBKCGRPBDILRFHET RFFKLLMESIKKKNNKASAFRYNVNTRATQRDLDNAGELGRBGB EQRGDEEBEGHTVDABABEGDADASDAKRKKQBEBVDYESEEB ERREGEENDDEDMOGBERRPHRSGAKTQBQDEBVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\SAMKEKQBEBVDYESEEB EERREGEENDDEDMOGBERRPHRSGAKTQBQDEBVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\SAMKEKQBEBVDYESEEB EERREGEENDDEDMOGBERRPHRSGAKTQBQDEBVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\SAMKEKQBEBVDYESEEB EERREGEENDGEBORGERRPHRSGAKTQBQDEBVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\SAMKEKQBEBVDYESEEB EERREGEENDDEDMOGBERRPHRSGAKTQBQDEBVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\SAMKEKQBEBVDYENSEE EERREGEENDDEDMOGBERRPHRSGAKTQBQDEBVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\SAMKEKQBEBVDYENSEH ANTYGIERAALRVIEKBIKDVPAVYGIAVDPRHLSLVADYMCF EGVYKPLNRFGIERSNSSPLQQMTFETSFQPLKQATMLGSHDBLR SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSGQRLPTVL*L*GPFGSCPCILSLEY*PGRHALPEIRFYINI TILKGDKGDDFGMGLDGYMGREGPGGBFGPGSKGDKGEMGSPG APCOKRFPAFSVGRRTALHSGEDPGTLLFERVFVNLDGCFDMAT GQFAAPLRGIYPFSLNVHSWNYKETYVHLMQKERAVILKYAQPS ERSIMGSQSVMLDLAYGDRVWYLFKRQRENATYSNDFDTYTTF SGGLIKAEDD 5385 326 799 LMVPFTKREAPAPFKAEAKAAL\KAKKAVLKDVHSHKKNKTHM SPTFRRPKTL*LRRQPKYPMKSTPRRKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKRGIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPFTKREAPAPPKAEARAKAL\KAKKAVLKDVHSHKKNKTHM SPTFRRPKTL*LLRRQPKYPMKSTPRRKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKRGIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGGWFVLGERRAGSLLASGYGFAMPGWVLFGRRWATA SDDLVFPGFFELVVRUMIGILTLYILMRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIRMCYMRGTICTMGPRKSMSKLLYIRL ALFEPTWAASJGGAWFUGGCORTVVNGIIATNVGSMIITIAA	ļ			
KEBUNHYSNEINKACMPFGLHRQFPENTLQLMVQSGAKGSTVMT MQISCLLGQIELEGRSTPLMASGKSLPCFBPYEFTPRAGGFVTG RFLTGIKPPEFFFHCMAGREGLUTJAVKTSRSGYLQRCIIKHLE GLVVQYDLTVRDSDGSVVQFLVGBEGLDIPKTQFLQPKQFPFLA SNYBVJMKSQHLHEVLJSRADPKALHHPRAJKKMQSHPPHTLAR RGAFLSYSQKIQEAVKALKLESENRNGR/RPWDS/G/RMLRMMY ELDEESRRKYQKKABACPDPSLSVWRPDIYBAVSTETTETKVDD YSQBWAAQTEKSYEKSELSLDFLRTLLQL\KWQRSLCEPGEAVG LLAAQSIGBPSTQMTLNTHPFAGRGEMNVTLGIPRLERLMVAS ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ ESPCMEEKQNKYQVYQLRPQFLPHLAYYQQBECLBPEDILRFHET RFFKLLMESIKKKNNKASAFRNVNTRRATRODLDNAGELGRGRG QEGEDEEGGHIVDAEABEGDADADAKRKKQDEEVDTKSEEE EEREGEENDDEDMQEERNPHREGARKTQBQDEEVGL/GH*GGPV PSRPPDAAPETHPQGAPGA\SAMERRVQAVREIHPPIDDYQYD TEBSLMCQVTVKLPLMKINFPMSSLVVSLAHGBVIVATKGITC LLMETTYNNNBKELVLNTEGINLPPLFKYABVLDLRRLVSNDTH AIANTYGIEAALRVIEKBIKDVPAVXGIAVDPRHLSLVADYMCF GGYXFLNRFGIRSNSSDLQQMTFETSFQFLKGATMLGSHDBLR SPSACLVVGKVVRGGTGLFELKQPLR SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSGGQRLPTVL*1*GPPGSCPCILSLF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGTMGREGGPGGPGPGGSKGNKGBNGSPG APCQKRFFAFSVGRKTALHSGEDPGTLIFPRVFVNLDGCFDMAT GQFAAPLRGIYFFISINVHSWYKYETYVHIHMNGKEAVILXQDS ERSIMGSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPFRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPPFRRPKTL*LRRQPKYPWKSTPRRKLDHHVIIKPPLTT**A VKKIENNSLLVFTVDVKANKHQIKQAYKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPFKAEARAKAL\KAKKAVLKOVHSHKKNKIHM SPPFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKPPLTT**A VKKIENNSLLVFTVDVKANKHQIKQAYKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGGWFVLGERRAGSLISASYGFFAMPGMVLPGRRWATA ALFFPEMWASLGAAWVADGVCQCRTVVNGIIATVVVSHIIIAA				I ·
MQISCLIGGIELBGRSTPLMASGKSLPCFEPYEFTPRAGGFVTG RFLTGIKPPBFFFCMAGREGLVUTAVKTSRSGYLQRCIIKHLE GLVVQYDLTVRDSDGSVVQFLYGEDGLDIPKTQFLQPKQPPFLA SNYSVIMKSQHLHEVLSRADPKKALHHPRAIKKWQSKHPNTLLR RGAFLSYSQKIQEAVKALKLESENRNGR/RPMDS/GJRMLRMWY ELDEESRRKYQKKAAACPDPSLSVWRPDIYPASVSETFETKVDD YSQBWAAQTEKSYEKSELSLDRLRTLLQLKWQRSLCEPGEAVG LLAAQSIGBBSTQMTLNTFHFARGGEMMVTLGI PIRKEILMVAS ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ ESSCMEEKQNKFQVYQLRPQFLPHAYYQQBKCLRPEDILRFMET RFFKLLMESIKKKNKNASAFRANTRATQRDDNAGELGRBRG EQEGDEEEGHIVDABABEEGDADASDAKRKEKQEEEVDYESEEE ERREGEENDDEDMGERRPHREGARKTQEQDEEVGL/GH*GGPV PSRPPDAAPETHEPPEDAPOATHEPPEDAPOXY PSRPPDAAPETHEPPEDAPOXY TEBSLMCQVTVKLPLMKINFDMSSLVVSLAHGAVIVATKGITRC LLNETTINNKNEKELVLNTEGINLPEHFKYABVLDLRRLYSNDIH AIANTYGIBAALRVIEKBIKDVPAVYGIAVDPRHLSIVADYMCF EGYYKPLNRFGIRSNSSPLQOMTFETSFQFLKQATMLGSHDELR SPSACLVVKKVVAGGTGLFELKQPLR SPSACLVVKKVVAGGTGLFELKQPLR 5384 196 886 QSGGRLPTVL*L*GPPGSCCILSLF\PGRPHALPEIRYPINI TILKGDKGDPGPMGLPGYMGREGPQGBFGPGSKGDKGBMGSPG APCOKRFPAFSVGRKTALHSGEDPGILFERVPVILDGCFDMAT GQFAAPLRGIYFFSLNVISWYKETYVHIHMNCKEAVILYAQPS ERSIMGSQSVMLDLAYGGRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKOVHSHKKNKHM SPTFRRPKTL*LRRQPKYPWKSTPRRKLDHHVIIKFPLTTE*A VKXIENNSLLVTVDVKANKIQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKOVHSHKKNKHM SPTFRRPKTL*LRRQPKYPWKSTPRRKLDHHVIIKFPLTTE*A VKXIENNSLLVTVDVKANKIQIKGNKL/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLISASYGTFAMPGMVLFGRRWATA SDDLVPPGFFELVVURVLWNIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICMPGPRKSNSKLLIYIRL ALFFPEMWASLIGAAWVADGVGCORTVVNGIIATVVVSNIIIAA				
RFLTGIKPEFFFENMAGREGLUDTAVKTSRSGYLQRCIIKHLE GLVVQYDLTVRDSGSVVQFLYGEDGLDIPKTQFLQFKGFFFLA SNYEVIMKSQHLHEVLSRADPKKALHIFRAIKKWQSKHPNTLLR RGAFLSYGKIQEAVKALKLESENRNGR/RPMDS/G/RMLRMMY ELDESRRKYQKKAAACPDPSLSVWRPDIYFASVSETFETKVDD YSGEMAAQTEKSYEKSELSLDRLRTLLQL\KWGRSLCEFGEAVG LLAAQSIGEBSTOMTLNTFHFAGRGEMUVTLGIPRLREILMVAS ANIKTPMMSVVYUNTKKALKSLKSQLTRVCLGEVLQKIDVQ ESFCMEEKQNKFQVYQLRFQFLPHAYYQQEKCLRPEDILRFMET RFFKLLMESIKKKNNKASAFRNNNTRRATQRDLDMAGELGRSRG EQEGDEESEGHIVDBABEADASDAKREKGEBEVDVESEEB EERGGEENDDEDMGEERNPHREGARKTQSQDEEVGL\GH*GGPV PSRPPDAAPETHPQPGAPGA\EAMERVQAVREIHPFIDDYQYD TEESLMCQVTVKLPLMKINFDMSLLVSLAHGAVIYATKGITRC LLMETTINKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH AIANTGIERALRVEIKERISDVAVGGIAPPHLSLVADYMCF EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSCGQKLPTVL*1-GPPGSCCTLSLF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHISGEDFGILLERVFVNLLDGCFDMAT GGPAAPLRGIYFFSLAVHSMYKETTVHTMHMQKEAVILYAQPS ERSIMOSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKXIENNSLLVPTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVLAPDYDDALVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKXIENNSLLVPTVDVVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCMFVTJGERTAGSLASGGTFAMFGMVLFGRRWAIA SDDLVPFGFFELVVRVILMNIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMCGTICNPGFRKSMSKLLVTILA ALFFPEMVWASLGAAWVALQVCDRTVVNGITATVVVSWIIIAA				
GLWVQYDLTVRDSDGSVVQFLYGEDGLDIPKTQFLQPKQFPFLA SNYEVIMKSQHLHEVUSRADPKKGLHIFRAIKKWQSKHPNTILIR RGAFLSYSQKIQEAVKALKLESENRING/RPMPS/G/RMLRMMY ELDEESRRKYQKKAAACPDPSLSVWRPDIYFASVSETFETKVDD YSQEWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEFGEAVG LLAAQSIGEBSTOMTLNTFHFAGRGEMNVTLGIPRLREILMVAS ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ ESFCMEEKQNKFQVYQLRFQFLPHAYYQQEKCLRPEDILRFMET RFFKLLMESIKKKNNKASAFRNNNTRATQRDLDNAGELGRSRG EQEGDEEEGHIVDABABEGDADASDAKREKQEBEVDVESEEE EERRGENDDEDMQEERNPHREGARKTQEDEVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIHFFIDDYQTD TEESLMCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC LLMETTINKNEKELVLNTEGINLPELFKYARAUDLRRLKYSNDIH AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF EGYYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVVRGGTG1EPEFFYNNLDGFFTWYNLDGFFTOMAT GQFAAPLRGIYFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSGVMLDLAYGBRWWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKXIENNSLLVPTVDVKANHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKXIENNSLLVPTVDVVKANHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVIGERAGSLSASGTFAMPGMVLFGRRMAIA SDDLVPPGFFELVVRVLWIGGILTLYLMRRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICTPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVASLGAWVRGVCDRTVVNGITATVVVSWIIIAA	1			
SNYEVIMKSÇİLHEVL SRADPKKALHIFRA IKKWQSKIPNTLIL RAPLISYŞÇKI QEAVKALKLESENRING / RIMLENMY ELDESRRKYÇKKABAÇDPSLSVIR PDI YPASVSSTFETKVDD YSQBWAAQTEKSYEKSELSLDRLRILQÜ, KWQRSLCEBGEAVG LLAAQSI GEPSTOMTLNTFHFAGRGEMIVTLGI PRLREILMIVAS ANIKTPIMISVYVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ ESPEMEEKQNKFQVYQLEFQFLPHAYYQQEKCLRPEDILRFMET RFFKLLMESI KKKNINKASAFRINVITRRATQRDLDNAGELGRSRG EQEGDEEEGHI VDABAEBGDADADARKKEQEESVDYESREE EEREGEENDEDDMOGERNPHREGARKTQEQDEEVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA \ Lametinnewselvukuruhipmsslvvslahadaviyartigitrc LLMETINNKEKELULNTEGI INLPELFKYAEVLDLRRLYSNDIH AIANTYGI ERASLRVUKUKURGTGLPELKQATMLGSHDELR SPSACLVVGKVVRGGTGLPELKQPLR SPSACLVVGKVVRGGTGLPELKQPLR SPSACLVVGKVVRGGTGLPELKQPLR SPSACLVVGKVVRGGTGLPELKQPLR SPSACLVVGKVVRGGTGLPELKQPLR GQFAAPLRGI YFFSLNVHSWIY KETYVHIMINQKAVILYAQPS ERSIMSOSVIMLDLAYGDRVWRLFKRQRENAI YSNDFDTYITF SGHLIKAEDD 5385 326 799 LMYPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRKLEDHDVILKFLTE*A VKKIENNSLLVFTVDVKANKQI KQAVKK/LCDIDVAKVNTLIQ SDGERKAYVLAPDYDALVVATKIGIT 5386 326 799 LMYPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKITI*LRRQPKYPMKSTPRRNKLDHHVIIKFPLITTE*A VKKIENNSLLVFTVDVKANKHQI KQAVKK/LCDIDVAKVNTLIQ SDGERKAYVLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVPFGFELVURVLMGI SLAYVKNGU KQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 4 PVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVPFGFFELVURVLMIGI SLAYLYMHRGKLDCAGGALLSSY LIVLMILLLAVVI CTVSAIMCVSMRGTI CNPGPRKSMSKLLYIRL ALPFPEMVWASLGAAWVADGVQCRTTVVNGI IATVVVSWI IIAA ALFFPEMVWASLGAAWVADGVQCRTTVVNGI IATVVVSWI IIIAA ALFFPEMVWASLGAAWVADGVQCRTTVVNGI IATVVVSWI IIIAA ALFFPEMVWASLGAAWVAGGVQCRTTVVNGI IATVVVSWI IIIAA ALFFPEMVWASLGAAWVAGGVQCRTTVVNGI IATVVVSWI IIIAA ALFFPEMVWASLGAAWVAGGVQCRTTVVNGI IATVVVSWI IIIAA ALFFPEMVASLGAAWVAGGVGCRTTVVNGI IATVVVSWI IIIAA ALFFPEMVASLGAAWVAGGVGCRTTVNGI IATVVVSWI IIIAA ALFFPEMVASLGAAWVAGGVGCRTTVNGI IATVVVSWI IIIAA ALFFPEMVAGACGAAULSSCAAWVAGGVGCRTTVNGI IATVVVSWI IIIAA ALFFPEMVAGCCACGAALLSSY LIVUMILLAVVI CTVSAIMCVSMGGTCNPGPRKSMSLLYIRI ALFFPEMVAGCCACGA	1			
RGAPLSYSQKIQEAVKALKLESENRNGR/RPWDS/G/RMLRMWY ELDESSRKYQKKAAACPDPSLSWRPDIYPASVSETTETKYDD YSQBWAAQTEKSYBKSELSDRLRTLLQL/KWQRSLCEGGEAVG LLAAQSIGEPSTQWTLNTFHFAGRGEMNVTTGIPRLREILMVAS ANIKTPMMSVPVLNTKKALKRVKSLKKQLITRVCLGEVLQKIDVQ ESSCMEEKQNKFQVYQLRFQFLPHAYYQQEKCLRPEDILRFMET RFFKLLMESIKKKNNKASAPRNVNTRRATQRDLDNAGELGRSRG EQEGDEEEGHIVDABABEEGDADASDAKRKEKQEEVDYYESEEE EERRGEENDDEDMGEERNPHREGARKTQEQDEEVGL/GH*GGPV PSRPPDAAPETHPQDGAPGA\CANGRUKYUSLAHGAVIYATKGITRC LLMETTINKMEKELVLNTEGINLDELFKYAEVLDLRRLYSNDIH AIANTYGIEAALRVIEKBIKDVFAVGLAVDPRHLSLVADVMCF EGVYKPLNRFGIRSNSPLQQMTFFTSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSCQGLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI TILKGDKGDDGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCOKRFFAFSVGRKTALHSGEDEGTLLFERVFVMLDGCFDMAT GQFAAPLRGIYFFSLNVHSWBYKETYVHIMINOKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWKVLFKQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVRANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVRANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVPFGFFELVURVLMMIGILITLYLMHRGKLDCAGGALLSSY LIVLMILLLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFFEMVWASLGAAWVAGDGVCCRTVVNGIIATVVSWIIIAA	1			
ELDEESRRKYQKKAAACPDPSLSVWRPDIYPASVSETTETKVDD YSQBWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEPGEAVG LLAAQSIGEPSTQMTLINTHFPAGRGEMNVTIGIPRLREILWVAS ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ ESFCMEEKQNKFQVVQLRFQFLPHAYYQQERCLRPEDILRFMET RFFFKLLMESIKKKNKKASAFRNVNTRATQRDLDNAGELGRSRG EQEGDEEEGHIVDAEABEEGDADASDAKRKEKQEEEVDYESEER EREGEENDDEDMGERRFHPEGARTTGEQDEVGL/GH**GGFV PSRFPDAAPETHQPGPAGA\EMERRVQAVREHPFIDDYQYD TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC LLMETTINKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH AIANTYGIEAALRVILEKBIKDVPAVVGIAVDPRHILSLVADVMCF EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQDLR SPSACLVVGKVVRGGTGLFELKQDLR GQCGQRLPTVL*L**GPPGSCFCILSLF\PGRPHALPRIRPYINI TILKGDKGDPGPMGLPGYMGREGPQCEPGPGGSKGDKGEMSSPG APCOKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMGSQSVMLDLAYGDRVWVLFKQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVFTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL**LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE**A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPFTKKEAPAPPKEARAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL**LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE**A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWATA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRRKSMLLLYFTV ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA				
YSQBWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEPGEAVG LLAAQSIGEPSTOWTLNTTHFAGRGEMNUTTLGIPRLREILMVAS ANIKTPMWSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ ESFCMEEKQNKFQVYQLRFQFLPHAYYQQEKCLRPEDILRFMET RFFKLLMESIKKKNKKASAFRNNNTRRATCRDLDNAGELGRSRG EQEGDEEEGGHIVDAEAEEGDADASDAKKEKQEEVDYESEEE EEREGEENDDEDMQEERNFHREGARKTQEQDEEVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREHPPFIDDYQYD TEESLWCQVTVKLPLMKINTGSINLPELFKYAEVLDLRRLYSNDIH AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF EGYYKPLNRFGIRSNSSPLQWTFFTSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTEFEKQPLW SSPACLVVGKVVRGGTGEFEKQPLW TILKGDKGDRGPMGLPGYMGREGPQGEPGPGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLLGCFDMAT GQFAAPLRGTYFFSLNVHSWNYKETTVHIMNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD SJ85 326 799 LMVPFTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRNKLDHHVIIKPPLTTE*A VKKIENNSLLVFTVDVKANKHQIKGAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPFTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRNKLDHHVIIKPPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVPFGFFELVURVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVUMILLAVVICTVSAIMCVSMRGTICTNPGPRKSMSKLLYFIL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA				
LLAAQSIGEPSTQMTLNTFHFAGRGEMNVTLGIPRLREILMVAS ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ ESFCMEEKQNKFQVVQLTPCHPLHATYQOEKCLHPEDILRFMBT RPFKLLMESIKKKNNKASAFRNVNTRRATQRDLDNAGELGRSRG EQEGDEEEGGIIVDAEAEEGDADASDAKRKEKQEEVDYSESEE EERRGEENDBEDMQERNPHREGARKTQEQDEEVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\EAMERVQAVREHPPTDDYQYD TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYARKGITRC LLNETTNNKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH AIANTYGIEAALRVIEKEIKDVPAVVGIAVDPRHLSLVADVMCF EGYVKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQPLR GGCGGRLPTVL*L*6PPGSCPCILSIF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCUKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLURGIYFFSLWHSWNYKETYHINNOKEAVILXQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRNKLDHHVIIKFPLTTE*A VKKIENNSLLVPTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVPFGFFELVURVLWIGILTLYLMHIGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLLYFIL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	1	1		
ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ ESFCMEEKQNKFQVYQLRFQFLPHAYYQQEKCLRPEDILRFMET RFFKLLMSIKKKNNKASAFRNVNTRRATQRDLDNAGELGRSRG EQSGDEEEGHIVDABABEEGDADASDAKKEKQEEVDYESEEE EERRGEENDDEDMQEERNPHREGARKTQBQEEVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIPPFIDDYQYD TEBSLWCQVTVLNPLMKINFDMSSLVVSLAHGAVIYATKGITRC LLNETTNNKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH AIANTYGIEAALRVIEKEIKDVFAVYGIAVDRHLSLVADYMCF EGYVKPLNEFGIRSNSPLQQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSCGQRLPTVL*L*GPPGSCPCILSF\PGRPHALPEIRPYINI TILKGDKGDPGFMGLPGYMGRGPQGBFGPQGSKGMKGFMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMYPRTKKEAPAPPFKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/CCDIDVAKVNTLIQ SDGERKAYVRLAPDALVVATXIGIT 5386 326 799 LMYPRTKKEAPAPPFKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/CCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATXIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFFGFFELVVRVLMWIGILTLYIMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSA MCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVMASLGAAWVADGVQCRTTVVNGILTATVVVSWIIIAA	ļ			_ · · · · · · · · · · · · · · · · · · ·
ESFCMEEKQNKFQVYQLRFQFLPHAYYQQEKCLRPEDILRFMET RFFKLLMSSIKKKNNKASAFRVNNTRRATQRDLDNAGELGRSRG EQEGDEEEGGHIVDAEAEEGGDADASDAKKEKQEEEVDYESEEE EEREGEENDDEDMQEERNPHRSGARKTQEQDEEVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIHPFIDDYQYD TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC LLMETTINKNEKEKELVLNTEGINLPELFKYAPEVLDLRRLYSNDIH AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF EGYYKPLNRFGIRSNSSPLQOMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQPIR 5384 196 886 QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGYMGREGPQGEPGPGSSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSMYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPMKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVXRANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPMKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFFGFFELVVRVLWMIGILTLYIMHRGKLDCAGGALLSSY LIVUMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVSWIIIAA	İ			
RFFKLLMESIKKNNKASAFRNVNTRRATQRDLDNAGELGRSRG EQECIDEEEGHIVDAEABEGDADASDAKRKERQEEETVYSSEEE EEREGEENDDEDMQEERNPHREGARKTQEQDEEVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\SAMERRVQAVREIHPFIDDYQYD TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC LLMETTINKNBKELVLINTEGINLPELFKYAEVLDLRRLYSNDIH AIANTYGIEAALRVIEKEIKDVPAVYGIAVDPMCFL EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSCGQRLPTVL*L*GPPGSPCGLESF\PGRPHALPEIRPYINI TILKGDKGDPGFMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMINQKEAVILVAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWATA SDDLVFFGFFELVVRVLWWIGILTLIXIMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVAGGVQCDRTVVNGIIATVVVSNIIIAA	1			
EQEGDEEEGHIVDAEAEEGDADASDAKRKEKQEEEVDYESEEE EEREGEENDDEDMQERRPHREGARKTQEQDEEVGL/GH*GGPV PSRPPDAAPBTHPQFGAPGA\EAMERRVQAVREIHPFIDDYQYD TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC LLNETTNNKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH AIANTYGIEAALRVIEKEIKDVFAVYGIAYDPRHLSLVADYMCF EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSCGQRLPTVL*L*GPPGSCFCILSLF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGYMGREGPQGEPGPGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKHHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKXIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKHHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKXIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYIMHRGKLDCAGGALLSSY LIVUMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	ł			
EEREGEENDDEDMQEERNPHREGARKTQEQDEEVGL/GH*GGPV PSRPPDAAPETHPQPGAPGA\EAMBRRVQAVREIHPFIDDYQYD TEESLWCQVTVKLPLMKINPDMSSLVVSLAHGAVIYATKGITRC LLNETTINKINEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSCGRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVULDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMWPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SFTFRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVUMGILTLYLMHRGKLDCAGGALLSSY LIVUMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	1	. *		
PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIHPFIDDYQYD TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC LLNETTNNKNEKELVLNTEGIINLPELFKYAEVLDLRRLYSNDIH AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSCGQRLPTVL*L*GPPGSCPCTLSLEYPGRHALPETRPYINI TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVEVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGWFVLGERRAGSLLSASGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADCVQCDRTVVNGIIATVVVSWIIIAA				.,
TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC LLMETTINKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGARWADGVQCDRTVVNGIIATVVVSWIIIAA				
LLNETTNNKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	1			
AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	1			1
EGVYKPLNRFGIRSNSSPLQMTFETSFQFLKQATMLGSHDELR SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA				
SPSACLVVGKVVRGGTGLFELKQPLR 5384 196 886 QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWATA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA				1 = 1 · · · · · ·
5384 196 886 QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA				
TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYPFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVPTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	5384	196	886	<u> </u>
APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	}		000	, · · · · · · · · · · · · · · · · ·
GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVPTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA				•
ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVPTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA				
SGHLIKAEDD 5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRPKTL*LRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRPKTL*LRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	1			
5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRPKTL*LRQPKYPWKSTPRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRPKTL*LRQPKYPWKSTPRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	1			
SPTFRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	5305	326	700	
VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRPKTL*LRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	2305	340	133	•
SDGERKAYVRLAPDYDALVVATKIGIT 5386 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRRPKTL*LRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA				
5386 326 799 IMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM SPTFRPKTL*LRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	ĺ	1		
SPTFRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	E200	336		
VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	2386	326	799	
SDGERKAYVRLAPDYDALVVATKIGIT 5387 2 2117 FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA				
5387 2 2117 FVVAASGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWATA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA				
SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA				
LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA	5387	2	2117	
ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA		ŀ		
			•	
TVVS111VFDPLGGKMAPYSSAGPSHLDSHDSSQLLNGLKTAAT				
	L			TVVSIIIVFDPLGGKMAPYSSAGPSHLDSHDSSQLLNGLKTAAT

Predicted Predicted en Incetin Predicted en Incetin In				
No:	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence Proline, Q-Gultamine, R-Arginine, Sequence Sequenc				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first maino acid residue of amino acid residue of amino acid residue of amino acid sequence solvente per per commine, Verlandine, Secriptine, Sec	NO:	nucleotide	_	Glutamic Acid, F=Pnenylalanine, G=Glycine,
to first amino acid residue of amino acid residue of amino acid sequence Septence #Typtophan, Y=Tyrosine, X=Unknown, *=Stop codom, y-possible nucleotide deletion, \possible nucleotide insertion) SVENTRIKELCCCIGKONTWAFSTRALE/STYTSDTDLYSSD TARGLALINGOONTRINGSPAGVYCHAGSSGEADLAELKUN HYMOPARAATGMPLITYINFELTICLICIGGEOCCRSRNGTONTM HYMOPARAATGMPLITYINFELTICLICIGGEOCCRSRNGTONTM HYMOPARAATGMPLITYINFELTICLICIGGEOCCRSRNGTONTM HYMOPARATGMPLITYINFELTICLICIGGEOCCRSRNGTONTM HYMOPARATGMPLITYINFELTICLICIGGEOCCRSRNGTONTM HYMOPARATGMPLITYINFELTICLICIGGEOCCRSRNGTONTM HYMOPARATGMPLITYINFELTICLICIGGEOCCRSRNGTONTM HYMOPARATGMPLITYINFELTICLICIGGEOCCRSRNGTONTM HYMOPARATGMPLITYINFELTICLICIGGEOCCRSRNGTONTM HYMOPARATGMPLITYINFELTICLICIGGEOCCRSRNGTONTM HYMOPARATGMPLITYINFELTICLICICIGGEOCCRSRNGTONTM HYMOPARATGMPLITYINFELTICLICICIGGEOCCRSRNGTONTM HYMOPARATGMPLITYINFELTICLICICIGGEOCCRSRNGTONTM HYMOPARATGMPLITYINGHALDSVORGENGOCCRANGTONTM HYMOPARATGMPLITYINGHALDSVORGENGOCCRANGTONTM HYMOPARATGMPLITYINGHALDSVORGENGOCCRANGTONTM HYMOPARATGMPLITYINGHALDSVORGENGOCCRANGTONTM HYMOPARATGMPLITYINGHALDSVORGENGOCCRANGTONTM HYMOPARATGMPLITYINGHALDSVORGENGOCCRANGTONTM HYM		location		
amino acid residue of amino acid sequence solvence whitepophan, 1=71yrosine, X-cünknown, *=Stop Codon, /=possible nuclectide deletion, 1-possible nuclectide disertion, 1-possible nuclectide insertion, 1-possible nuclectide disertion, 1-possible nuclectide disertion, 1-possible nuclectide insertion, 1-possible nuclectide disertion, 1-possible nuclectide disertion, 1-possible nuclectide insertion, 1-possible nuclectide disertion, 1-possible nuclectide, 1-possible		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
amino acid residue of amino acid sequence solvence whitepophan, 1=71yrosine, X-cünknown, *=Stop Codon, /=possible nuclectide deletion, 1-possible nuclectide disertion, 1-possible nuclectide insertion, 1-possible nuclectide disertion, 1-possible nuclectide disertion, 1-possible nuclectide insertion, 1-possible nuclectide disertion, 1-possible nuclectide disertion, 1-possible nuclectide insertion, 1-possible nuclectide disertion, 1-possible nuclectide, 1-possible		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
menio acid amino acid sequence Sequence			residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence Codom, /-possible nucleotide deletion, -possible nucleotide insertion) SVMETRIKLICCTIGEDDHTRUAPSSTARLESTYPSDTDLVPSD LARGIALHGQQDMIRMORGENAPGSSGARDLDAELKOK HNYMOFARARVOWELVITNEPLTGLCRIGGCCRSKRFQTHT/M VGCDQLQ/CTSAF LHHTHRARVOGLAPGCLAPGLAFTER KGISQARYVYGRIHMODILGAGRIADFULDEVELTPPLVA LDHRKESVWANGTMSLQDVLTDLSARSSWLDVSCDVODRLAH KGISQARYVYGRIHMODILGAGRIADFULDVSCDVODRLAH KGISQARYVYGRIHMODILGAGRIADFULDVSCDVODRLAH KGISQARYVYGRIHMODILGAGRIADFULDVSCDVODRLAH KGISQARYVYGRIHMODILGAGRIADFULDVSCDVODRLAH KGISQARYVYGRIHMODILGAGRIADFULDVSCDVODRLAH KGISQARYVYGRIHMODILGAGRIADFULDVSCDVODRLAH KGISQARYVYGRIHMODILGAGRIADFULDVSCDVODRIAH FORDINGTSUTNEDLAGGRIADFULDVSCDVODRIAH FORDINGTSUTNEDLAGGRIADFULDVSCDVODRIAH FORDINGTSUTNEDLAGGRIADFULDVSCDVODRIAHVSLOF GONNALTDEMODILGAGRIHMOPPLICSTCGSFYGNPR TROMGSVCYKEHLGRQNSSNORISFPYQCTDGSVPRAGRAARS FSKILIGFMKILDEMODILGAGRIHMOPPLICSTCGSFYGNPR TROMGSVCYKEHLGRQNSSNORISFPYQCTDGSVPRAGRALDST TROMGSVCYKEHLGRQNSSNORISFPYDGAVPTEROVASVS DTAQQFSEQSSELEVANIKKELAVSCAGRIMDLLGAGRAGAGRIADFULDRAY TVYYTYCMYTTLITTTGQLLANFVYGCTDGSVPRAGRADST TROMGSVCYKEHLGRQNSSNORISFPYGCTDGSVPRAGRADST KONTOLANYQKGHLAVQLANMAQETHISACYPALCSTGCSFYGNPR TROMGSVCYKEHLGRQNSSNORISFPYGCTDGSVPRAGRADST TROMGSVCYKEHLGRQNSSNORISFPYGCTDGSVPRAGRADST TROMGSVCYKEHLGRQNSSNORISFPYGCTDGSVPRAGRADST TROMGSVCYKEHLGRQNSSNORISFPYGCTDGSVPRAGRADST TROMGSVCYKEHLGRQNSSNORISFPYGCTDGSVPRAGRADST TROMGSVCYKEHLGRQNSSNORISFPYGCTDGSVPRAGRADST TROMGSVCYKEHLGRQNSSNORISFPYGCTDGSVPRAGRADST TROMGSVCYKEHLGRQNSSNORISFPYGCTDGSVPRAGRADST TROMGSVCYKEHLGRGNSSNORISFPYGCTDGSVPRAGRADST TROMGSVCKYKHLGRGNSSNORISFPYGCTDGSVPRAGRADST TROMGSVCKYKHLGRGNSSNORISFPYGCTDGSVPRAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMGSVCKYKHLGAGRADST TROMG	<u>'</u>			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence				Codon /=possible nucleotide deletion,
SVMETRIKLICCTIGRODHTRAJESTTÄLETTYPSDTDIVPSD LARGIALHGQOONITRINGEPAQVCHAPGSSGENDLOBLEKING HYMOFARANYOMININGEPAQVCHAPGSSGENDLOBLEKING HYMOFARANYOMININGEPAQVCHAPGSGENDLOBLEKING LOHRESSVVANGTININGEPAQVCHAPGOLDHITFETELEPTIVA LOHRESSVVANGTINISLODVITULGASSEVLUVSCEVODRLAH KGISQARAYYOGINITULGASSEVLUVSCEVODRLAH KGISQARAYYOGINITULGIAGASISKULDIVSCEVODRLAH KGISQARAYYOGINITULGIAGASISKULDIVSCEVODRLAH EDVIPTISVINIELDEKRI ILVVANGTOKSKYKILLIGHAVITELEG GINNILPTELLOGGOOSVITOPLIGGGSLITRISPASSESSEPL DSPRYVPPLYPPGGI HILOGEGAGGRIGCGGARHYAKNISHAB FSKILLIGEMILTDEMPDILMRALDSVVSORRACVSCPAQGVSSV DVA TADCGAGGGGGRAGAGWERHYLYPPTGGYSRERAACOAERPAARS FSKILLIGEMILTDEMPDILMRALDSVVSORRACVSCPAQGVSSV DVA TONICALAYQKSILLIQURAMAQCENHAQOPHICSTOCGYSNPR TROMCSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TROMCSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TROMCSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCYKERLIGROSSNORTSPVOCTIOSVPEAGSALDST TONICSVCKARAGAGSASSLORGENCACARROMILLIGHANGVMP TONICSVCKARAGAGSASSLORGENCACARROMILLIGHANGVMP TONICSVCKARAGAGSASSLORGENCACARROMILLIGHANGVMP TONICSVCKARAGAGSASSLORGENCACARROMILLIGHANGVMP TONICSVCKARAGAGSASSLORGENCACARROMILLIGHANGVMP TONICSVCKARAGAGSASSLORGENCACARROMILLIGHANGVMP TONICSVCKARAGAGSASSLORGENCACARROMILLINGENTUCH TONICSVCKARAGAGSASSLORGENCACARROMILLINGENTUCH TONICSVCKARAGAGSASSLORGENCACARROMILLINGENTUCH TONICSVCKARAGAGSASSLORGENCACARROMILLINGENTUCH TONICSVCKARAGAGSASSLORGENCACARROMILLINGENTUCH TONICSVCKARAGAGSASSLORGENC			sequence	\=nossible mucleotide insertion)
TAGGIALIAGOGONIANOGEPAQVVCHAGGSSORADIDAELNOC HHYMOPANAAYOMPILYREPITGICEGOCCRSREPOTITY // VGGDQLQL/CTSAPILHHERANVGUHPROLEWITFIELPELVA LDHREKSTVVANKORISQOVITOLSASERVLUVSCOVDRIAN KGISQARSYVYQRLINDGILSQOFSITARPINIVIGSISLOGGAN ALLATWARANYOCKYPAPPPROHIMSKARGAPSTORFYSISULG GOVIPRISVYTNIEDLERBILRVANICRKRYKYLLHGIANYELPG GINNHLPTELDGGORVLYTOPLIGBGSLITHER PAYSPSSOPL BSSPKYPPLYPPKGILHQEBGASGRFGCCSRAHYSAXGSHERA FSKILIGERKILDEMBDILRARLDSVUSDRAACVSCAGGVSSV UNA STADGGAGGGGERQAGVERHYLYPPTGGYRERBAACQAERPAARS KDTDLAAYQKGHLGVQLENMAGCFINEGVYPHLCSTGCGFTGNP TNGMCSVCYKEBLGROSSGRRISFYDGCTDSSVPEAQGALDST TVYYTTCMTITLATITTGOLLENFYPCOGPTSSVPEAQGALDST TVYYTTCMTITLATITTGOLLENFYPCOGPTSSVPEAQGALDST TVYYTTCMTITLATITTGOLLENFYPCOGPTSSVPEAQGALDST TLEHLGITEN 5389 1569 753 7DAGGAGGGGRRQAGVERHYLYPPTGGYERBAACQAERPAARS KDTDLAAYQKGHLGVQLENMAGCTHEQOYPHLCSTGCGFTGNP TNGMCSVCYKEBLGRONSSNGRISFYPCGTDSVPEAQGALDST TLEHLGITEN TOMOCSVCYKEBLGRONSSNGRISFYPCGTDSVPEAQGALDST TLEHLGITEN TOMOCSVCYKEBLGRONSSNGRISFYPCGTDSVPEAQGALDST TNGMCSVCYKEBLGRONSSNGRISFYPCGTDSVPEAQGALDST TOMOCSVCYKEBLGRONSSNGRISFYPCGTDSVPEAQGALDST TOMOCSVCYKEBLGRONSSNGRISFYPCGTTGSVPEAQGALDST TOMOCSVCYKEBLGRONSSNGRISFYPCGTTGSVPEAQGALDST TOMOCSVCYKEBLGRONSSNGRISFYPCGTTGSVPEAQGALDST TOMOCSVCYKEBLGRONSSNGRISFYPCGTTGSVPEAGGALDST TOMOCSVCYKEBLGRONSSNGRISFYPCGTTGSVPEAGGALDST TOMOCSVCYKEBLGRONSSNGRISFYPCGTTGSVPEAGGALDST TOMOCSVCYKEBLGRONSSNGRISFYPCGTTGSVPEAGATGAGA TVYYTTCMTITLATITTKOLLENFYPCGGFTSGGSTGCGLEEVARS TOMOCSVCYKEBLGRONSSNGRISFYPCGTTGGARDAGA TOMOCSVCYKEBLGRONSSNGRISFYPCGTTGGARDAGA TOMOCSVCYKEBLGRONSSNGRISFYPCGTTGGARDAGA TOMOCSVCYKEBLGRONSSNGRISFYPUTTGGESTGGARGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGA		sequence		
HHYMGFAAAAYGMELITYRNPLTGLCRIGGOCKSRIPGTYTY V VGCDQLQL/CTSAELHITHRANQCGHAPGQLPWTFTELPPLVA LDHRKSSVVVANRTWSLQDVLTDLSAESSVLDVECEVQDRLAH KGISQAARYYQRLINGILSQSFIAPERILVIVGHSLGGGAA ALLATMVRAAYPQVRCYAFSPPRGUMSKALQBYSQSFIVSUVLG KDVIPRLSVYNLEDLKRRILEVVANCKOKPYKILLHGLWYSLFG GNPNNLPPELDGGQDEVLTQPLLGGGSLLTRWSPAYSFSSSPL DSSPKYPPLIVPRGILKGRESKGFTCCSAAHYSHSWSHEAE FSKILLIGBKMLTDHMPDILMRALDSVVSDBAACVSCPAQGVSSV DVA 5388 1569 753 **TANGCAGCGGRRQAGVERHYLYPPTGGYRRBAACQAEEPAAS RDTDLAAYGKSLGVDJENBAGVTSCGFYGNPR TROMCSVCYKEHLGRQSSSNGRISPPVQCTDGSVPEAGSALDSF SSSMQPSPVGNSLLSSVASSQLDSTSVVAKVPETDGVASVS DTAQQPSEGGSLSLNNRKKRLAVSCAGRKDLLGLANGVSMP TVYVTTOMTTLAITIKKNLKNSVCAGRKDLLGLANGVSMP TVYVTTOMTTLAITITKCHLKNSVCAGRKDLLGLANGVSMP TVYVTTOMTTLAITITKCHLKNSVCAGRKDLLGLANGVSMP TVYVTTOMTTLAITITKCHLKNSVCAGRKDLLGLANGVSMP TVYTTOMTTLAITITKCHLKNSVCAGRKDLLGLANGVSMP TVYTTOMTTLAITITKCHLKNSVCAGRKDLLGLANGVSMP TVYTTOMTTLAITITKCHLKNSVCAGRKDLLGLANGVSMP TVYTTOMTTLAITITKCHLKNSVCAGRKDLLGLANGVSMP TVYTTOMTTLAITITKCHLKNSVCAGRKDLLGLANGVSMP TVYTTOMTTLAITITKCHLKNSVCAGRKDLLGLANGVSMP TVYTTOMTTLAITITKCHLKNSVCAGRKDLLGLANGVSMP TVYTTOMTTLAITITKCHLKNSVCAGRKDLLGLANGVSMP TVYTTOMTTLAITITKCHLKNSVCAGRKDLLGLANGVSMP TVYTTOMTTLAITITKCHLKNSVCAGRKDLLGLANGVSMP TVYTTOMTTLAITITKCHLKNSVCAGRKDLLGLANGVSMP TVYTTOMTTLAITITKCHLKNSVCAGRKDLAGCLASKTSTNUL LDTVYCAGRKRDINGSCEDFERSLVCLTDFOADARACGLASKTSTNUL LDTVYCAGRKRDINGSCEDFERSLVCLTDFOADARACGLASKTSTNUL LDTVYCAGRKRDINGSCEDFERSLVCLTDFOADARACGLASKTSTNUL LDTVYCAGRKRDINGSCEDFERSLVCLTDFOADARACGLASKTSTNUL LDTVYCAGRKRDINGSCEDFERSLVCLTDFOADARACGLASKTSTNUL LDTVYCAGRKRDINGSTARAAQAA\GICVTTSTDAGS SAPICAGRAVATARAUGUSSCEDFTARAAQAA\GICVTTSTDAGS LEDIVIAAPGGRRGATURULGJSSVCATARAUGUSTACRAVUL LDTCCRSVAEINRINGUSSLANGVSRITURULGJSSVCATAGRAUGUSTACRAVUL ALALGAKCIFLGDALLANGVSRLAV VKRAAGRSGFFTAGGGCERAFGTVWERRLGVARAVYRENGGSF OPPCKIKMINGGGLAVAFVOGUSTARAUGUSTACRAVULA LTCCRSVAEINRINGUSSLAVENGVSTLAVSTLANGVSTLAVSLAVENG ALALGAKCIFLGDALLANGVSRLAV VKRAAGRSGFTAGGGCERAFGTVWERRLGVARAVYRENGGSF OPPCKIKMINGGGSGGAGGGGGDAAAPHLLKQCGSVATARAVILAGLEGGSSV VYMGGRELLGLAVATACTVATTRUVTTRUVTHAGGEBFTLANGV	_	ł	ł	
VGGDIGLI, CTSAPILHTERRAVGGIHERGLEWIRTELEPILU LDERKES VUVANFORTSLODVILDSASESULDVECKYODELAH KGISQARAYYYGRINDGILSGAFSIAPETRUVIVGHSIGGGA ALLATWRARAYYORCYCAFSEPREMIKSALQEYSGYISULG KDUTPRISVYNILEDLKREI LEVVAMCHKEPKYKILLHGIMYELFE GNENNILPTELDGGODGEVITOPLIGEGSILATRINS PAYSFSISDEL DSSPKYPPLYPRGII HLQBEGASGRFGCCSARHYSAKMISEAB FSKILLIGPKHITOPHOPLIMBALDSVYSDRAACVSCPAGVSSV DVA TADGGAGGGERBOAVERHYLYPPTGGYBREBAACQAERPAARS FONDLAAVGKSLOVURHYLYPPTGGYBREBAACQAERPAACBAACHTGGSFONDLAAVGKSLOVURHYLTTRAGGABCAACGAACGAACGAACGAACGAACGAACGAACGAA		1	Ì	TAAGLALLHQQQDNIRNNQEPAQVVCHAPGSSQEADDDAEDRAC
LDIRKES WVAVRATINS LODVITUS ARSSEVLD VECEVORE LANK KGISOARAY YORKING LISOS PETAPET KINVIVORISIGGIAA ALLATIWARAY POWECYAS SPREMINSKALDEN SOSFI VISITUS KUTUPEL SVINLED KER I LEVVALGKOR PETAPET KILLIGAMY PELOG CINPINLE PIEL DES DES VEYPEL PY PETAPET INLEGES GASE PETAPET KILLIGAMY PELOG CINPINLE PIEL DES DES VEYPEL PY PETAPET INLEGES GASE PETACES AND VAR SERVEPL PY PETAPET INLEGES GASE PETACES AND VARIANCE PER FEXILIGEM LICHEMA PETAPET AND VARIANCE		1	l	HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGDCCRSKNPQTWT/M
KGISQARYYYQRLINGGILSQAFSIAPEYRIVIVGHSLGGGAA ALLATWRAAYYOQRCYAFSPFRGWSKAIQEYSQISULGU KDYIPRLSVYNLEDLKREILBVVAHCNEPKYKILLHGLMYELF GNPNNLPTELLGGGOBUTNOPELLGGSLILTRIKS PAYSFSSDSPL DSSPKYPPLYPGRIIHLDGGSLILTRIKS PAYSFSSDSPL DSSPKYPPLYPGRIIHLDGGSLILTRIKS PAYSFSSDSPL DSSPKYPPLYPGRIIHLDGGSLILTRIKS PAYSFSSDSPL DSSPKYPPLYPGRIIHLDGGSLILTRIKS PAYSFSSDSPL DSSPKYPPLYPGRIIHLDGGSLILTRIKS PAYSFSSDSPL DSSPKYPPLYPGRIIHLDGGSLILTRIKS PAYSFSSDSPL DSSPKYPPLYPGRIIHLDGGSLILTRIKS PAYSFSSDSPL DSSPKYPPLYPGRIIHLDGGSLITRIKS PAYSFSSDSPL DSSPKYPPLYPGRIIHLDGGSLITRIKS PAYSFSSDSPL TROMGSVCYKEHLDGROSSNORIS PYVQCTDGSVPERQSALDGST SSSMOPSPVENGSLISSVASGLOBSTSVKAVPETEDVQASVS DTAQQPSEGGSLSENSKASGLOBSTSVKAVPETEDVQASVS DTAQQPSEGGSRGAVERHYLYPPTGGYRRBAACQAERPAARS KDTDLAAYQKGHLGVQLSKNAQETHISQVPMLCSTGGGFYGNF TVYYTYTOMTITALITIKOMLKNFVQOEKKSFGSFHQQLLEYK ILBHLQTTKN TOMOCVCKEHLDRONSORSICHE PPVQCTTGGSVPRAF TNOMCSVCKEHLDRONSORSICHE PPVQCTTGGSVPRAF SSSMOPSPVENGSLLSSVASGLDSTSVKAVPETEDVQASVS DTAQQPSEGGSKSLVNRKKRLAVSCAGRMBULGIANGVSMS TVYYTTOMTITALITIKOMLKNFVYQOEKKSFGSFHQQLLEYK ILBHLQTTKN TVYYTTOMTITALITIKOMLKNFVYQOEKKSFGSFHQQLLEYK ILBHLQTTKN TVYYTTOMTITALITIKOMLKNFVYQOEKKSFGSFHQQLLEYK ILBHLQTTKN TVYYTTOMTITALITIKOMLKNFVYQOEKKSFGSFHQQLLEYK ILBHLQTTKN TVYYTTOMTITALITIKOMLKNFVYQOEKKSFGSFHQQLLEYK ILBHLQTTKN TVYYTTOMTITALITIKOMLKNFVYQOEKKSFGSFHQQLLEYK ILBHLQTTKN TVYYTTOMTITALITIKOMLKNFVYQOEKKSFGSFHQQLLEYK ILBHLQTTKN TVYYTTOMTITALITIKOMLKNFVYQOEKKSFGTHTTTQTLAKYCHTOMAPTALOG SSCALTSTGFHCHWPDGGMSTARAAQAAAJACAGCSKRTOMTITALITIK SAPICATOMAPTALOFICH SCHOOL TARABAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Ì			VGGDQLQL/CTSAPILHTHRAAVQGLHPRQLPWTRFTELPFLVA
ALLATWIRANTPOURCHASPERGENSKALGETSGEFIUSLULG KDVTPRLSVTNLEGHKRITLKUVALGENGERVILHGLMYBLIGG GNRNILPTELDGGDGEVLTNOPLIGGGSLITMS PAYSFSSDEP DSSPKYPPLYPPGGT HILDGESGSGEGCGANAPSFSSDEP DSSPKYPPLYPPGGT HILDGESGSGEGCGANGAPSSPKYPSDA 5388 1569 753 TADGGGGGGRQAVREHYLTYPTGGYBRERAGGGEEDARA KOTDLAAVGKGHGVQLRIMAGETNISQVPMLGSTGGFYGNRP KOTDLAAVGKGHGVQLRIMAGETNISQVPMLGSTGGFYGNRP TOMOGSVCYKEHLGRQNSSNGRISPVQCTDGSVPBAGGALDST SSSMGPSFVSNGSLISSSVASSGLDSTSVDRAVPETEDVQANSV DTAQQPSEEGASSLES NRRKKRIAVSCAGRKROLLGARAVENF TVYTYTVMTTIAHITITKGMLKNFVYQGEFKSFGSFHQGLLEFK ILBELGTRN 5389 1569 753 TADGGGGGGRQAVGRHYLYPFTGGYBRERAGCQAEPAARS KOTDLAAVGKGHGVQLRIMAGETNISQVPMLGSTGGGFYGNRP TNGMCSVCYKEHLGRQNSSNGRISPVQCTDGSVPBAGGALDST SSSMGPSFVSNGSLISSSVASGLDSTSVDRAVPETEDVQANSV TNGMCSVCYKEHLGRQNSSNGRISPVQCTDGSVPBAGGALDST SSSMGPSFVSNGSLLSSVASSQLDSTSVDRAVPETEDVQASVS DTAQQPSEEGASSLENSVASGLDSTSVDRAVPETEDVQASVS TNGMCSVCYKEHLGRQNSSNGRISPVQCTGGSVPBAGGALDGEF SSSMGPSFVSNGSLLSSVASSQLDSTSVDRAVPETEDVQASVS DTAQQPSEEGASSLENSVASGLDSTSVDRAVPETEDVQASVS DTAQQPSEEGASSLENSVASGLDSTSVDRAVPETEDVQASVS DTAQQPSEEGASSLENSVASGLDSTSVDRAVPETEDVQASVS DTAQQPSEEGASSLENSVASGLDSTSVDRAVPETEDVQASVS TVYTTOMYTIALITIKKQMLKNPVQCFKSFGSFGGGFYGQLEFK TLEHLGTRN 100000000000000000000000000000000000	J	†	}	LDHRKESVVVAVRGTMSLQDVLTDLSAESEVLDVECEVQDRLAH
EDUTPILEUTRILEUTRICLEGGSLITRINFEPATSFSISSE DSSEXPPELYP PORT I HILOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGESTER POWER OF THE THOMAS OF THE THOM			•	KGISQAARYVYQRLINDGILSQAFSIAPEYRLVIVGHSLGGGAA
EDUTPILEUTRILEUTRICLEGGSLITRINFEPATSFSISSE DSSEXPPELYP PORT I HILOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGCESARTY SANKHEAE FSXLLIGPMILTDHMP I LIHOSEGASGERGESTER POWER OF THE THOMAS OF THE THOM		1	(ALLATMVRAAYPOVRCYAFSPPRGLWSKALQEYSQSFIVSLVLG
GNPNNLPPELDGODGUTTOPLIGEGGSLITRMSPAYSPSSSPSIPL DSSPKYPELTP PGRI THIGGEGGASGREGGGGARATYSANNSHEAB FSXLIIGPKMLTDHMPDILMRALDSVVSDRAACVSCPAGGVSSV DVA TADGGAGGGGRQAGVRHYLYFFTGGYRRERAACQAEVBARS KOTTLAAYQKSHLGVQLRMAGGTMHSQVFHLCSTGCGFYGNPR TROMCSVCYKRHGLQKNSSNGLBSPVQCTGDSVPERQSALDST SSMOPSPVSNOSLLSBSVASSQLDSTSVDKAVEETEDVQASVS DTAQQSSEGGSKSL&\NRNKRALVSCAGRKADLLGLANGVEMF TVYYTYTOMYTIALTITGOMLKNFVFQOGFKSFGSHQLLEYK LEHLDTKN TADGGAGGGGEQGAGGAGGARAFTANAVEETEDVQASVS DTAQGSSEGGSKSL&\NRNKRALVSCAGRKADLLGLANGVEMF TVYYTYTOMYTIALTITGOMLKNFVFQOGFKSFGSHQLLEYK LEHLDTKN TADGGAGGGGEQGAGGAGGARATHSQUAMCSTGCGFYGNPR TROMCSVCYKHLQRQNSSNGGTSPPVQCTDGSVPEAQSALDST SSSMQPSPVSNQSLLSBSVASSQLDSTSVDKAVPETEDVQASVS DTAQQSSEGGKSL&\NRNKKRIAVSCAGRKMDLLGLANGVEMF TVYYTYTOMYTIALTITGOMLKNFVFQOGFKSFGSFFQQLLEYK LEHLDTKN DTAQQSSEGGKSL&\NRNKKRIAVSCAGRKMDLLGLANGVEMF TVYYTYTOMYTIALTITKOMLKNFVFQOGFKSFGSFFQQLLEYK LEHLDTKN DTAQQSSEGGKSL&\NRNKKRIAVSCAGRKMDLLGLANGVEMF TVYYTTOMYTIALTITKOMLKNFVFQOGFKSFGSFFQQLLEYK LEHLDTKN DTAQQSSEGGKSL&\NRNKKRIAVSCAGRKMDLLGLANGVEMF TVYYTTOMYTIALTITKOMLKNFVFQOGFKSFGSFFQQLEYK LEHLDTKN SCAGGADSITTRDMIAAFKTRAPFYLRDVSSVTPRTTQGEET SSSMQPSFVSNGSLLSESVASSQLDSTSVDKAVPSTTDQGASVATAVAVSCAGT SSSMQPSFVSNGSFFQAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG		1	1	KDVIPRLSVTNLEDLKRRILRVVAHCNKPKYKILLHGLWYELFG
DSSPKYPELYPEGRIIHLGEGASGREGCGSAAHYSAKNSHEAE FSKILIGEMALTDHMPDILMRALDSVVSDRACVSCPAGGVSSY DVA TADGGAGGGGRQAGVRHYLVEPTGGYRRRBAACQAEEPAARS KDTDLAAYGKRUGUGURMAQETHHSQVPMLCSTGCGFYGNPR TNOMCSVCYKEHLQRQNSSNGRISFPVQCTDGSVPERGSALDST SSSMGPSPVSNGSLESSVASSGLDSTSVDKAVEETEDVQASVS DTAQQPSEEQSRSLE\NENKRLAVSCAGRKWDLLGELNGGWBF TVYVTYTOMYTLITITROLKHYFYQGGFKSFGSFHQQLLEYK LIBHLGTKN TADGGAGGGGRQAGGREUVLYPPTGGYRRBAACQAEEPAARS KDTDLAAYQKGNLGVQLRNMAQETHHSQVPMLCSTGCGFYGNPR TNOMCSVCYKEHLQRQNSSNGRISFPVQCTDGSVPERGSALDST SSSMGPSFVSNGSLLSSEVASSGLDSTSVDRAVPETEDVQASVS KDTDLAAYQKGNLGVQLRNMAQETHHSQVPMLCSTGCGFYGNPR TNOMCSVCYKEHLQRQNSSNGRISFPVQCTDGSVPERGSALDST SSSMGPSFVSNGSLLSSEVASSGLDSTSVDRAVPETEDVQASVS KDTDLAAYQKGNLGVQLRNMAQETHHSQVPMLCSTGCGFYGNPR TNOMCSVCYKEHLQRQNSSNGRISFPVQCTDGSVPERGSALDST SSSMGPSFVSNGSLLSSEVASSGLDSTSVDRAVPETEDVQASVS LIBHLGTKN TNOMCSVCYKEHLQRQNSSNGRISFPVQCTDGSVPERGSPHQQLLEYK LIBHLGTKN TURNATITALITITROLKNEYFYGGERFSFGSFHQQLLEYK LIBHLGTKN LIBHLGT		1		CNPNNI, PTEL DGGDOEVI TOPLLGEOSLLTRWSPAYSFSSDSPL
FSXILIGEMILTHMEDILMRALDSVVSDRAACVSCPAGGYSV DVA 5388 1569 753 TADGGGGGERDAGVRRHYLYPTGGYRRRAACQAERPARS KDTDLAAYQKONLOVQLRMAQGTHMSOVPHLCSTGGGYRNPR TNOMGSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST SSSMQPBPVSNOSLLSESVASSQLDSTSVDKAVPETEDVQASVS DTAQQSEEGSKEL%NRNKKHAVSCGRKWDLLGLRAGVSWS TVYYTYTOMYTIALTITKOMLKNFVFQGEKSFGSHQLLEKK ILBRLQTRN 5389 1569 753 **TADGGAGGGGRQAGVRRHYLYPTGGYRRRAACQAERPAARS KDTDLAAYQKONLGSVASHAQSTHSQVPUNCSTGGGFYGNPR TNOMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST SSSMQPSPUSNOSLLGSEVASSQLDSTSVDKAVPETDVQASVS DTAQQPSEEQSKSLE\NRNKKRLAVSCAGRKWDLLGLNAGGEMF TOYYTYTTGMYTIALTITKQMLKNFVFQGEFKSFGSHQLLEYK LEHLQTRN 5390 217 1332 **EDFFRKLMEDKNWSECEGFEMSLVCLTDFQAHAREQLSKSTRDFI GGADDSITRDNIAPKRTRLRFPYLRDVSSVTRTTTQGEET SAFICTAPTGFHCLWWPGSMSTARAAQAA\GICYTTSTFASCS LEDLVLAAPEGLNRFQLVYUPDGLINKGLLYSSLFFKALVIT LLDTPVCANRENDIARFKTRLRFPYLRDVSSVTRTTTQGEET SAFICTAPTGFHCLWWPGSMSTARAAQAA\GICYTTSTFASCS LEDLVLAAPEGLNRFQLVYUPDGLINKGLLYSSLFFKALVIT LLDTPVCANRENDIARFKTRLFPYLRDVSSVTRTTTQGEET SAFICTAPTGFHCLWWPGSMSTARAAQAA\GICYTTSTFASCS LEDLVLAAPEGLNRFQLVYUPDGLINKGLLYSSLFFKALVIT LLDTPVCANRENDIARFMTTATDLASPKKENANIPYPTMTIS **TSCWNDLSWFQSTTRDFILKSLTKTTLDGSPKKANAIPYPTMTIS TSCWNDLSWFQSTTRDFILKSLTKTTLDGSPKKANAIPYPTMTIS TSCWNDLSWFQSTTRDFILKSLTKTTLDGSPKKANAIPYPTMTIS **TICCRSVAREIRRIUTGFSRL **TICCRSVAREIRRIUT		1	1	DCCDVVDDLVDDCDTTHLOFFGASGRFGCCSAAHYSAKWSHEAE
5388 1569 753 KDTOLAAYQKENLOVLENMAQETHISOVPHICSTOCGFYONPR TNOMCSVCYKEHLORINSOUTHLCSTOCGFYONPR TNOMCSVCYKEHLORINSOUTHLCSTOCGFYONPR TNOMCSVCYKEHLORINSOUTHLCSTOCGFYONPR TNOMCSVCYKEHLORINSOUTHLCSTOCGFYONPR TNOMCSVCYKEHLORINSOUTHLCSTOCGFYONPR TVYTTYTOMYTIALTITKOHLKMPTYOCGFYSETSSTHOOLAUSY DTAQOPSEEQSKSLEVNENKKRIAVSCAGRIMOLLALBAGVEMF TVYTTYTOMYTIALTITKOHLKMPTYOCGFYSETSSTHOOLAUSY LIBHLOTIN 5389 1569 753 MOTOLAAYQKONLOVQLENMAQETHISOVPHICSTOCGFYONPR TNOMCSVCYKEHLORINSOUTHISOVPHICSTOCGFYONPR TNOMCSVCYKEHLORINSOUTHISOVPHICSTOCGFYONPR TNOMCSVCYKEHLORINSOUTHISOVPHICSTOCGFYONPR TNOMCSVCYKEHLORINSOUTHISOVPHICSTOCGFYONPR TNOMCSVCYKEHLORINSOUTHISOVPHICSTOCGFYONPR TNOMCSVCYKEHLORINSOUTHISOVPHICSTOCGFYONPR TVYTTYTOMYTIALTITKOHKMPTYOCGFSFORSPHOOLLEYK TILBHLOTKN 5390 217 1332 EDFEKKMEDKWISSEGFPEMSUCLTDFOAHAREOLSKSTRDFI SGADDSITRDDNIAAFKRILARPYLROVSSUNTETTOGEEI LEDIVIAAPEGRINFOLLYWHPDIALBKOLIQVUSSIGFKALVIT LITTOCHNOLEMPOSITRIDINIAAFKRILARPYLROVSSUNTETTOGEEI SAPICIAPPOFHICLWERDEMSTARAAOAI(SYTTSTFASCS LEDIVIAAPEGRINFOLLYWHPDIALBKOLIQVISSIGFKALVIT LITTOCHNOLEMPOSITRIDINIAAFKRILARPYLROVSSUNTETTOGEEI SAPICIAPPOFHICLWERDEMSTARAAOAI(SYTTSTFASCS LEDIVIAAPEGRINFOLLYWHPDIALBKOLIQVISSIGFKALVIT LITTOCHNOLEMPOSITRIDINIAAFKRILARPYLROVSSUNTETTOGEEI SAPICIAPPOFHICLWERDEMSTARAAOAI(SYTTSTFASCS LEDIVIAAPEGRINFOLLYWHPOLALKSUNTUNIAVINOGGIIVS NIGGROLDEVIASIDALTVOLAKKRILARVINVOGIIVS NIGGROLDEVIASIDALTVOLAKKRILARVINVOGIIVS NIGGROLDEVIASIDALTVOLAKKRILARVINVOGIIVS NIGGROLDEVIASIDALTVOLAKKRILARVINVOGIIVS RELECTIOLIAARVINVOGIIPLIAARVINVOGIIPLIAARVINVOGIIVS RRILETELDOLIRIYVOJIVHOLLOLAKSUNTUNIAVINOGIIVS RRILETELDOLIRIYOTGOSSORLORIPATOVINVOR RRILETELDOLIRIYOTGOTSTOPISPIKAS OQATYLSILABOTYTEOUI LIYOGGSSSULARVINVO DPACKKSPIMESPIKASITOTOTSTOTSTOPISIKAS TROVIGRELSIGBWINGSPIKARATOVSTILEVINSPISHVISS VCRCUPHERAHCCHPSCPSOPRCHAPGRAAAPHILLOROPPIXLE VYAPAKDEPILLOPISTOTOTSTOPISTIKASILPHTY RTOVITRAINIAHEAUPOVORGSWKKARMINALASVIKSINERPA GRISIIHISTOLISISVAPROTOTOTSTOPISIKASILPHTYN RTOVITRAINIAHEAUPOVORGSWKKARMINALOROPSILISHTYNIST PGEPPI GGIVSAURIPHENDARVINGOSSORJAGGRO	1	}	1	BOART TODAMI ADMODIT MONT DERIGODO NACAGEA
TADGGGGGGREDGURERTYLYPTGYPRERBACQBREPANS	1	1	ļ	1
KDTDLAAYQKONLGVQLRNMAQETNISQVPMLCSTGCCFYGNPR TNGMCSVCVKEHLQRONSSNGRISPPVCTSVPEDVASVD SSMQPSPVSNGSLLESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEGQSRSLESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEGQSRSLESVASSQLDSTSVDKAVPETEDVQASVS TVYYTYTQMYTTALTITKQMLKMFVYQGEFKSFGSFHQQLLEYK ILBHLQTKN 5389 1569 753 TADGGAGGGRRQAGVRHYLYPPTGGYRRRAACQAERPAARS KDTDLAAYQKONLGVQLRNMAQETNISQVPMLCSTGCGFYGNPR TNGMCSVCVKEHLQRONSSNGRISPPVGTGSVPEARGALDST SSMQPSPVSNGSLLGESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRLAVSCAGRKHDLLGLANGGVBM TVYYTTYCMYTTALTITKQMLKNFVYQGEFKSFGSFHQQLLEYK ILBHLQTKN 5390 217 1332 EDPFKLMBEDKMSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI EGGADDSITRDDNTAAFKRIRLRRYLRDVSEVDTETTQGEET SAPICTAPTGPHCLWMPDGEMSTARAAQAA\GCYTTTSTPASCS LEDIVTAPEGHENDISNORTHITLTDLOSGFKALVIT LDTPVCNGNRHDIENQLRRUTLTLDGSEJKRALVIT LDTPVCNGNRHDIENQLRRUTLTLDGSUSKANLPYPGMYDIS TSLCWNDLSWFQSITRLPIILKGILTKEDABLAVKHNVGGILVS NHGGRQLDEVIASIBLATEVVAAVKKIEVILDGVRTNODVLK ALALGAKCTLGDAILMALASKGEHGVKEVINILTMEPHTSMA\ LTGCRSVAEINRHLVQFSEL VKRAAGRSKGFFTAGGGCGEAPGTVMERRLGVRAWVKENRGSF QPPVCNKLMIGSGLKWFVGGFNTRKDYHIESGSEVYQLSBGM VLRVLLGGGRHEDVINGGS IFTLLARAV PHSCPTVLUVER RRLETELDGLRYYVGDTMDVLFEKMFYCKOLGTQLAPITORFFK SEQURTGKFIPDQLLKEPPPPLSTRSIMPSDLAWLUSHHREL QAGTFILLGEDFTYBTQUIAYGGSSSGLRQNVDWLWQLEGSSV VTMGGRELSLGPWMGSENGLKAARTQVSTLEVPSLPNNSSPHYLSV VCRCUPHRPAHCCHEPPSCPSQFCHAPGRAAAPHLLWQTQPTAL PULPGGLPPPPLLIPIELJCTCTSTSTPSIKAS 1623 1623 1RGSNAQKVVGASGGGAGGGPOPDPAGFGGYPALAAAALGACEPR RGMSISHIETGDLSLSVATRQVTANHHBSISPAGGGTDMTD YVAYAKDOFINGRACHTLECCGGLAQSISTSVAGGGERIFKQVY LHSPPKXAGEBSCHGLKAARTQVSTLEVPSLFNNSSPHYLSV VCRCUPHRPAHCCHEPSCPSQFCHAPGRAAAPHLLWQTQPTAL PULPGGLPPPALPIPILSLQTCTSTSTPRSIKAS FIRKPARGMLHPDARVLGGVSVVVRMGCIEVLRSMRSLDFNT RTQVTRBAINRHEAVPGVRGSBKRKAPMKALBSVILKSNIFFA GMSISHIETGDLSLSVAPTRQVTANHHBSISPAGGGTDMTD YVAYAKDPINGRACHTLECCGGLAQSISTSVAGGREDFKKQV LHSPPKXAGLPPPRLAGPESSANGDEDBSPKKLLFKNNFFA GMSISHIBTGDLSLSVAPTRQVTANHHBSISPAGGGDTDMTD YVAYAKDPINGRACHTLECCGGLAGSISTGCGGAGGAGGEBFKKQV LHSPPKXAGLPPPRLAGPEBSANGDEDBSPKKLLFNNNSIPGKEPPL GGLVDSRLAALTOPCALTALDGGPSSLRHYNNSIPGKEPPL GGLVDSRLAALTOPCALTAL	1		<u> </u>	
TINGMCSVCYKERLIGRONSSINGEIS FPVQCTIDGSVPÄGGALIDST SSSMØPSPVNSGLISESVASSGLDSTSVKAVPETEBOVOANVS DTAQQPSECSKSLE\NRNKKRLAVSCAGRKMDLIGLKAGVEMF TVYYTYTOMYTIALTITKOMLKNFVFQGEFKSFGSFHQQLLEYK LIEHLIGTKN 5389 1569 753 TADGGAGGGGRQAGVERHYLYPFTGGYRREAACQAERPAARS KOTDLAAAVQKORLGVQLRMMAQETHHSQVPMLCSTGCGFYGNPR TOMCSVCYKERLIGRONSSINGEIS PPVQCTIGGSVPÄGGALDST SSSMQPSPVSNQSLLSESVASSGLDSTSVKAVPETEBOVAGNUS DTAQQPSEEQSKSLE\NRNKKRLAVSCAGRKWDLLGLNAGVEMF TVYYTYTOMYTIALTITKOMLKNFVFQGEFKSFGSFHQQLLEYK LIEHLIOTKN 5390 217 1332 EDPRKLMEDKMISSCEGPEMSLVCLTDFQAHAREQLSKSTEDFI LEGHLOTKN EGGADDSITEDDIN LAFKERLRLEPFYLADVSEVDTRETTIQGEEI SAPICIAPTGPHICLWEDGEMSTARAAQAA GICYITSTFASCS LEDIVIAAPEGLRWFQLYVHPDLQINKQLIQKVESLIGFKALVIT LDTTVCGNRRHDIRNQLRRHLITKEDAELKANINVGGITY NHGGRQLDEVLASIDALTEVVAAVKKIEVYLDGGVRTSNDVLK ALALGAKCIFLGDALLAMLASKGEHGVKEVINILTMEFHTSMA\ LTGCRSVAEINNNLUVSSRL 1292 VKKAAGRSRGFPTAGGQRCEAPGTYMERRIGVAWKKRNGGSF SOVRTKAGEPTAGGORCEAPGTYMERRIGVAWKRNGGSF RRLETELDGIRTYVGDTMOVLEFKWFYCKLDGTALAFILGEFEN RRLETELDGIRTYVGDTMOVLEFKWFYCKLDGTALAFILGEFEN SAGVRTKERPIPDLIKKEPPPLSTRESIDEPMSLDAHLDSHHREL QAGTPLSLEGDWINGLIVLSWGGEST INEPMSLDAHLDSHHREL QAGTPLSLEGDWINGLIVLSWGGEST INEPMSLDAHLDSHHREL QAGTPLSLEGDWINGLIVLSWGGEST INEPMSLDAHLDSHHREL QAGTPLSLEGDWINGLIVLSWGGEST INEPMSLDAHLDSHHREL QAGTPLSLEGDWINGLIVLSWGGEST INEPMSLDAHLDSHHREL QAGTPLSLEGDWINGLIVLSWGGST INEPMSLDAHLDSHHREL QAGTPLSLEGDWINGLIVLSWGGST INEPMSLDAHLDSHHREL QAGTPLSLEGDWINGLIVLSWGGST INEPMSLDAHLDSHHREL QAGTPLSLEGDWINGLIVLSWGGST INEPMSLDAHLDSHHREL QAGTPLSLEGDWINGLIVLSWGGST INEPMSLDAHLDSHHREL QAGTPLSLEGDWINGLIVLSWGGST INEPMSLDAHLDSHHREL GALVSKLAUTOPGAVAVARGSGGGGGPOPDPAGGGVPALAANICAGCEFR GEGSAGNEWTGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	5388	1569	753	TADGGAGGGRRQAGVRRHYLYFFTGGYRRRAACQAERPAARS
SSSMQPSPVSNOSILJESSVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKIEL, NAMKKRLAVSCRWDLLGIAVAGVEMF TVYYTTQMYTTLATITKQMLKNFVFQQEFKSFGSFHQQLLEYK ILBEHLQTKN TADGGGGGRRQAGVRRHYLYPFTGGYRRRRAACQAERPAARS KDTDLAAYQKGNLGVQLRNMAQBTNHSQVPMLCSTGCGFYGNPR TNONCSUCVCKEHLQRQNSSINGLISPVCHGSVEPAGAALDST SSSMQPSPVSNQSILLSESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKIE, NRNKKRLAVSCAGRKWDLLGLNAGVEMF TVYYTVTQMYTTALTITKQMLKNFVFQOEKSFGSFRQQLLEYK ILBHLOTKN DEPKLMREDEMMSECEGPEMSLVCLTDFQAHAREQLSKSTEDFI EGGADDSITRDDNIAAFKRIRLRPRYLEDVSEVDTRTTIQGEBI SAPICIAPPGFHCLWWEDGEMSTARAAQAA\GICYITSTFASCS LEDIVIAAPEGGRWFQLYVHPDLQLINKQLIQRVESLGFKALVIT LDTPVCGNRRHDIRNQLRRNLTITDLGSPKKGNAIPYFQMTPLIS TSLCWNDLSWFQSTTRIPJILKSGLITKAGLLGVKENGGIVS NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\ LTGCRSVAEINRNLVQPSRL 1 1292 VKKAAGRSRGFFTAGGGCEEAFGTVMERRLGVRAWKENRGSF QPPVCNKHMIQRQLKVMFVGGPNTKRDYHIEGGEBYFYQLEGDM VLRVLEQGKHRDVVIRQGEIFLLDPARVPHSFQRFANTVGLVVER RRLETELDGLRYYYGDTWOLTEFKMFVDHIEGGEBYFYQLEGDM VLRVLEQGKHRDVVIRQGEIFLLDPARVPHSFQRFANTVGLVVER RRLETELDGLRYYYGDTWOLTEFKMFVDHIEGGEBSSV VTMGGRISLGTWMBSLLVLJWMGPSYLAWKENGSSSV VTMGGRISLGTWMBSLLVLJWMGPSYLAWKENGSSP SEQXRTGKFIPDQLKEPFPLSTRSIMEPMSLDAWLDSHREL QAGTFLSLGFWHSPLSLJVLJWMGPSYLAWKENGSSP VTMGGRISLGTWMSLLVLJWMGPSYLAWKENGSSP VTMGGRISLGTWMSLLVLJWMGPSYLAWKENGSSP VTMGGRISLGTWMSLLVLJWMGPSYLAWKENGSSP VTMGGRISLGTWMSLLVLJWMGPSYLAWKENGSSP SEQXRTGKFIPDQLKEPPFPLSTRSIMEPMSLDAWLDSHREL QAGTFLSLFGDTYFTQVLATGGSSEGGRRGNAGGAAAPAHPLLWQOPPTAL PVLPGGLPPAFLCRGAGSGGRGRGGRGAGASGDAAAARENIRKGS FIHKPAHGWLHPDARVLGPGSSVVVVYMGCIEVLRGMRSLDFNT RTQVTRERAINGLIBEAPGVARGSMKKANKALASVUGKSNIRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISPAGGDTDMTD VYAYVALDPERLAGPESSAMGDEBOSLEINTYNSIFGKEPPL GGLVDSRIALTGPCALTALDQGFSSAMGDEBOSLEINTYNSIFGKEPPL GGLVDSRIALTGPCALTALDQGFSPSLRDAGSLDWOGSTGTAP PGGGVAGDARGPPBERLYVNTQGDFLURGVTNGGVYLTGMH AGQPKHLLLVDFGGVVRTKOVLPESISHLIDHHLQNGQPIVAAB SSLHLRGGVYSREP GGGDSAGMWTGNSONVCPRNLWILLDPLTVLLLLLASADSQAAAP	J.			KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
DTAQQPSEEQSSLE\NRNKRELAVSCAGEKWDLLIGLNAGVEMF TVYYTVTVMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK ILBHLQTKN 5389 1569 753 TADGGAGGGGRQAGVURHYLLYPFTGYTRERAACQAERPAARS KDTDLAAVQKGNLAVQLRNMAQETHHSQVPMLCSTGCGFYGNPR TXQKCSVCVKERLORQNSSNGRISPVQCTLGSVPBAQSALDST SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRLAVSCAGEKWDLLGLNAGVEMF TVYYTVTQMYTIALTITKOMLNNFVFQQEFKSFGSFHQQLLEYK ILBHLQTKN 5390 217 1332 EDFRKLMEDENMSECEGPEMSLVCLTDFQAAAREQLSKSTRDFI LEGLOTKN EGGADDSITRDDNIAAFKRIRLRPRYLRDVSEVDTRTTIQGEBI SAFICLAPGSHRWDQLYVHPDJQLNKQLIQRVESLGFKALVIT LDTFVCANRHDIRNOLGRRNLTLTIDLSPKKGRAIPYFGMF1S LEDIVIAAPEGLRWDQLYVHPDJQLNKQLIQRVESLGFKALVIT LDTFVCANRHDIRNOLGRRNLTLTIDLSPKKGRAIPYFGMF1S TSLCWNDLSWFQSITRUPIILKGILTKEDABLAVKINVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKKRIVEYDLOGVRTGNDVLK ALALGAKCIFLCDALLMALASKGEHGVKEVLNILTTREPHTSMA\ LTGCRSVAEINNLVQPSRL VKKAAGRSGPPFDAGGOREBAPGTVMERRLGVRAWVKENRGSF QPPVCNKLMHQBQLKVMFVGGPNTRKDVHLEBGEEVFYQLBGDM VLRVLEGGKHRDVVLRQGGSGGREDAFGTVMERRLGVRAWVKENRGSF RRLETELDGHTYYVGDTWDVLFEKMFYCKDLGTQLAPIIQBFFS SBOYRTCKPIPDDLLKEPPFPLSTRSINEPMSHLVVLVER RRLETELDGHTYYVGDTWDVLFEKMFYCKDLGTQLAPIIQBFFS SBOYRTCKPIPDDLLKEPPFPLSTRSINEPMSHLVLVE QDAGTPLELSLGGDTLYATVGGSSGLRQNVDVMLWQLGGSSV VTMGGRRLSLGPWMDSLLVLSWGPSV\AW\RRTQGSVALSVT\Q DDACKKSPNGBPSCGLKAATGVPSTLEVPSLPNNSSPHYLSV VGRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTTAPRRSIKAS FIHKBALGHPDARVLGPGVSVVVFYMGCIEVLRSMRSLDPNT TYQVTREBINHLEAUPAVURGSKSKKKANAKALASVLJKSKNLRFA GMSISHHSTDGLSLSVPATRQVIANHMPSISPAGGDTDMTD VVAYAKOPINQRACHILECCGGL\GADEPEDSFKDLEFKOY LHISPFKVALPPBRLAGPEBSAWGDEBDSLEINYYNSIPGKEPDI GGLVDSRLALTQCGALTALDQGSPSLRDAGSLEPKNOY LHISPFKVALPPBRLAGPEBLYVNTYGLSTTAVAPTEEQ LRQEWYHGRMSRRAAERMLRADGDFLVSBOTTRAPVAPTEEQ LRQEWYHGRMSRRAAERMLRADGDFLVSBOTTRAPVAPTEEQ LRQEWYHGRMSRRAAERMLRADGDFLVSBOTTRAPVAPTEEQ LRQEWYHGRMSRRAAERMLRADGDFLVSBOTTRAPVAPTEEQ LRQEWYHGRMSRRAAERMLRADGDFLVSBOTTRAPVAPTEEQ LRQEWYHGRMSRRADERHLYVNTQLBTSTALDPHTVAACH AGQPKHLLLVDPGGVORTKKDVLPESISHLLDHLLQNGQPIVARA	1			TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST
DTAQQPSEEQSSLE\NRNKRELAVSCAGEKWDLLIGLNAGVEMF TVYYTVTVMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK ILBHLQTKN 5389 1569 753 TADGGAGGGGRQAGVURHYLLYPFTGYTRERAACQAERPAARS KDTDLAAVQKGNLAVQLRNMAQETHHSQVPMLCSTGCGFYGNPR TXQKCSVCVKERLORQNSSNGRISPVQCTLGSVPBAQSALDST SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRLAVSCAGEKWDLLGLNAGVEMF TVYYTVTQMYTIALTITKOMLNNFVFQQEFKSFGSFHQQLLEYK ILBHLQTKN 5390 217 1332 EDFRKLMEDENMSECEGPEMSLVCLTDFQAAAREQLSKSTRDFI LEGLOTKN EGGADDSITRDDNIAAFKRIRLRPRYLRDVSEVDTRTTIQGEBI SAFICLAPGSHRWDQLYVHPDJQLNKQLIQRVESLGFKALVIT LDTFVCANRHDIRNOLGRRNLTLTIDLSPKKGRAIPYFGMF1S LEDIVIAAPEGLRWDQLYVHPDJQLNKQLIQRVESLGFKALVIT LDTFVCANRHDIRNOLGRRNLTLTIDLSPKKGRAIPYFGMF1S TSLCWNDLSWFQSITRUPIILKGILTKEDABLAVKINVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKKRIVEYDLOGVRTGNDVLK ALALGAKCIFLCDALLMALASKGEHGVKEVLNILTTREPHTSMA\ LTGCRSVAEINNLVQPSRL VKKAAGRSGPPFDAGGOREBAPGTVMERRLGVRAWVKENRGSF QPPVCNKLMHQBQLKVMFVGGPNTRKDVHLEBGEEVFYQLBGDM VLRVLEGGKHRDVVLRQGGSGGREDAFGTVMERRLGVRAWVKENRGSF RRLETELDGHTYYVGDTWDVLFEKMFYCKDLGTQLAPIIQBFFS SBOYRTCKPIPDDLLKEPPFPLSTRSINEPMSHLVVLVER RRLETELDGHTYYVGDTWDVLFEKMFYCKDLGTQLAPIIQBFFS SBOYRTCKPIPDDLLKEPPFPLSTRSINEPMSHLVLVE QDAGTPLELSLGGDTLYATVGGSSGLRQNVDVMLWQLGGSSV VTMGGRRLSLGPWMDSLLVLSWGPSV\AW\RRTQGSVALSVT\Q DDACKKSPNGBPSCGLKAATGVPSTLEVPSLPNNSSPHYLSV VGRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTTAPRRSIKAS FIHKBALGHPDARVLGPGVSVVVFYMGCIEVLRSMRSLDPNT TYQVTREBINHLEAUPAVURGSKSKKKANAKALASVLJKSKNLRFA GMSISHHSTDGLSLSVPATRQVIANHMPSISPAGGDTDMTD VVAYAKOPINQRACHILECCGGL\GADEPEDSFKDLEFKOY LHISPFKVALPPBRLAGPEBSAWGDEBDSLEINYYNSIPGKEPDI GGLVDSRLALTQCGALTALDQGSPSLRDAGSLEPKNOY LHISPFKVALPPBRLAGPEBLYVNTYGLSTTAVAPTEEQ LRQEWYHGRMSRRAAERMLRADGDFLVSBOTTRAPVAPTEEQ LRQEWYHGRMSRRAAERMLRADGDFLVSBOTTRAPVAPTEEQ LRQEWYHGRMSRRAAERMLRADGDFLVSBOTTRAPVAPTEEQ LRQEWYHGRMSRRAAERMLRADGDFLVSBOTTRAPVAPTEEQ LRQEWYHGRMSRRAAERMLRADGDFLVSBOTTRAPVAPTEEQ LRQEWYHGRMSRRADERHLYVNTQLBTSTALDPHTVAACH AGQPKHLLLVDPGGVORTKKDVLPESISHLLDHLLQNGQPIVARA	1			SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
TVYTTYONYTIALTITKOMLKNFVFQQEFKSFGSFHQQLLEYK ILBHLOTKN TADGGAGGGRRQAGVRRHYLYPFTGGYRRRAACQAERPAARS KDTDLAAYQKGNLGVQLRMMAQETNHSQVPMLCSTGCFYFONST TROMCSVCYKEELQRQNSSNGRISFBYVQCTUGSVPEAQSALDET SSSMQPSPVSNQSLLSESVASSQLDSTTSVRKAYPETEDVQASVS DTAQQPSEBQSXSIE.YMRKKRIAVACGRKWBLIGLMAGGVMF TVYYTVTQMYTIALTITKOMLKNFVFQQEFKSFGSFHQQLLEYK ILBHLQTKN 5390 217 1332 EDPFKLMEDROMWSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI EGGADDSITRDDNIAAFKRIRLRPRYLADVSEVDTRTTIQGEBI SAPICLAPPOSHCLWUPDGMSTARAAQAGIGCYTTSTFASCS LEDIVLAAPEGLRNFQLYVHPDLQLNKQLIQRVESLGFKALVIT LDTPVCGNRRHDIRNQLRRHLITLIDLSPKKGNAIPYPQMTP1S TSLCWNDLSWFQSITRLPILLSLLIKEDBELAVKHNVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKSKIEVVLDGGYTSNDVLK ALALGAGKTIGDATLAMLASKGEHEVKEVINILTNEPHTSMA LTGCRSVAEINNLVQPSRL 1 1292 VKKAAGRSRGFFTAGGGREEAPGTVMERRLGVRAWKENRGSF OPPVCNLMHQSQLKVMFVGGNYTKRDTHIESGEBVFYQLSGDM VLRVLEGGKHRDVVLRQGEIFLLPARVPHSDGFANTVGLVVER RRLETEILDGLRYYVGDTMVLTEKMFYCKDLGTQLAPIIOFFS SBQYRTGKPIPDOLLKEPPPLSTRSIMEPMSLDANLDSHREL QAGTPLSLEGDLTYYTGVIAYGGSSEGLRQNVDVULMQLEGSSV VTMGGRRLSLGDWNDSLLVLSWGPSY\AM\RRTQGSVALSVT\Q DDACKSPMGEPSCHGLKAATGYPSTLEVPSLDNSFSBHYLSV YCRCVPHRAHCCHPSCPSOPRCHAPGRAAPHLLWQTQPTAL PULPGGLPPAPLDPIDLSLQTDCGSTSTPRRFSIKAS 5392 1 1623 TRSNAGKVVGASGSGGAGGPQFDPAGGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSGSGRGGRAGSGDAAAAPHLLWQTQPTAL PULPGGLPPAPLDPIDLSLQTDCGSTSTPRRFSIKAS FIHKBAHGWLHPDARVLGPGVSVVVWMGCIEVLREMRSLDFNT RTQVTREAINRHEAPLAVPOVGSNSKKKARNAALASVLGKSNLFFA GMSISHHSTDGLSLSVPATRQVIANHHMPSISPASGGTDMTD YVAVVAKDPINQRACHILECCEQL\QASIISTVGQAPELRFKQY LISPPKVALPPBRLAGGPESSAMCDEBGLSLENTYNSIPGKEPPL GGLVDSRLALTQCALTALDQGSPSLRRACSLDWDVGSTGTARP PEGDALKHESCVAAGVTAAPLPLECOMPSPFTRAPVAPTEEQ LKQPWYHGRMSRRAAGRMLRADGDFLVRBVTGDVTTARP PEFDALKLHESCVAAGVTAAPLPLEDQWPSPFTRAPVAPTEEQ LKQPWYHGRMSRRAAERMLRADGDFLVRBVTGDVTTARP PEFDALKLHLECCEGVARGFPREHLYVNTQCGVTTARAPTERP LAGGGPADARGPPDHERHLYVNTQCGVTTARDVTTAMH AGQPKHLLLVDPEGVVRTKGVPFESISHLIDHHLQNGQPIVAAB SSLHLRGVYSREP GGGSAGMWBTONSONVCPRNLWILLDEPLUSVTGGTTATA	1			DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
ILBHLOTKN		ĺ	·	TVVYTVTOMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
TADGGAGGGRRQAGVRRHYLYPFTGGYRRRAACQERPAARS KDTDLAAYQKRILGVQRINMAQETHINSQUPMLCSTGCGFYGNPR TNGMCSVCYKEHLQRQNSSNGRIEPPVQCTDGSVPEAQSALDST SSSMQPSPVSNGSLLSESVASSQLDSTSVDKAYPETEDVQASVS DTAQQPSEQSKSLE\NRNKRILAVSCAGRKWDLLIGLNAGVEMF SSSMQPSPVSNGSLLSESVASSQLDSTSVDKAYPETEDVQASVS DTAQQPSEQSKSLE\NRNKRILAVSCAGRKWDLLIGLNAGVEMF ILEHLQTKN 5390 217 1332 EDPRKIMEDEMMSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI EGGADDSITRDNIAAFKRIRLRPRYLRDVSSVDYRTTIQGEEI SAPICIAPPGFHCLWWPDGEMSTARAAQAA\GICYITSTPASCS LEDIVIAAPEGIRWPQLYVHPDLQLNKQLIQRVESLGFKALVIT LDTPVCGNRRHDIRNQLRRNITLTDLQSPKKGNATPYPQMTPIS TSLCWNDLSWPQSITRLPILLWEITEADBLAVKHNVGGIIVS NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILWALASKGEHGVKEVLAHLITNEFHTSMA\ LTGCRSVAEINRHLUGFSRL VKKAAGRSRGPPAGGQRCEEAPGTVWERELGVRAWVKENKGSF QPPVCNNILMHQBQLKVMFVGGPNTRKUPHIEBGEEVFYQLBGDM VLRVLEQGKHRDVVIRQCEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGIRYYVGDTMDVLFERMFYCKDLGTOLAPIIGFFS SBOYRTGKPTPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHREL QAGTPLSLEGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV VTMGGRELSLGWMDSLLVLSWGFSY\AN\BERGSSVATGKPTDGLUKEPPFPLSTRSIMEPMSLDAWLDSHREL QAGTPLSLEGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV VTMGGRELSLGWMDSLLVLSWGFSY\AN\BERGGSSVATGKPTDABLSHREL QAGTPLSLEGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV VTMGGRELSLGWMDSLLVLSWGFSY\AN\BERGGSSVATGKPTDFTAL PVLPGGLPPAPLLPIPLSLQTCCTSTPRREPSIKAS 1623 1623 1623 1623 1623 1623 1623 1624 1625 1625 1625 1626 1626 1626 1627 1627 1627 1628 1628 1628 1629 1629 1629 1629 1629 1620 1629 1620 162]	1		N control of the cont
KDTDLAAYQKGRILGVQLRINMAQETNISQVPMLCSTGGCFYGNRR TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPBAQSALDST SSSMQPSPVSNGSLLSESVASSQLDSTSVDRAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKMDLLGLINAGVENF TVVTVTYOMYTIALTITKOMLKNFVFQGEFKSFGSFGQGLLEYK ILEHLQTKN 5390 217 1332 EDPRKIMEDKMNSECEGFPEMSLVCLTDFQAHAREQLSKSTRDFI EGGADDSITEDDNIAAPKRIRLBRRYLRDVSSVDYTRTTIQGEBI SAPICIAPTGFHCLWWPDGEMSTARAQAAA-GICYITSTFASCS LEDIVIAAPBGLRWFQLVYHPDLQLIKQLIQKVGLIGKALDIT LDTPVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFQMTPIS TSLCWNDLSMFQSITRLPIILKGILTKEBABLAVKHNVQGIIVS NHGGGQLDEVLASIDALTEVVAAPKIEVYLDGGVGRGNDVLK ALALGARCIFLGDAILWALASKGBHGVKEVINILTNEPHTSMA\ LTGCRSVAEINRNLVQFSLL VKKAAGRSGFFPTAGGQRCEBAPGTVMERRLGVRAWVKENRGSF OPPVCNNLMIGGGLKWMFVGGFITLBAPVHHSQBEKFYQLBGDM VLRVLGGGKHRDVIRGGEIFLDARVPHSPQRFANTVGLVVER RRLETELDGLRYYVGDTMDVLFEKMFYCKDLGTOLAPIIORFFS SEQYRTCKFPTPQLLKEPPFPLSTTRIMEPMSLDAWLDSHHELL QAGTTBLSLFGDTYTETQVIAYGGSSGGLRQNDVDVLMQLBGSSV VTMGGRRISLGPWMDSLLVLSWGPSY\AV\ERTQGSVALSVT\Q DDACKKSPWGBPSCHLKAATGVSSGGLRQNDVDVLMQLBGSSV VTMGGRRISLGPWMDSLLVLSWGPSY\AV\ERTQGSVALSVT\Q DDACKKSPWGBPSCHALKAATGVSTEVSLFVNSPSPSHVLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLGVTGSTSTPRRSIASS FIHKPAHGWLHPDARVLGPGVSYVVRYMGGIELTRARSSLFMT RTQVTREAINRLHEAVPGWGSWKKKAPNRALASVLGKSNLFFA GMSISHHSTDGLSLSVPATRQVIANHIMPSISFASGGDTDMTD VAYAYAKDPINQRACHILECCGLAQSIISTGGAPELRFKQY LHSPPKVALPPERLAGPESAWGDEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQCALTALDQGPSPSLRDASLPWDVGSTGTAP PGDGTVQADARGPPDLEBLLYNTYGLDAPEPBDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQMPSPTRRAPVAPTEQ LLQEPWYHGRMSRRAARBARLARDQSYLDGSVTUNDSVTTNGOTYLTGAP PGDGTVQADARGPPDLEBLLYNTYGLDAPEPBDSPKKDLFDMR PFEDALKLHLCSVAAGVTAAPLPLEDQMPSPTRRAPVAPTEQ LRQEPWYHGRMSRRAARBARLARDQSYLDGSVTUNDSVTTNGOTYLTGAP PGDGTVQADARGPPDLEBLLYNTYGLDAPEPBDSPKKDLFDMR PFEDALKLHLCSVAAGVTAAPLPLEDQMPSPTRRAPVAPTEQ LRQEPWYHGRMSRRAARBARLARDQGYVLTSGSTTTAP		1560	753	
TINGMCSVCYKEHLORONSSINGRISPPVGCTTGSVPEAQSALDST SSSMQPSPVSNQSLLGSVASSQLDSTSVDKAVPEATDVQASVS DTAQQPSEEQSKSLENRKKKIAVSCAGRKWDLLGLNAGVEMF TVVYTVTQMTIALTITKOMLKNFVFQQEFKSFGSFRQQLLEYK LLEHLQTKN 5390 217 1332 EDPRKLMEDKMWSECGSPEMSLVCLTDFQAHAREQLSKSTRDFI EGGADDSITRDDNIAAFKRIRLRPRYLKDVSEVDTRTTIGGESI SAPICIAPTGFHCLWPDGGEMSTARAQAA\GICYITSTFASCS LEDIVIAAPEGLRWFQLVYHPDLQINKQLIQRVSSLGFKALVIT LDTFVCGNRHDIRNQLRRNLTLTDLQSPKKGNAIPYFQMTPIS TSLCWNDLSWFQSITRLPILLKGILIKEDABLAVKHNVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\ LTGCRSVAEINRILVQFSRL LTGCRSVAEINRILVQFSRL UKKAAGRSGGFPTAGGGGCEAPGTVMERLGVRAWVKENRGSF OPPVGNKLMIGGGLKWMFVGGFNTRGVHIEGGEBVFYQLBGDM VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGLRYYYGDTMOVLEFKWFYCKDLGTQLAPILQBFFS SGOVRTGKPIBOQLLKEPPFPJSTRSIMSPMSLDAWLDSHIRGL OAGTPLSLFGDTYSTQUIAYGGGSSEGLRQNVDVALWGLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSV\AV\EXTOGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPARCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PULPGGLPPAPLLPIPLSLGTQCSTTPRRPSIKAS 5392 1 1623 TRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR CAAPCPLEALSRCGAASSGSAAAGSGAAAARWIRKGS FIHKRPHGWLHDARVLGGGVSVVVRYMGCIEVLSKMSLDFNT RTQVTREAINRLHEAVPOVRGSWKKAPMALASVLGKSNLRFA GMSISIHISTTGLSLSVPATRQVIANHHMPSISPASGGDTDMTD YVAYAKDPINGACHTLECCEGL\AQSIISTVGQAFBLRRKQT LHSPPKVALPPERLAGPESAWGDEBDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQPSPPSLRDAGSLPMVGSTGTAP PGDGTYQADARGPPDHEEHLYVNTQGLDAPEPEDSPKOLFDMR PPEDALKLHECSVAAGTTAAPLPLEDQWSPSPTRRAPAPPTEG LRQEPWHGMSRRAASRMAGDFLVADSVTNPQGYVLTGMH AQQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP GGSAGMTWETTOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	5389	1569	153	VDTDI AAVOVGNI GUOLDIMAOETNISOUPMI.CSTGCGEVGNPR
SSSMOPSPUSNOSLLESVASSOLDSTSVDKAVPETEDVQASVS DTAQQPSEBQSKSLE\nrnkkriavscagrkwdllglnayemf TVVTVTQMTILALTITKOMLKNFVFQOEFKSFGSFAQGLLEYK ILEHLQTKN 5390 217 1332 EDPRKLMEDKMWSECBGPEMSLVCLTDFQAHAREQLSKSTRDFI EGGADDSITREDDNIAAFKRIRLRFRYLRDVSEVDTRTTIQGEIL SAPICIAPTGFHCLVWPDGEMSTARRAQAA\GICYITSTFASCS LEDIVIAAPEGLRWPQLVYHPDJQLNKQLIQRVSSLGFKALVIT LDTFVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFQMTPIS TSLCWNDLSWFQSITRLPFILKSILITKSDALAVKHNVCGILVS NHGGRQLDEVLASIDALTEVVAVKKSKEVVLLOGGVRGNDVLK ALALGAKCIFLGDAILWALASKGEHGVKEVINILTNEFHTSMA\ LTGCRSVAEINRNLVQFSRL VAKKAGRSRGFPTAGGGCEBAPGTVMERGJGVRAWVKENRGSF QPPVCNKLMHQEQLKVMFVGGPNTRKDYHLEGGEVFYQLEGDM VIRVLEQGKHRDVVIRQGEIFLLPRAVYHSPQRFANTVGLVER RRLETELDGLRYYGGDTMOYLEKWFYCKDLGTQLAPFIQBFFS SEQYRTGKPIPDQLLKEPPPPLSTRSIMSPMSLDAWLDSHRELL QAGTFLSLFGDTYTETQVIAYGGGSSEGLRQNVDVWLWQLEGSSV VTWGGRRLSLGPMMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSFWGEPSCHGLKAATGYPSTLEPFSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQFTAL PVLPGGLPPAFLDFIPLSTGTCSTSTRRPSIKAS 5392 1 1623 1RGSNAQKVVGASGSGGAGFQPDPAGFGGFAAAAPHLLWQTQFTAL PVLPGGLPPAFLDFIPLSLSVDATGCTSTSTRRPSIKAS GMSISIHISTDGLSLSVPATRQVIANHHPMSLFSAGGDTDMTD TVAYYAKDFINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPESAWGDEEDSLEHNYNSSIFGKPPI GGLVDSRLALTOPCALTALDOGFSPSLRDACSLPPNVSSTTAP PGDGTVQADARGPPDHEEHLYVNTQGLDAPEPDSPKKDLFDMR PPEDALKLHECSVAAGVTAAPLPLEDQWSPPTRRAPVAPTEEQ GGLVDSRLALTOPCALTALDOGFSPSLRDACSLPPNVSSTTAP PGDGTVQADARGPPDHEEHLYVNTQGLDAPEPDSPKKDLFDMR PPEDALKLHECSVAAGVTAAPLPLEDQWSPPTRRAPVAPTEEQ GELVDSRLALTOPCALTALDOGFSPSLRDACSLPPNVSSTTAP PGDGTVQADARGPPDHEEHLYVNTQGLDAPEPDSPKKDLFDMR PPEDALKLHECSVAAGVTAAPLPLEDQWSPPTRRAPVAPTEEQ LRQEBWYHGKRSRRARSRMRARAGDDFLVRDSVTNDGQVYLTCMM AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SSLHLRGVVSREP GGSAGMTMETTOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	ļ		ł	MICHOGRAPHIC OPONIC MCD TERROUCCEDGGUBEAGAI.DET
DTAQQPSEQSKSLE\NRNKKRIAVSCAGRKWDLLGLINAGVEMF TVVYTVTQMYTIALTITKQMKNFVFQQEFKSFGSFHQQLLEYK ILEHLQTKN 5390 217 1332 EDFRKLMEDKMWSECGFEMSLVCLTDFQAHAREQLSKSTRDFI EGGADDSITRDDNIAAPKET,RLRPRYLRDVSEVDTRTTIGGESI SAPICIAPTGFHCLVWPDGBMSTARAAQAA\GICYITSTFASCS LEDIVIAAPEGLRWFQLYVHPDLQLMKQLIQRVESLGFKALVIT LDTPVCGMRRBIDINOA,RKRILTDLQSPKKGMAIPYFGMTPIS TSLCWNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKGRIEVYLDGGVRTGNDVLK ALALGAKCIFLGDALIMALASKGEHGVKEVINILTMEFHTSMA\ LTGCRSVAEINRNLVQPSRL VKKAAGRSGPFTAGGQRCEEAPGTVMERRLGVRAWVENRGSF QPPVCNKLMHGBQLKVMFVGGPNTRKDYHIEBGGEVFYQLBGDM VLRVLEQGKHRDVVIRQGEIFLLPRAFVHSPGRFANTVGLVVER RRLETELDGLRYYVGDTMDVLJEKKMFYCKDLGTQLAFIIGBFFS SBQNKTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSSSV VTMGGRISLGGWMDSLLVLUSWGPSY\AW\SRTGGSVALSVSV\Q DPACKKSPWGBPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHARGRAAPHLLWQTQPTAL PVLPGGLPPAFLDFILDFLSLQTQCSTSTPRRPSIKAS 1 1623 1 RGSNAQKVVGASGSGGAGPQPDPAGFGGVPALAAAVLGACEPR CAAPCPLPALESRCAGASKGSRGRGAAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVYREAINRHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA RTQVYREAINRHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA RTQVYREAINRHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA RTQVYREAINRHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA RTQVYREAINRHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISHISTDGLSLSVPATRQVIANHHMPSISPASGGDTDMTD YVAYVAKDPINGRACHLLECCEGL\AGSIISTVGQAFELRFKQY LHSPPKVALPPBRLAGPESSAWGDEBDSLEINYYNSITGKRPPL GGLVDSRLALTOPCALTALDQGPSPSLENDGSLPMVVSSTGTAP PGGGYQADARGPPDHEEHLVVNTGGLDAPEPGDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDGWPSPTRRAPVAPPTERG GGLVDSRLALTOPCALTALDGGPSPSLENDGSLPMVSSTGTAP PGGGYQADARGPPDHEEHLLVNTTGGLDAPEPGSPSKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDGWPSPTRRAPVAPPTERG LRQEPWHGRMGRRRAAERMADGGFLVRDSVTTRAPVAPTEEG LRQEPWHGRMGRRRAAERMADGGFLVRDSVTTRAPVAPTEEG LRQEPWHGRMGRRRAAERMADGGFLVRDSVTTRAPVAPTEEG SELHLRGWSREP GGSSAGMTETGTMSONVCPRNLWLLQPLTVLLLLASADSQAAAA		ł		TNGMCSVCYKENDQRQNSSNGRISPPVQCIDGSVPEAQSADDSI
TVVYTYTOMYTIALTITKOMLKNFVFQQEFKSFGSFHQQLLEYK ILEHLQTKN EDPRKLMEDKMWSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI EGGADDSITRDDNTAAPKRIRLRPRYLRDVSEVDTRTTIQGESI SAPICIAPTGFHCLVWPDGEMSTARAAQAA\GICYITSTFASGS LEDIVIAAPEGLRWFQLYVHPDLQLMKQLIQRVESIGFKALVIT LDTPVCGNRRHDIRNQLRRNLTITDLQSPKKGNAIPYFOMTPIS TSLCWNDLSWFQSITRLPIILKGLITKEDBALAVKHNVGIIVS NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILMALASKGEHGVKEVLNILTMEFHTSMA\ LTGCRSVAE INRNLVQPSRL VKKAAGRSRGFFTAGGGRCEEAPGTVMERRLGVRAWVKENRGSF QPPVCNKLMHQSQLKVMFVGGPNITKNYHIEBGEBVYYQLBGDM VLRVLEQGKHRDVVIRQGE IFLLPARVPHSPGRPANTVGLVVER RRLETELDGLKYVYGDTMDVLFEKWFYCKDLGTQLAPIIQBFFS SBQNXTGKPIPDOLLKEPFFPLSTTSIMEPMSLDAWLDSHHREL QAGTPLSLFGDTYFTQVILAYGGSSEGLRQNDVDWLWQLGSGSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGBPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAPHLLWQTQFTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTFRRPSIKAS 1 1623 IRGSNAQKVVGASGSGGRGFQAPGGVPPABAAVLGACEPR CAAPCLPPALEARCKGAGSGSGGRGGAGSGDAAAABWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLFPA GMS1SIH1STGLSLSVPATRQVIANHHMPSISPASGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPESSMGDEBSLEINYYNSIPGKEPPL GGLVSRLALTOPCALTALDGPSPSLRDAGSLEWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLEDMR PFEDALKLHECSVAAGVTAAPLPLEEDGWPSPFTRRAPVAPTEQ LKQEPWYHGRMSRRAAEMRRADGFFLVRDSVTTPGGYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SSELHLRGVVSREP GGSSAGMTETGMSRRAAEMRRADGFFLVRDSVTTPGGYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE			1	SSSMQPSPVSNQSLLSESVASSQLDSTSVDAAVPEIEDVQASVS
ILEHLOTKN		1		DTAQQPSEEQSKSLE\NRNKKRLAVSCAGRKWDLLGLNAGVEMF
EDPRKLMEDKMWSECEGPEMSLVCLTDFOAHAREQLSKSTRDFI EGGADDSITRDNITAAFKRIRLRPRYLRDVSVDTRTTIQGEEI SAPICIAPTEPHCLWMPDGEMSTARAAQAA\GICYITSTFASCS LEDIVIAAPEGLRWPQLYVHPDLQLIKQLIQRVESLGFKALVIT LDTPVCGNRRHDIRNQLRRNLTITLDLQSPKKGNAIPYFQMTPIS TSLCWNDLSWPQSITRPLFIILKGILTKEDAELAVKHNVGGILVS NHGGRQLDEVLAS IDALTEVVAAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILWALASKGEHGVKEVINILTMEPHTSMA\ LTGCRSVAE INNILVQFSRL 1 1292 VKKAAGRSRGPPTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF QPPVCNKLMHQSQLKVMFVGGPTVTKRVYHIEBGEEVFYQLEGDM VLRVLEQGKRRDVIRQGEFTLLPARVPHSPQRFANTVCLVUSK RRLETELDGLRYYVGDTMDVLFEKWFYCDLGTOLAPIIQBFFS SEQYNTGKPIPDVOLLKEPPFPLSTRSIMEPMSLDAWLDSHREL QAGTPLSLFGDTYFTQVIAYGGSSSGLRQNUDVWLWQLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGBPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPQPRCHAPGRAAAPHLLWQTQFTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRPSIKAS 1623 IRGSNAQKVVGASGSGGAGPQDPAGAGAGAGAAAHAAVLGACEPR CAAPCPLPALSRCRGGSRGSRGGRGAAASGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSVVWFYMGCIEVLRSMRSLDFNT RTQVTREAINRHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISHIETDGLSLSVPATRQVIANHHMPSISPASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\QSIISTVQQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEBDSLEHNYYNSIPGKEPPL GGLVDSRLALITOPCAITALDQGFSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYUTTQGLDAPEPEDSPKKDLFDMR PPEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LKQEPWHERGMSRAAAERMLRADGDET.VRDSVTNPGQYVLTCMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAGA SSLHLBRGVVSTEB		1		TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
EGGADDSTRDDNIAAFKRIRLRPRYLROVSEVDTRTTIGGEEI SAPICIAFTGFHCLVWPDGEMSTARAAQAA\GICYITSTFASCS LEDIVIAAPEGLRWPGLYVHPDLQLNKQLIQRVESLGFKALVIT LDTPVCGRRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFOMTPIS TSLCWNDLSWFQSITRLPIILKGILITKEDAELNKHNVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTCHNDLUK ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\ LTGCRSVAEINRNLVQFSRL 1 1292 VKKAAGRSRGPFTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF OPPVCNKLMHQBQLKVMFVGGPNTRKDYHIEBGEEVFYQLEGDM VLRVLEQGKHRDVVIRQGEIFLLPRAVPHSPQRFANTVGLVVER RRLETELDGLRYYYGDTMDVLFKWFYCDLGTOLAPIIQBFS SEQYRTGKPIPPOLLKEPFFPLSTRSIMEPMSLDAWLDSHHREL OAGTPLSLEGDTYFTQVIAYGGGSSGLRQNDVDWLWQLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPMGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPSCPSQPRCHAPGRAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLGYCTSTPRRPSIKAS 1623 IRGSNAQKVGASGSGAGPQPDPAGFGGVPALAANVLGACEPR CAAPCPLPALSRCRGAGSRGSRGRGRAGSGDAAAAEWIRKGS FIHKPAHGMLHPDARVLGFGVSVVKYMGCIEVLRSMRSLDFNT RTQVTREALANTRHEAVPGVGRSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTGPCALTALDQGFSPSLRDACSLPWDVGSTGTAP PGGGYVQADARGPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PPEDALKLHECSVAAGVTAAPLPLEQQWPSPPTRRAPVAPTEGQ LKQEPWHGRMSRRAAERMLRADGDELVRDSVTNPGQYVLTIGMH AGQPKHLLLVDPERVARGNTAABCHLRDDAPSPPTRRAPVAPTEGU LKQEPWHGRMSRRAAERMLRADGDELVRDSVTNPGQYVLTIGMH AGQPKHLLLUVDREP	ļ		1	ILEHLQTKN
EGGADDSTRDDNIAAFKRIRLRPRYLRDVSSVDTRTTIQGEI SAPICIAPTGPHCLVWPDGEMSTARAAQAA\GICYITSTFASCS LEDIVIAAPEGLRWPQLYVHPDLQLNKQLIQRVESLGFKALVIT LDTPVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFGMTPIS TSLCWNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS NHGGRQLDEVLASIDALTTVVAAVKGKLEVYLDGGVRTCHNDLUK ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\ LTGCRSVAEINRNLVQFSRL VKKAAGRSGFPTAGGORCEAPGTVMERRLGVRAWVKENRGSF QPPVCNKLMHQEQLKVMFVGGPNTRKDYHIEBGEEVFYQLBGDM VIRVLEQGKHRDVVIRQGEIFLLPRAVPHSPQRFANTVGLVVER RRLETELDGLRYYYGDTMDVLFEKWFYCDLGTOLAPIIQBFFS SEQYNTGKPIPPOLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL QAGTPLSLFGDTYTCTVIAYGGGSSGRLRQNVDVMLWQLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSV\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS TRISNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSGRGRGGAGGGDAAAAEWIRKGS FIHKPAHGMLHPDARVLGFGVSVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRHEAVPGVGRSWKKKAPNXALASVLGKSNLRFA GMSISHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILBCCGGL\AQSISTTVQAFELRFKQY LHSPPKVALPPERLAGPEESAMGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTGPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGGGYVQADARGPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLELQWPSPPTRRAPVAPTEGV LRQEPWHGRMSRRAAERMLRADGDELVRDSVTNFQQYVLTGMH AGQPKHLLLUDPBGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP GGGSAGMTMETOMSONVCPRNLWILGPLTVLLLLASADSQAAAP	5390	217	1332	EDPRKLMEDKMWSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI
LEDIVIAAPEGLRWFQLYVHPDLQLNKQLIQRVESLGFKALVIT LDTPVCGNRRHDIRNQLRNLTITDLQSPKKGNAIPYFQMTPIS TSLCMNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\ LTGCRSVABEINRNLVGPSRL 1 1292 VKKAAGRSRGFFTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF QPPVCNKLMHQBQLKVMFVGGPNTRKDYHIEEGEEVFFYQLEGDM VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQBFFS SEQYRTGKPIPPDLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL QAGTFLSLFGDTYTETQVIAYGQGSSEGLRQNVDVWLWQLEGGSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLEV YCRCVPHRPAHCCHPPSCPSQFPCHAPGARAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGGAGFQPDPAGFGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSGGRGRAGSGDAAAAABWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLFA GMSISHISTDGLSLSVPATRQVIANHHMPSISFAGGDTDMTD YVAYVAKDPINQRACHLLECCEGL\AQSISISTGAGFELFKQY LHSPPKYALPPERLAGGEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGGGYQADARGPPDHEEHLYVNTQGLDAPEFDDSFKUDLFDMR PFEDALKLLECSVAAGVTAAPLPLEDQWSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAASRMLRADGDFLVRDSVTNPQQYVLTGMH AGQPKHLLLVDPEGVVRKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP GGDSAGMTMETOMSONVCPRNIWLLQPLTVLLLLASADSQAAAP		1		EGGADDSITRDDNIAAFKRIRLRPRYLRDVSEVDTRTTIQGEEI
LEDIVIAAPEGLRWFQLYVHPDLQLNKQLIQRVESLGFKALVIT LDTPVCGNRRHDIRNQLRNLTITDLQSPKKGNAIPYFQMTPIS TSLCMNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\ LTGCRSVABEINRNLVGPSRL 1 1292 VKKAAGRSRGFFTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF QPPVCNKLMHQBQLKVMFVGGPNTRKDYHIEEGEEVFFYQLEGDM VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQBFFS SEQYRTGKPIPPDLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL QAGTFLSLFGDTYTETQVIAYGQGSSEGLRQNVDVWLWQLEGGSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLEV YCRCVPHRPAHCCHPPSCPSQFPCHAPGARAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGGAGFQPDPAGFGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSGGRGRAGSGDAAAAABWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLFA GMSISHISTDGLSLSVPATRQVIANHHMPSISFAGGDTDMTD YVAYVAKDPINQRACHLLECCEGL\AQSISISTGAGFELFKQY LHSPPKYALPPERLAGGEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGGGYQADARGPPDHEEHLYVNTQGLDAPEFDDSFKUDLFDMR PFEDALKLLECSVAAGVTAAPLPLEDQWSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAASRMLRADGDFLVRDSVTNPQQYVLTGMH AGQPKHLLLVDPEGVVRKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP GGDSAGMTMETOMSONVCPRNIWLLQPLTVLLLLASADSQAAAP		1		SAPICIAPTGFHCLVWPDGEMSTARAAQAA\GICYITSTFASCS
LDTPVCGNRRHDIRNQLRRNITLTDLQSPKKGNAIPYFQMTPIS TSLCWNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILWALASKGEHGVKEVUNILTNEFHTSMA\ LTGCRSVAEINRNLVQFSRL 1 1292 VKKAAGRSRGFPTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF OPPVCNKLMHQEGLKWMFVGGENTRRDYHIEEGESVFYQLEGDM VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTGLAPIIQBFFS SEQYRTGKPIPPQLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\SRTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHHLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGGAGPQPDPAGFGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGSRGSAGSAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRWMGCLEVLRSMRSLDFWT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISHISTDGLSLSVPATRQVIANHHMPSISPASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPESSAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGFSPSLRDACSLPMDVGSTGTAP PGDGYYQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFFDALKHHEGVSARGVTAAPLPLEDQWPSPTRRAPVAPTEEQ LRQEFWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP SCHLHLRGVVSREP	ł	1	}	LEDIVIAAPEGLRWFOLYVHPDLQLNKQLIQRVESLGFKALVIT
TSLCWNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\ LTGCRSVAEINRNLVQFSRL 1 1292 VKKAAGRSRGPPTAGGQRCEEAPGTVMERRLGURAWVKENRGSF QPPVCNKLMHQGQLKVMFVGGPNTRKDYHIEBGEEVFYQLBGDM VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGLRYYVGDTMDVLFEKKFYCKDLGTQLAPIIQBFFS SEQYRTGKPIPDQLLKEPPFPLSTRSIMSPMSLDAWLDSHHREL QAGTPLSLFGDTYETQVIAYQGSSEGLRQNVDVWLWQLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAPHLLWQTQPTAL PVLPGGLPPAFLLPIPLSUTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAEWIRKGS PIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPMKALASVLGKSNLFPA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVQQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPDVGSTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGGPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP SELHLRGVVSREP GGDSAGWTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	ļ			LDTPVCGNRRHDIRNOLRRNLTLTDLQSPKKGNAIPYFQMTPIS
NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDALLWALASKGEHGVKEVLNILTNEFHTSMA\ LTGCRSVAEINRNLVQFSRL 1 1292 VKKAAGRSGFPTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF QPPVCNKLMHQBQLKVMFVGGPNTRKDYHIESGEBVFYQLEGDM VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGLRYYVGDTMDVLFEKMFYCKDLGTQLAPIIQBFFS SBQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGBPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAFLLPIPLSTRGTPRFSIKAS 1 1623 IRGSNAQKVVGASGSGGAGPQPDPAGFGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAENIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISPFASGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSKLALTGQPCATTALDGPSPSLRDACSLEWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPPEDSPKCDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGGPKHLLLIVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP GGDSAGWTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP				TSLCWNDLSWFOSITRLPIILKGILTKEDAELAVKHNVQGIIVS
ALALGAKCIFLGDAILWALASKGEHGVKEVINILTNEFHTSMA\ LTGCRSVAEINRILVGFSRL VKKAAGRSRGPPTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF QPPVCNKLMHQSQLKVMFVGGPNTRKDYHIEBGEEVFYQLEGDM VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQBFFS SEQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL QAGTPLSLFGDTYETQVIAYGGGSSEGLRQNVDVWLWQLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGAGPQPDPAGFGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGRGRAAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISHHSTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPBRLAGPESAWGDEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGTTAAPLPLEDQWPSPTTRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTCMH AGGPKHLLIVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP SSHLRGVVSREP	1	:		NHCCROLDEVIASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK
LTGCRSVAEINRNLVQFSRL 5391 1 1292 VKKAAGRSGPPTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF QPPVCNKLMHQEQLKVMFVGGPNTRKDYHIEEGEVFYQLEGDM VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQBFFS SEQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL QAGTPLSLFGDTYETQVIAYGGSSSEGLRQNVDVWLWQLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGBPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS 5392 1 1623 IRGSNAQKVVGASGSGAGFQPDPAGFGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGAGAGSQDAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSWRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHLLECCSGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAASRMLRADGDFLVRDSVTNPGQVVLTCMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETONSONVCPRNLWLLQPLTVLLLLASADSQAAAP	1.	1	1	AT AT CANCIFIC DATE WALLASK GERGVKEVINIL THE FHTSMA
1 1292 VKKAAGRSGPPTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF QPPVCNKLMHQBGLKVMFVGGPNTRKDYHLEEGEEVFYQLEADM VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGLRYYVGDTMDVLFEKMFYCKDLGTOLAPIJQBFS SEQYRTCKPIPPOLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV VTMGGRRLSLGBWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEFR CAAPCPLPALSRCRGAGSGRGSRGRGRAAGSGDAAAAAEWIRKGS PIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLFFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPESSAWGDEEDSLEINYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGGGYVQADARGPPDHEEHLYVNTQSLDAPSPEDSFKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGGYVLTCMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP				
QPPVCNKLMHQEQLKVMFVGGPNTRKDYHIEEGEEVFYQLEGDM VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQBFFS SEQYRTGKPIPDQLLKEPPFFLSTRSIMEPMSLDAWLDSHHREL QAGTPLSLBFGDTYBTQVIAYGQGSSEGLRQNVDWWLWQLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSQTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGGAGPQPDPAGFGGVPALAAAVLGACEPR CAAPCPLPPLSRCRGAGSRGGRGAAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP				TAKKA Y OD CO DEBY COOK CERY DOMINIED DI GILD YMINENDOGE DIOCKO AND TRUMPA ON DEBY DOMINIED DI GILD YMINENDOGE
VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVER RRLETELDGLRYYVGDTMDVLFEKMFYCKDLGTQLAPIIQBFFS SEQYRTGKPIPDQLLKEPFFPLSTRSIMEPMSLDAWLDSHHREL QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGAGPQPDPAGFGGVPALAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHLIECCEGLAQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP SELHLRGVVSREP	5391	1	1292	VKRAAGKSKGPPTAGGQCCEAPGTVIERKLIGVAANVKERKGSP
RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQBFFS SEQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGBPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	1			Obbacukrwhórórkawa agabatkym tyregera a tóregom
SEQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV VTMGGRRLSLGDWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS CAAPCPLPALSRCRGAGSGGAGPQPDPAGPGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGRGAAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVARGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AQQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	1		,	VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER
QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	1	1		RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQEFFS
VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	1	ļ		SEQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL
VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	1.	1	' '	QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV
DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISHISTDGLSLSVPATRQVIANHHMPSISPASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAFVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	1			VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q
YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGSRGAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	1	}		DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV
PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS 1 1623 IRGSNAQKVVGASGSGAGPQPDPAGPGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGSRGAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	1		j	YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL
1 1623 IRGSNAQKVVGASGSGAGPQPDPAGPGGVPALAAAVLGACEPR CAAPCPLPALSRCRGAGSRGSRGAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQFSPSLEDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	1			PVI.PGGI.PPAPLLPIPLSLOTOCSTSTPRRPSIKAS
CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	L	 	1603	TEGENAOKINGASGSGGAGPODDPAGPGGVPALAAAVI.GACKPR
FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDGGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	5392	1	1623.	CANDODE DATEDODOGGOE OF DETACT GOVERNMENT DOTOETH
RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP				CHAPCARATION INDIVIDES COGNOTION IN ACCUSED DEMOGRAPHED LINES
GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP		1	1	FINKPAHGWENPUAKVEGPGVSIVVKIMGCIEVEKSMKSEDFRI
YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP			1	RTQVTREAINRDHEAVPGVRGSWKKKAPNKALASVDGRSNDKFA
LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP		j	1	GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD
GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETQMSONVCPRNLWLLQPLTVLLLLASADSQAAAP			1	YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY
PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP	1		1	LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL
PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP			1	GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP
PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP				PGDGYVOADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR
LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP	1		1	PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ
AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	j	1	1	LROEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGOYVLTGMH
SELHLRGVVSREP 5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP				ACODKHILL VDPEGVVPTKDVI. FESTSHILTDHHLONGOPIVAAE
5393 2 982 GGDSAGMTMETOMSONVCPRNLWLLQPLTVLLLLASADSQAAAP	1		1	
5393 2 982 GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLLASADSQAAAP PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG				
PKAATKTEbbmtuatG/EDSAltacGeabGb/ FK2D216m54m2	5393	2	982	GGDSAGMTMETQMSQNVCPRNLWbLQPLTVhbbhASADSQAAAP
			<u> </u>	KWAPKPERSMINATO/EDSAIDLEGGWADAS EKSDSTÖMEUNG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A≈Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
Į	sequence		\=possible nucleotide insertion)
 -		 	\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
i	1 '	1	LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFONGK
}		}	· · · · · · · · · · · · · · · · · · ·
		İ	SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
	1	l .	QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
		J.	STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
			RAPTDDDKNIYLTLPPNDHVNSNN
5394	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
	1	1	PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG
		İ	\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
		ł	LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK
	J	j	SOKFSHLDPTFSIPOANHSHSGDYHCTGNIGYTLFSSKPVTITV
		1	QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
	1		}
	ļ		STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
		<u></u>	RAPTDDDKNIYLTLPPNDHVNSNN
5395	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
	l'		SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
		1	KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
		!	LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
			RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
		[SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
		1	PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
			POOSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
	Ĭ	(ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
	j	j	TPAATPETPPVISAVVHATDEEKLAVTNOKWTCMTVDLEADKOD
		Į.	~
		í	YPQPSDLSTFVNETKFSSPTEELDYRNSYEIBYMEKIGSSLPQD
	ļ]	DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
			ALVNTAAKNQHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP
	i	i	SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
		1	PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
			PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
•		1	\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
	1		YOALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
	1.	1	CRV\DALERTLEOKNKEIEELTKICDELIAKMGKS
5396	3135	531	RASDAKNOEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
3320	1: 3233	}	SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKOTTK
	1		KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
	I]	LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVONSPPVG
			· · · · · · · · · · · · · · · · ·
•	1	1	RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
	1	ļ	SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
	ļ		PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
			PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
		1	ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
	1		TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
	}]	YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
			DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFBETE
	1		ALVNTAAKNOHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP
		1	SEAIRITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
]		
	[PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
	1	}	PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
	l		\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
	1		YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
			CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5397	3135	531	RASDAKNOEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
			SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
			KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
	1		1
			LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
	1		RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
	}		SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPBKLDNTPASP PRSPABPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL

PCT/US00/34263

		n - 22 - 5 - 2 - 5 - 5	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
!	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
1	to first	amino acid	S=Serine, T=Threonine, V=Valine,
[]	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
{	sequence		\=possible nucleotide insertion)
			POOSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
1			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
į.			TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
ļ		}	YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
ĺ		1	DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
{			ALVNTAAKNOHPVPRGLAPNOESHLOVPEKSSOKELEAMGLGTP
Ì		j	SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
1			PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
1	ł	į	PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
1	1	1	\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
1	1	}	YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
			CRV\DALERTLEQKNKEIBELTKICDELIAKMGKS
5398	56	5426	SGEVCRMESNFNQEGVPRPSYVFSADPIARPSEINFDGIKLDLS
3330)	}	HEFSLVAPNTEANSFESKDYLQVCLRIRPFTQSEKELESEGCVH
			ILDSOTVVLKEPQCILGRLSEKSSG\QM\AQKFSFFPGFLGPAT
			TQKEFFQGCIMHP\VKDLLKGQSRLIFTYGLTNSGKTYTFQGTE
j			ENIRILPRTLNVLFDSLQERLYTKMNLKPHRSREYLRLSSEQEK
l l			EEIASKSALLRQIKEVTVHNDSDDTLYGSLTNSLNISEFEESIK
1			DYEQANLNMANSIKFSVWVSFFEIYNEYIYDLFVPVSSKFQKRK
			MLRLSQDVKGYSFIKDLQWIQVSDSKEAYRLLKLGIKHQSVAFT
1			KLNNASSRSHSIPTVKILQIEDSEMSRVIRVSELSLCDLAGSER
1	/		TMKTQNEGERLRETGNINTSLLTLGKCINVLKNSEKSKFQQHVP
1			FRESKLTHYF/QSFFNGKGKICMIVNISQCYLAYDETLNVLKFS
1	[AIAQKVCVPDTLNSSQEKLFGPVKSSQDVSLDSNSNSKILNVKR
ł	1		ATISWENSLEDLMEDEDLVEELENAEETED/VGETKLLDEDLDK
İ			TLEENKAFISHEEKRKLLDLIEDLKKKLINEKKEKLTLEFKIRE
[EVTQEFTQYWAQREADFKETLLQEREILEENAERRLAIFKDLVG
	1	}	KCDTREEAAKDICATKVETEBATACLELKFNQIKAELAKTKGEL
ł		ľ	IKTKEELKKRENESDSLIQELETSNKKIITQNQRIKELINIIDQ
ŀ	}		KEDTINEFQNLKSHMENTFKCNDKADTSSLIINNKLICNETVEV
1			PKDSKSKICSERKRVNENELQQDEPPAKKGSIHVSSAITEDQKK
1			PKDSKSKICSERRRVNENELQQDEPPARKGSINVSSAITEDQKK SEEVRPNIAEIEDIRVLQENNEGLRAFLLTIENELKNEKEEKAE
1			SEEAKBNIVETERIKATÖRINE ORKALTIRI IENERVINETERIK
l			LNKQIVHFQQELSLSEKKNLTLSKEVQQIQSNYDIAIAELHVQK
ſ			SKNQEQBEKIMKLSNEIETATRSITNNVSQIKLMHTKIDELRTL
}			DSVSQISNIDLLNLRDLSNGSBEDNLPNTQLDLLGNDYLVSKQV
1			KEYRIQEPNRENSFHSSIEAIWEECKEIVKASSKKSHQIEELEQ
Ï			QIEKLQAEVKGYKDENNRLKEKEHKNQDDLLKEKETLIQQLKEE
}			LQEKNVTLDVQIQHVVEGKRALSELTQGVTCYKAKIKELETILE
			TOKVERSHSAKLEQDILEKESIILKLERNLKEFQEHLQDSVKNT
			KDLNVKELKLKEEITQLTNNLQDMKHLLQLKEEEEETNRQETEK
1	1		LKEELSASSARTQN\LNADLQRKEEDYADLKEKLTDAKKQIKQV
			QKEVSVMRDEDKLLRIKINELEKKKNQCSQELDMKQR\TIQQLK
1	(1	EQLINOKVEEAIQOYERACKOLNVKEKIIEDMRMTLEEQEQTQV
1	1	,	EQDQVL\EAKLEEVERLATELDRWRVKCNDLETKNNQRSNKEHE
		1	NNTDVLGKLTNLQDELQESEQKYNADRKKWLEEKMMLITQAKEA
	(1	ENIRNKEMKKYAEDRBRFFKQQNEMEILTAQLTEKDSDLQKWRB
	j		ERDQLVAALEIQLKALISSNVQKDNEIEQLKRIISETSKIETQI
		1	MDIKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCEV
1			STENDQSTRFPKPELBIQFTPLQPNKMAVKHPGCTTPVTVKIPK
	j	}	ARKRKSNEMEEDLVKCENKKNATPRTNLKFPISDDRNSSVKKEQ
1		1	KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS
1		1	PSILQSKAKKIIETMSSSKLSNVRASKENVSQPKRAKRKLYTSE
!			ISSPIDISGOVILMDQKMKESDHQIIKRRLRTKTAK
5399	705	230	GPRMAKFLSODQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG
3333	1 ,03	1	ASPTPGEVORHLOTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE
			ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE
1	Ĭ	į	\ADIEPNGKVKYDEFIHKITSYLDGTY
5400	931	248	SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK
3400	931		CASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE
-			TAPEVNFTFEGETGKNPDEEDNTFYQRLKSMKEPLEAQNI\PDN
	L		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
- {	sequence	•	\=possible nucleotide insertion)
			FGNVSPEMTLVLHLAWVACGYIIWQNSTEDTWYKMVKIQTVKOV
		}	QRNDDFIELDYTILLHNIASQEIIPWQMQVLWHPQYGTKVKHNS
l		Ì	RLPKEVOLE
5401	3	1360	TGWSYGPTTSLAFLAPRDFPFPPKLLIHPQAVVRLSCGAGSMGS
			QAAAEWRNWASWEGSSSLSGCSMGCFKDDRIVFWTWMFSTYFME
1		ł	KWAPRQDDMLFYVRRKLAYSGSESGADGRKAAEPEVEVEVYRRD
			SKKLPGLGDPDIDWEESVCLNLILQKLDYMVTCAVCTRADGGDI
1			HIHKKKSQQVFASPSKHPMDSKGEESKISYPNIFFMIDSF\EE\
1			VFSDMTVGKGEMVCVELVASDKTNTFQGVIFQGSIRYEALKKVY
l			DNRVSVAARMAQK\MSFGFSKYSNMEF\VR\MKGPQGKGHABMA
	I		VSRVSTGDTSPCGTEEDSSPASPMHERVTSFSTPPTPERNNRPA
]		FFSPSLKRKVPRNRIAEMKKSHSANDSEEFFREDDGGADLHNAT
	1		NLRSRSLSGTGRSLVGSWLKLNRADGNFLLYAHLTYVTLPLHRI
			LTDILEVRQKPILMT
5402	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
		1	PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDDTL
			TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS
			PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ
ļ			PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL
[ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
1			MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE
1			DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK
1	'		PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ
			PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
1	·		MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
			VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
			ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS
1			QVAMKQNELLEPNSF
5403	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
			PGADILNSYAGLACVEEPNDMITESSLDVAEBEIIDDDDDDITL
			TVEASCHDGDETIETIBAAEALLNMDSPGPMLDEKRINNNIFSS
· ·			PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ
.			PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL
·			ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
			MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE
	•		DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK
			PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ
1 .			PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP
			RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
			MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
1	1		VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
	İ		ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS
5404	187	1111	QVAMKQNELLEPNSF
		TTTT	LPVTLIFAKMKTLQSTLLLLLLVPLIKPAPPTQQDSRIIYDYGT DNFEBSIFSQDYEDKYLDGKNIKEKETVIIPNEKSLQLQKDEAI
			TPLPPKKENDEMPTCLLCVCLSGSVYCEEVDIDAVPPLPKESAY
j l			LYARFNKIKKLT\AKDFADIPNLRRLDFTGNLIEDIEDGTFSKL
]	[SLVEELSLAENQLLKLPVLPPKLTLFNAKYNKIKSRGIKANAFK
	1		KLNNLTFLYLDHNALESVPLNLPESLRVIHLQFNNIASITDDTF
			CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSYF
5405	2199	1220	QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDYEREIQPTA
-		~~~	ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPROEKHERTHEII
]	ļ		PINVNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS
į (1		NSSASSEQGLLGRSPPTRPVPGHRSERAIRTOPKOLIVDDLKGS
1	1		LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE
	1		SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR
1	l		YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS
			NTVYCKLESCPSRGQGKPS
5406	279	2732	RWRTYNVEGPLTFMDVAIEFCLEEWQCLDTAQQNLYRNVMLENY
		· · · · · · · · · · · · · · · · · · ·	

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1 -	\=possible nucleotide insertion)
	1	ļ <u></u>	RNLVFLG/IIAVSKPDLITCLEQEKEPWEPMRRHEMVAKPPVMC
1			SHFTQDFWPEQHIKDPFQKATLRRYKNCEHKNVHLKKDHKSVDR
1		l	CKVHRGGYNGFNQCLPATQSKIFLFDKCVKAFHKFSNSNRHKIS
l	1	\$	HTEKKLFKCKECGKSFCMLSHLAQHKIIHTRVNFCKCEKCGKAF
1	ļ	ł	NCPSIITKHKRINTGEKPYTCEBCGKVFNWSSRLTTHKKNYTRY
1		1	KLYKCEECGKAFNKSSILTTHKIIRTGEKFYKCKECAKAFNQSS
1			KLIKCEECGKAFNKSSIBIIHKIIKIGERFIKCKECAKAFNQSS
ł	Í		NLTEHKKIHPGEKPYKCEECGKAFNWPSTLTKHKRIHTGEKPYT
ł		}	CEECGKAFNQFSNLTTHKRIHTA\EKFYKCTECGEAFSRS\SNL
1			TKHKEIHTEKKPYKCEECGKAFKWSSKLTEHKLTHTGEKPYKCE
1			KCGKAFNCPSIITKHNRINTGEKPYTCEECGKVFNWSSRLTTHK
1	1		KNYTRYKLYKCEECGKAFNKSSILTTHKKIHIEKKFYKCEECGK
1	İ		AFKWSSKLTEHKITHTGEKPYKCEECGKAFNHFSILTKHKRIHT
1			GEKPYKCEECGKAFTQSSNLTTHKKIHTGEKFYKCEECGKAFTQ
l			SSNLTTHKKIHTGGKPYKCEECGKAFNQFSTLTKHKIIHTEEKP
1			YKCEECGKAFKWSSTLTKHKIIHTGEKPYKCEECG\KAFKLSST
1			LSTHKIIHTGEKPYKCEKCGKAFNRPSNLIEHKKIHTGEQPYKC
	1	Į.	EECGKAFNYSSHLNTHKRIHTKEQPYKCKECGKAFNQYSNLTTH
1		1	NKIHTGEKLYKPEDVTVILTTPQTFSNIK
	 	659	RPRRRQSSCCTGWLAGWLLRAAPRFCRRTETDMEQGKGLAVLIL
5407	3	039	AIILLQGTLAQSIKGNHLVKVYDYQEDGSVLLTCDAEAKNITWF
1	1	Ì	KDGKMIGFLTEDKKKWNLGSNAKDPRGMYQCKGSQNKSKPLQVY
1			
1			YRMCQNCIELNAATISGFLFAEIVSIFDLAVGVYFIAGTGMEFR
		Í	QS\RASDKQTLLP\NDPAPTQPLKDPRKMTQYSHLQGN\QLRRN
5408	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP
		1	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL
- [APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF
1			STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP
		1	RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE
			VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM
ı			NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD
}			LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL
1	•	1	LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS
	j		IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL
i			EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL
1			LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP
,			TOTDFSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNTVVPCGTEK
1			NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR
	1		
		İ	PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH
1	1		AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
1	1		DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ
1	1		VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
1			LPPILIIHLKRFQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
i			ALCOHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS
1	1	}	PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS
1			KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH
1		1	VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG
i	1	(NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
	1	1	PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK
1			TDGKKMADTSSMDEDFESDY\EKYCVLQ
5409	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP
1 3303	, ,,,,	V.20	HAROHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL
1			APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF
1		1	STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP
			RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE
1			KPLIDDITGGAMENITE SYCONI DERING TO BE CONTOURNED ON CONTOURN
1			VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM
1			NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD
		}	LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL
1			LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS
			IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL
1	J		EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL
-			LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
""	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L-Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P-Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1 .	sequence	sequence	\=possible nucleotide insertion)
	Bequence		TOTDFSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNTVVPCGTEK
1 -			NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSOKNR
		l .	PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH
1			AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
ł	1		DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAO
1	ì		VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
			LPPILIIHLKRFQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
1			ALCOHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS
ł			PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS
<u> </u>			KGRLRLPQIGSKNKLSSSKENLDASKENGAGOICELADALSRGH
i			VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG
1			NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
į.			PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK
1.			TDGKKMADTSSMDEDFESDY\EKYCVLQ
5410	2	710	LRFPGOARHVWLAARMOAPHKEHLYKLLVIGDLGVGKTSIIKRY
			VHQNFSSHYRATIGVDFALKVLHWDPETVVRLQLWDIAGQERFG
			NMTRVYYREAMGAFIVFDVTRPATFEAVAKWKNDLDSKLSLPNG
1			KPVSVVLLANKCDQGKDVLMNNGLKMDQFCKEHGFVGWFETSAK
1			ENINIDEASRCLVKHILANECDLMESIEPDVVKPHLTSTKVASC
ļ			SG\CAKILVGTFAGVW
5411	1302	289	TGPAAAGRRKALGSFGKPSPVTGLRAARRRTRPSAPAAPSVGC
ĺ			GKRRESDAGAGGERASVRTGSGRRGGRTMAGDSEOTLONHOOPN
			GGEPFLIGVSGGTASGKSSVCAKIVQLLGQNEVDYRQKQVVILS
	ļ		QDSFYRVLTSEQKAKALKGQFNFDHPDAFDNELILKTLKEITEG
	· .		KTVQIPVYDFVSHSRKEETVTVYPADVVLFEGILAFYSQER/IR
			DLFQMKLFVDTDADTRLSRRVLKDISERGRDLEQILSSSTLRFV
			KPA\FEEFCLPPK\KYADVIIPR\GADN\RVPINLIVQHIQ\DI
			LNGGPS\NRQTNGCLNGYTPSRKRQASESSSRPH
5412	3180	313	QGISNFFHKEANFWFEVSGYLISPLRSPFVDPALEWSLMASPWN
1		,	KMEGESSRFEIHTPVSDKKKKKCSIHKERPQKHSHEIFRDSSLV
			NEQSQITRRKKRKKDFQHLISSPLKKSRICDETANATSTLKKRK
	·		KRRYSALEVDEEAGVTVVLVDKENINNTPKHFRKDVDVVCVDMS
1	1,50		IEQKLPRK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQR
		•	KAASWESQRA\RDTLPQSEFPTQEESWLSVGPGGEITELP\ASA
1	V.		HKNKSKKKKKSSNREYET\LAMPEGSQAGREAGTDMQESQPTV
		,	GLDDETPQLLGPTHKKKSKKKKKKKKSNHQEFESLAMPEGSQVGS
1		i	EVGADMQES\RPAVGLHGETAGIPAPAYKNKSKKKKKKSNHQEF
1			EAVAMPESLESAYPEGSQVGSEVGTVEGSTALKGFKESNSTKKK
1	}	•	SKKRKLTSVKRARVSGDDFSVPSKNSESTLFDSVEGDGAMMEEG
			VKSRPRQKKTQACLASKHVQEAPRLEPANEEHNVETAEDSEIRY
			LSADSGDADDSDADLGSAVKQLQEFIPNIKDRATSTIKRMYRDD
			LERFKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLALTGIESAD
			KLLYTDRYPEEKSVITNLKRRYSFRLHIG\RNIARPWKLIYYRA
			KKMFDVNNYKGRYSEGDTEKLKMYHSLLGNDWKTIGEMVARRSL
1			SVALKFSQISSQRNRGAWSKSETRKLIKAVEEVILKKMSPQELK
1	1		EVDSKLQENPESCLSIVREKLYKGISWVEVEAKVQTRNWMQCKS
	[KWTEILTKRMTNGRRIYYGMNALRAKVSLIERLYEINVEDTNEI
			DWEDLASAIGDVPPSYVQTKFSRLKAVYVPFWQKKTFPEIIDYL
			YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPFRDIFYYEDD
F444			SEGGGHRKRKRRPRRHAWFTPVIPVLWEAKAGWII
5413	3753	1304	RPPAGVAPRRAMANVSKKVSWSGRDRDDEEAAPLLRRTARPGGG
			TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP
.			HPFPKEIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR
			TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKGNID
		j	KFTEKGGLSFSLLLWATLNAAFVLVGSVIVAFIEPVAAGSGIPQ
			IKCFLNGVKIPHVVRLKTLVIKVSGVILSVVGGLAVGKEGPMIH
		l	00011777070000000000000000000000000000
			SGSVIAAGISQGRSTSLKRDFKIFEYLRRDTEKRDFVSAGAAAG
			VSAAFGAPVGGVLFSLEEGASFWNQFLTWRIFFASMISTFTLNF
			VSAAFGAPVGGVLFSLEEGASFWNQFLTWRIFFASMISTFTLNF VLSIYHGNMWDLSSPGLINFGRFDSEKMAYTIHEIPVFIAMGVV
			VSAAFGAPVGGVLFSLEEGASFWNQFLTWRIFFASMISTFTLNF

Deginning No:				Amino acid segment containing signal peptide
No:	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Corresponding to first amino acid amino acid residue of amino acid amino acid amino acid amino acid sequence Sequence				(A=Alanine, C=Cysteine, D=Aspartic Actu, D=
to first manno acid residue of mino acid sequence sequence sequence sequence sequence sequence sequence sequence sequenc	NO:			Giutamic Acid, Fernenylaianine, Gegrycine,
to first amino acid residue of amino acid sequence ##Tryptophan, Y=Tyrosine, X=Unknown, **Stop Codon, A-possible nucleotide deletion, V=possible nucleotide nucleotide deletion, V=possible n				H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence sequence sequence codon, /-possible nucleocide deletion, -possible nucleocide de			1 -	L=Leucine, M=Methionine, N=Asparagine,
meino acid sequence ### Tryptophan, Y=Tytoshe, X=Unknow, **sScp Codon, /=possible nuclectide deletion, V=possible nuclectide deletion, V=possible nuclectide labertion) ### SUSUEMPROSYNPIPULGHTWIFFELCOWYGUTYSAGVFIP SULIGAMGRISISTICMALIMADROKYALMGARAQIGGIV ### HIGGSVPFLHWEAPVTSSILTARAKIWGYPTELGAREKVGVIT UNLSDTARAKIWGYPTELGAREKVGVITUNG ### HIGGSVPFLHWEAPVTSSILTARAKIWGYPTELGAREKVGVITUNG UNLSDTARAKIWGYPTOGENERGAREKVGVITUNG ### LIGAMGRISISTICMALIMADROKYALMGARAQIGGIV ### HIGGSVPFLHWEAPVTSSILTARAKIWGYPTOGENERGKUGUT LUTKKOLARYRIGGRGLESISLAOT ### SUSUEMPROSYNPIPUTGGRGLES				P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence Codon, /=possible nucleotide desettion) SVVSLEHDPPSYNPLTLSLFTLVYFFLACHTOINTSMAYFIF SLLIGAMOGLEGISLSVILAGAMADPSYNAMAAAQLGGIV RMTLSLTVIMMEATSMYTGFPIMLVMTAKINGBVFIRGUNGVIT BLICHAMOGLEGISLSVILAGAMADPSYTCLERREKUVAV UVLSDTASNINGFPVVEHADDTOPARLGGLILASGUIVLLHKKV FVERSLLGARRWSTSSLTAREWSFTVTCLERREKUVAV UVLSDTASNINGFPVVEHADDTOPARLGGLILASGUIVLLKHKV FVERSLLGARRWSTSSLTAREWSFTVTCLERREKUVAV UVLSDTASNINGFPVVEHADDTOPARLGGLILASGUIVLLKHKV FVERSLLGARRWSTSSLTAREWSFTVTCLERREKUVAV UVLSDTASNINGFPVVEHADDTOPARLGGLILASGUIVLLKHKV FVERSLLGARRSSPKTVTVOSINGSVORGUNGVA LUTRKULARRIGKGRESSISLATAVENTSTPROTARMYS SQUASAMDRALFSFLLSFTSRVFATSPROVSTETGRARMYS ROMADPDIGNYFHIGDSSSCLIGVVVISSYMULAPVORGOPROFISS SPENSTREGGSSFALGLYGARLIAVALCITILLANDROVG AGADAPDDIGNYFHIGDSSSCLIGVVISSYMULAPVORGARY RYLMCGLAFWSLAVINGSFTGORFFATAVENDROW RYLMCGLAFWSLAVINGSFTGORFFATAVENDROW RYLMCGLAFWSLAVINGSFTGORFFATAVENDROW RYLMCGLAFWSLAVINGSFTGORFFATAVENDROW RYLMCGLAFWSLAVINGSFTGORFATAVENGGRAV STIAPTLIADLFVADQRSMMSITYFFAIPVOSGLGYTAGSKVO MAGDMINALAVTHGLGAVALLIFLVVINGSFATARAFOLUSLIFSKA RYLMGGLAFFYLIGLISSFTGORFATAVFTGGGRAF RYLMCGLAFFYLIGHTSPROTACHTOLICASAPPLFISLACARGSIVATYLF SRRVLEISSFTPALDROSCSSSDLIFSFRAAPFOLUSLAGA SRRVLIGHTSPROTACHTOLICASAPPLFISLACARGSIVATYLF FIGGETLASHOPLAVALTIFLUTYLTTMTSFATAFOLUSLAGA AFFIGTAHLH SRRVLEGETPPCLAGARGAGATIFERVALCAFVOLIGA AAFIGTAHLH SRRVLEGETPPCLAGARGAGATIFERVALCAFVOLIGA AAFIGTAHLH SRRVLEGETPPCLAGARGAGATIFERVALCAFVOLIGA AAFIGTAHLH SRRVLEGETPPCLAGARGAGAGATIFERVALCAFVOLIGA AAFIGTAHLH SRRVLEGETPPCLAGARGAGAGATIFERVALCAFVOLIGA AFFIGTAHLH SRRVLEGETPCLAGETYTVEEMINGSFOLGARGAGAGAGASGUSCHAL RYHSVSTEPPBRKOFSFSAHAHLOSGGRAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence Codon, /=possible nucleotide desettion) SVVSLEHDPPSYNPLTLSLFTLVYFFLACHTOINTSMAYFIF SLLIGAMOGLEGISLSVILAGAMADPSYNAMAAAQLGGIV RMTLSLTVIMMEATSMYTGFPIMLVMTAKINGBVFIRGUNGVIT BLICHAMOGLEGISLSVILAGAMADPSYTCLERREKUVAV UVLSDTASNINGFPVVEHADDTOPARLGGLILASGUIVLLHKKV FVERSLLGARRWSTSSLTAREWSFTVTCLERREKUVAV UVLSDTASNINGFPVVEHADDTOPARLGGLILASGUIVLLKHKV FVERSLLGARRWSTSSLTAREWSFTVTCLERREKUVAV UVLSDTASNINGFPVVEHADDTOPARLGGLILASGUIVLLKHKV FVERSLLGARRWSTSSLTAREWSFTVTCLERREKUVAV UVLSDTASNINGFPVVEHADDTOPARLGGLILASGUIVLLKHKV FVERSLLGARRSSPKTVTVOSINGSVORGUNGVA LUTRKULARRIGKGRESSISLATAVENTSTPROTARMYS SQUASAMDRALFSFLLSFTSRVFATSPROVSTETGRARMYS ROMADPDIGNYFHIGDSSSCLIGVVVISSYMULAPVORGOPROFISS SPENSTREGGSSFALGLYGARLIAVALCITILLANDROVG AGADAPDDIGNYFHIGDSSSCLIGVVISSYMULAPVORGARY RYLMCGLAFWSLAVINGSFTGORFFATAVENDROW RYLMCGLAFWSLAVINGSFTGORFFATAVENDROW RYLMCGLAFWSLAVINGSFTGORFFATAVENDROW RYLMCGLAFWSLAVINGSFTGORFFATAVENDROW RYLMCGLAFWSLAVINGSFTGORFATAVENGGRAV STIAPTLIADLFVADQRSMMSITYFFAIPVOSGLGYTAGSKVO MAGDMINALAVTHGLGAVALLIFLVVINGSFATARAFOLUSLIFSKA RYLMGGLAFFYLIGLISSFTGORFATAVFTGGGRAF RYLMCGLAFFYLIGHTSPROTACHTOLICASAPPLFISLACARGSIVATYLF SRRVLEISSFTPALDROSCSSSDLIFSFRAAPFOLUSLAGA SRRVLIGHTSPROTACHTOLICASAPPLFISLACARGSIVATYLF FIGGETLASHOPLAVALTIFLUTYLTTMTSFATAFOLUSLAGA AFFIGTAHLH SRRVLEGETPPCLAGARGAGATIFERVALCAFVOLIGA AAFIGTAHLH SRRVLEGETPPCLAGARGAGATIFERVALCAFVOLIGA AAFIGTAHLH SRRVLEGETPPCLAGARGAGATIFERVALCAFVOLIGA AAFIGTAHLH SRRVLEGETPPCLAGARGAGAGATIFERVALCAFVOLIGA AAFIGTAHLH SRRVLEGETPPCLAGARGAGAGATIFERVALCAFVOLIGA AFFIGTAHLH SRRVLEGETPCLAGETYTVEEMINGSFOLGARGAGAGAGASGUSCHAL RYHSVSTEPPBRKOFSFSAHAHLOSGGRAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence N=possible nuclectide insertion			1	Codon, /=possible nucleotide deletion,
SVYS_BHIDPOSYND_TILG_FTLYYFFLACWYG_ITVSAGVFT S SILLGAMKGILFGILSYLICAGALMADGKYLMAGAAGLGGIV RMTLS_LTVIRMEATSNUTGSP_IMLVLATAKUGDVFIGG_ITR HIQG_SVP_HIMBASTNUTGSP_IMLVLATAKUGDVFIGG_ITR UV_SVP_HIMBASTNUTGSP_IMLVLATAKUGDVFIGG_ITR UV_SVP_HIMBASTNUTGSP_IMLVLATAKUGDVFIGG_ITR VVESSILGLUQRILLENGPROATPSPIG_SILRSGLUV_LLHKUV VVESSILGLUQRILLENGPROATPSPIG_SILRSGLUV_LLHKUV VVESSILGLUQRILLENGPROATPSPIG_SILRSGLUV_LLHKUV VVESSILGLUQRILLENGPROATPSPIG_SILRSGLUV_LLHKUV UV_TKRULARVILLGKSGLESILS_GOT GVSSADDRALFSPILLSYTSRVPRTSPPRCVSTTGREDARVYS SPESSTRRGCASSPACLD_FCRSALLVAVLCYINLLNYMBPFVV AGVALORIUNGGIAFSPILLSYTSRVPRTSPPRCVSTTGREDARVYS RSPESSTRRGCASSPACLD_FCRSALLVAVLCYINLLNYMBPFVV AGVALOPIDIRG_PFNIGDSSSGLIQTVFISSYMVLADVFCYILGGRXY RYLMCGGIAFWSLUTGSSFILGGTHSILLLTRGLUGGGASY STIAPPLIADLFVALOGSSRSLIGTVFISSYMVLADVFCYILGGRXY RYLMCGGIAFWSLUTGSSFILGGTHSILLLTRGLUGGGASY STIAPPLIADLFVALOGSSSSSLIGTUS-ISSTULLATORSLUXGUE SRELRISSRPRADPLVCATGLIGSAP_PLFISIACARGSIVAYIL SRRVLAGSTPFCLEGDSCSSSSLIGTSIGLTCLTGVLGVGLGVEL SRRLRISSRPRADPLVCATGLIGSAP_PLFISIACARGSIVAYIL SRRVLAGSTPFCLEGDSCSSSSLIGTSIGLTCLTGVLGVGLGVEL SRRLRISSRFADPLTCATGLIGSAP_PLFISIACARGSIVAYIL SRRVLAGSTPFCLEGGSCSSSSLIGTSIGLTCTTCTCHSHLGD AGSPYLIGLISDRLERNWPPSFLSEFFALQSSIMLCAFFGAG SRPLIGLISDRLERNWPPSFLSEFFALQSSIMLCAFFGAG SRRLRISSRFADPLTCAGSAP_PLFISIACACAGSIVAYILG SRRLRISSRFADPLTCAGSAP_PLFISIACACAGSIVATICHSHLGD AGSPYLIGLISDRLERNWPPSFLSEFFALQSSBLLSGSSSSHIPS SRLDENGERSTERNELNGGATTSRSALLGSFBANGAGGABSISTATAGS RIBGERSTERNELNGGATTSRSALLGSFBANGAGGABSISTATAGS SRRLRISSRSSHIPSSLSSLGEDPRSC_PRATER RIDMKRKKARSITSSLESSLGSGAFFANGAGCAGSSSSHIPS SRRLRISSRSGLAGAGGAGGATTSRCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG			2-4	\=possible nucleotide insertion)
SILIGAMGRIPGIELSYLTGALIWADDGKYLAMGAAQLOGIV MINISLITYIMMEATSIVTYGYPHINUTHAKTKYGPYPIGGYTM HIOLOSVPPHMEAPV7SHSLTAREWMSTPVTCLRREEKVOVTV DVLSPTSARNINGEPVEHADDTOPARLGGLIRKSCULLULHKU FYESSILGIVORRIELKDPRADYSPPPIGSTHYSODERCTUD LSEMMPSSTYTUGCASLERWKIKERGIGELSAGT GVASAMDRALFSFLISTSTWERTSPRCVSTTYTGREDARVYS GVASAMDRALFSFLISTSTWERTSPRCVSTTYTGREDARVYS QUCSVIQUKLPVSGRTSLAVUSILLSPASSPRKVGITVGROGAR AGAAPPDIGNRYRHSPSSARMTTGTGCLAPRGCOPPGTRSP RSPESSTRRGCSSSGLGTVTSILLSPASSPRKVGITVGROGAR AGAAPPDIGNRYRHSPSSARMTTGCLAPRGCOPPGTRSP RSPESSTRRGCSSSGLGTVTSILLSPASSPRKVGITVGGTGAR RKYLMCGILARWSLUTLGSSTIDGESGLGTVTTSSYWLAWPGVGIGORYN RKYLMCGILARWSLUTLGSSGLGTVTTSISTSWALAWPGVGIGORYN RKYLMCGILARWSLUTLGSSGLGTVTTATAPTVGSLGALVAGSKVKO MAGDHHALRVTFGLGVVAAVLLELUVREPPRAVETSGDLAPTY RKYLMCGILARWSLUTLGSSGLGTVTTAPTVGSKVKA MAGDHHALRVTFGLGVVAAVLLELUVREPPRAVETSGDLAPTY RKYLMCGILARWSLUTLGSSGLGTVTTAPTVGSKVKA MAGDHHALRVTFGLGVVAAVLLELUVREPPRAVETSGDLAPTY RKYLMCGILARWSLUTLGSSGLGATTYTAPTVGSLAVATY SERLENSADDLARVSTRAVETSGLGARVAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG		Beddenee		SVVSTEHDERGSYNPITIGLETLVYFFLACWTYGLTVSAGVFIP
RMTLSLTVIMMEATSNYTGSPIMLUMTAKUVGDVFIGGLTYM HIOLOGVPPHIMBARYVSISHLAREWSTVYCLRRERVGVIV DVLSDTASNINGFEVVERLADTORARLGGLILRSGLTVLLHHUV FVERSHLGLUGRILLGDVRDAFFEPIGSIHNGOGERECTMO LSERMØPSFITVPQGASLRVWKLFRALGGRHLVVDNRNQVG LVTKKULARYHLGKRGLESISLAGO GVGAVLDARYHLGKRGUESISLAGO GCGAVLGKLBVSGRUESISLAGO GCGAVLGKLBVSGRUESISLAGO GCGAVLGKLBVSGRUESISLAGO GCGAVLGKLBVSGRUESISLAGO GCGAVLGKLBVSGRUESISLAGO GCGAVLGKLBVSGRUESISLAGO GCGAVLGKLBVSGRUESISLAGO GCGAVLGKLBVSGRUESISLAGO AGAPDUHGRVRHERDSSARRVTETTGCCLARGGCOFFGTREF RSTRERTRGCSASPACLD/CCSALLVAULCYLLLAVDGREAV RSTLAPHLADLFAGASSHLSITTYLSVAULCYLLAVDGREAV RSTLAPHLADLFAGASSHLSITTYLSVAULAPVEGYLGGRY RKYLMCGGIAFMSLVTLGSSFIPGENFULLLFREWGUNGEAV RKYLMCGGIAFMSLVTLGSSFIPGENFULLLFREWGUNGEAV RKYLMCGGIAFMSLVTLGSSFIPGENFULLLFREWGUNGEAV RKYLMCGGIAFMSLVTLGSSFIPGENFULLLFREWGUNGEAV RKYLMCGGIAFMSLVTLGSSFIPGENFULLLFREWGUNGEAV RKYLMCGGIAFMSLVTLGSSFIPGENFULLLFREWGUNGEAV RKYLMCGGIAFMSLVTLGSSFIPGENFULLLFREWGUNGEAV RKYLMCGGIAFMSLVTLGSSFIPGENFULLLFREWGUNGEAV RKYLMCGGIAFMSLVTLGSSFIPGENFULLLFREWGUNGEAV RKYLMCGGIAFMSLVTLGSSFIPGENFULLGSSGLSLVAUSKUNG RRERISSPRADELVCATGLIGGSSFILTGASFICTUATI- SRERRISSPRADELVCATGLIGGSAFFALGFSLINLGASFIVATI- FIFGETLLSMMALVAGILLTVVTREPFRADFFALGFSLINLGAFFALGF RSRVTGSFIPGLFFALGFSLINLGAFFALGFAGAFGAFGAFGAFGAFGAFGAFGAFGAFGAFGAFGAFG		j	}	CITTCAAWCDI.FCTSI.SVI.TGAATWADDGKYAI,MGAAAOI.GGIV
HIQLGSVPPLHMEAPVISHSLTAREWSTEVTCLRRREXVOYUV UNLSDYTANNINGE VEHADIOTORALGGILRSOLTULAHKU FYERSHLGLVORRILLKDEPRDAYER PPICSHIVSODERECTUD LSERMPSETVIVOERALDRIVERSPAGICRHLVVVDNINGVUG LSERMPSETVIVOERALDRIVERSPAGICRHLVVVDNINGVUG UNTEKDLARVRILGKEGLESLAOT GYAGAMDRAIFSETLESPTSVPRSTSPROVSTETGERDARVS AGAAPEDRIKSVRILGSPSSVPRSTSPROVSTETGERDARVS AGAAPEDRIKSVRIERSSARMSTTTOCOLARRGGOGEGOTESP REYBESTROGGSASPACLE/CRSALIVAVLCYINILAYMDREYV AGVLPDIRGYPRINGSSSARMSTTTOCALARRGGOGEGOTESP REYBESTROGGSASPACLE/CRSALIVAVLCYINILAYMDREYV AGVLPDIRGYPRINGSSSARMSTTYPALFVUSGLGYTAGSKVX REYLMGGSIAPSKUTUGSSST IGGENVALVILGVURSPROVALDEVICKIORYX REYLMGGSIAPSKUTUGSSST IGGENVALVILGVURSPROVALDEVICKIORYX REYLMGGSIAPSKUTUGSSST IGGENVALVILGVURSPROVALDEVICKIORYX REYLMGGSIAPSKUTUGSST IGGENVALVILGVURSPROVALDEVICKIORYX REYLMGGSIAPSKUTUGSST IGGENVALVILGVURSPROVALDEVICKIORYX REYLMGGSIAPSKUTUGSST IGGENVALVILGVURSPROVALDEVICKIORYX REYLMGGSIAPSKUTUGSST IGGENVALVILGVURSPROVALDEVICKIORYX REYLMGGSIAPSKUTUGSST IGGENVALVILGVURSPROVALDEVICKIONE SERLERISMPRADEVICKTGILGSAPPLETSIACAGGSIVATYIT FIGURILISMMADISTICHTUTUTUSHILGARAGGIVATICHSHLOO AASIGTAHHH SRVLYIGITGDERRAMPSSTLESPALOPSIMICAPGALOR AASIGTAHHH SRVLYIGITGDERRAMPSSTLESPALOPSIMICAPGALOR AASIGTAHHH SAGPYLIGURANDILLAYUTUTUSHILGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA		\$		DAME OF WITHMEN TONGTOCKED INT. VI.MTAKTVCDVFTFGI.YDM
DVLODTASNINGEPVVERADTOPARICGLIRSOLITULIS LIitulisen liituliitaliitaliitaliitaliitali		1		
FYERSKLIGHVORKILIKOPRIDAYPREPTIGS HHYGODERICAL LERMORPS TYPOGRASL PRAVEL PRALICIAL HYDODROGUMENT LYTRICHARY PLACKROLESISANOT GUGSWICHOVSGRISLACYBS ILLS PRASPETS PREVISTED GROBARVIS ORGANICAL PROBLEM PROSPETS PREVISTED GROBARD AGAA PROHECT WHEN PERSAR PREVISTED GROBARD AGAA PROHECT WHEN PERSAR PREVISTED FOR PROSPETS OF THE PROSPET ORGANICAL PROBLEM TO THE AGAIN WALL THE AGAIN WA		Ì	l	
LSEFMMPSPTYPQEASIBRYFKLFRALGERILVVUDNENGVUG LYTRKDLARYBLGKØRGESIBLAOT GVASAMDRALFSPLLSPTSRYPTSPFRUSTETGRRDBAVLG GKGSVLQGKLDVSERPSLACHSTSPRAVETSPREVUSTETGRRDBAVLG GKGSVLQGKLDVSERPSLACHSTSLESPASSPREVIJVGGTGRB AGAAPRDHGRVRHRPSSARMTETTGGCLADRGCGPPTETGR REPRINTERGCSASPACLP/CRSALIVAVLCYINLLATWODEFTV AUVLPDIEQFFRINDISSEGIIGTVFISSMVLAPVFGYLGDRYN REYLMCGGTAWBLVTLOSSFTEGBHWALLLATWOLDFTV AUVLPDIEQFFRINDISSEGIIGTVFISSMVLAPVFGYLGDRYN REYLMCGGTAWBLVTLOSSFTEGBHWALLLATWOLDFTV STIAPTLIADLFVADQRSMMSISTFYAIFUSGGSTALGAVPAFLL RERVINGETPFCLEGDSCSSDSLIFGLITCLTCUTGVLSVLGUNTYFF RERRENSPRADPLVCATGLIGSAFTFYAIFUSGGSTALAWAPAFLL RERVINGETPFCLEGDSCSSSDSLIFGLITCLTCUTGVLSVLGUNTYFF IFIGETLLSMMWALVADILLFVVVIETRRSTARAFQIVLSHLLGD ASSPYLIGLISDRIRRNBPSFYSISFRALGSSTALWAPAFLL RERVINGETPFCLEGDSCSSDSLIFGLITCLTCVLSVLGVLGVIYFF IFIGETLLSMMWALVADILLFVVVIETRRSTARAFQIVLSHLLGD ASSPYLIGLISDRIRRNBPSFTSSFFALGSSTALWAPAFLL RERVENSPRETPELSBERINGFFFISFRALGFSIALWAPAFLL RERVENSPLIGHTENDEVCATHLIGSAGTTVERTRGGGSTALWAPAFLL REPRESENTERINGRAMAINGSCHARAGTGGUNTAR RICHTERSPRETERINGRAMAINGSGSTTVERTRHSMRQGIFF REXTENSELRERUMGRATILGHPIECQBPDPARASSFORDSSSHLPP EPALSPOQAPRARANTISHPSTECQBPDPARASSFORDSSHLPP REXTENSELRERUMGRATILGHPIECQBPDPARASSFORDSSHLPP REXTENSELRERUMGRATILGHPIECQBPDPARASSFORDSHLINKS RICHTERSPRETPCLREVTTWERMISTTGRSKIKFDMEMMSHAVG GVP\RHRIBGEINGFSCAGDILLHMSERGKIKFDMEMSHAVG GVP\RHRIBGEINGFSCAGDILLHMSERGKIKFDMEMSHAVG GVP\RHRIBGEINGFSCAGDILLHMSERGKIKFDMELKKYRDD VGYCGLISFVAGILLLHMSERGKIKHFSSLRKCHARDLLKOKANDLLANK ASGPHEFTMERFTADFFDMITGLGGVFTRVSLLGGARGUNDLANKFYLLIGHER LETTUPDIKSTLPHLIGUMGRATINGVPSDQTAKGLGAVEVYFV VLQEELIDSSPLSDNORMMLEKERTNSLRKCHARDLLGULGVAN RIGSLBATIEKLLSSBEKKLGAMLTTLELEGBRATHQWTFGEI SAPAAPTTSLMSSTINGMATHAUTKTLETERREGGRATHQWTFGEI REPRLASFGGGMTSTUTTSLESPTOTTISHTSTELELSSCHAMACHARDLANG ALALKEKLELBENGER RESVAUGABERMMDIVVYHRGSRGCEDARANGTLURANGCUGHTHORM VECSTORILERFFCQLTALMMALDENGLONGANA ANDERVERSTGGGGGSVDVTVCSPRCCASSELUMDENGLINGS REVSYGDDPVGSLENDVYLGKRTTALGGGLYNDFHILLIK NINLEEWESIGGGGGSVDVTVCSPRCCASSRGVWTEANGVITCHLING REVS		ļ.		DVLSDTASNHNGFPVVEHADDTQPARLQGLILKSQLIVLLKAKV
5414 2130 390 GUGASANDRALES PLASPISAVETS PERCUSTETGREDARUS GASANDRALES PLASPISAVETS PERCUSTETGREDARUS GACSANDRALES PLASPISAVETS PERCUSTETGREDARUS GACSANDRALES PLASPISAVETS PERCUSTETGREDARUS AGAAPRIGE VIRIAGE SARMTETTOCLANDROCGOPEGTES REPRESTERGCASPACLP/CRSALIVAVLCYINILAVIADEPTY ACVLPDIEGFFNIGISSSGLICTVETS SEMILAVEROLIGORYA REYLMCGGIAFWELVILOSS TEGHENWILLINGUNGGASY STIAPTITADLFVADQRSRMLSIFTFAIFVGGGGYLAGRENGDLPEL NETSWADDLRALARNSSYLSSIGTTAVAFVTGSLALWAPAFLL RERVYLGETP PELEPGISCSSSBLITGLITCUTGVALUSUGUET SREARUSHSPRADPLVCATGLIGSAPFLETSLACARGSIVATY I PICETLLSMWSALVADILAGENPUTPISLACARGSIVATY I PICETLLSMWSALVADILAGENPUTPISLACARGSIVATY I PICETLLSMWSALVADILAGENPUTPISLACARGSIVATY I PICETLLSMWSALVADILAGENPUTPISLACARGSIVATY I PICETLLSMWSALVADILAGENPUTPISLACARGSIVATY I PICETLLSMWSALVADILAGENPUTPISLACARGSIVATY I PICETLLSMWSALVADILAGENPUTPISLACARGSIVATY I PICETLLSMWSALVADILAGENPUTPISLACARGSIVATY I PICETLLSMWSALVADILAGENPUTPISLACARGSIVATY I PICETLLSMWSALVADILAGENPUTPISLACARGSIVALVADILAGE SERURISMSRADALVADILAGENPUTPISLACARGSIVALVAT REDARMAN ALABIANA VADILAGENPUTPISLACARGSIVAL PROPERPOT REMATSREDENBERGEN VAN ALABIANA VADILAGENPUTPISLACARGSIVAL PROPERPOT REMATSREDENBERGEN VAN ALABIANA VADILAGENPUTPISLACARGO POPPARA REMATSREDENBERGEN VAN ALABIANA VADILAGENPUTPISLATAR VAN ALABIANA REMATSREDENBERGEN VAN ALABIANA VADILAGENPUTPISLATAR VAN ALABIANA REMATSREDARI VAN ALABIANA VAN ALABIANA VAN ALABIANA REMATSREDARI VAN ALABIANA VAN ALABIANA REMATSREDARI VAN ALABIANA VAN ALABIANA REMATSREDARI VAN ALABIANA VAN ALABIANA REMATSREDARI VAN ALABIANA VAN ALABIANA REMATSREDARI VAN ALABIANA VAN ALABIANA REMATSREDARI VAN ALABIANA VAN ALABIANA REMATSREDARI VAN ALABIANA VAN ALABIANA REMATSREDARI VAN ALABIANA VAN ALABIANA REMATSREDARI VAN ALABIANA VAN ALABIANA REMATSREDARI VAN ALABIANA		l .		FVERSNLGLVQRRLRLKDFRDAYPRFPPIQSIHVSQDERECTMD
5414 390 GVASAMDRALFSPLLSPTSRVPRTSPRRVIJVOGTGRR AGAAPDRHGRVRHERPSSARMTTTGGCLAPRGCGSPRETEL REPSRTRRGGSARMTTTGGCLAPRGCGSPRETEL REPSRTRRGGSARPACLY/CREALIVALVCTINLIATMORPTY REVERSTRRGGSARPACLY/CREALIVALVCTINLIATMORPTY REVERSTRRGGSARPACLY/CREALIVALVCTINLIATMORPTY REVILOGIA FROM THE RESPRETE REPSRRVILOGUE FROM THE REVERSE REPSRRVILOGUE FROM THE REVERSE REPSRRVILOGUE FROM THE REVERSE REPSRRVILOGUE FROM THE REVERSE REPSRRVILOGUE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE REVERSE FROM THE REVERSE R		}	1	LSEFMNPSPYTVPQEASLPRVFKLFRALGLRHLVVVDNRNQVVG
OMCSVLOGILLPVSGRTSLACVRSILLSPASSPRIVGITVGGTGRA AGAAPAPEHGRVWHRRPSSARMTTTTGCLAGEGGGRGTGSP RSPESRTRGCCSASPACLP/CRSALIVANUCYINLLNYMDEPTV AGVUPDIEGPPWIGDSSSGLIGTVTTISSWVLAPVGGVLGRAVI RKYIMCGGIAFWSLVTLGSSPIPGEHFWLLLLTRGLIVGVGBAY STIAPTLIADLEVALORSMILSIPYTA PROSGIVATIAGSKVKO MAGDWHARLAVPFELGGVACKSSELSIPSTLTAPAFVGGLAVARGKVKO MAGDWHARLAVPFELGGVACKSSELSIPSTLTAPAFVGGLAVARPAFLL RSRVULGETPFELGGDCSSSSELSIPSTLTGLTGVLGVGLAVET SRRUHSHNPRADPILVCATGLGSAPFIFISLACARGSIVANYIF IFIGGTLLSMNNAVADILLVAVI PTRETSTAPAFVLSHLLOD AGSPYLIGLISDRIRRWPPSSLSEFFALQFSIMLCAFVGLAG AAFLGTAHLH ASSPYLIGLISDRIRRWPPSSLSEFFALQFSIMLCAFVGLAG AAFLGTAHLH SSPLIGLISDRIRRWPPSSLSEFFALQFSIMLCAFVGLAG AAFLGTAHLH ITSPLRCLFERKQKEHHIGEMKQTSQMAAENIGSLPPSALTR RLDMLNKKARSLTSSLSSILSGENARACLQSHSISVDSSLSSLPSALTR RLDMLNKKARSLTSSLSSILSGENARACLQSHSISVDSSLSSLPSALTR RLDMLNKKARSLTSSLSSILSGENARACLQSHSISVDSSLSSLPSALTR RLDMLNKKARSLTSSLSSILSGENARACLQSHSISVDSSLSSLPSALTR RLDMLNKKARSLTSSLSSILSGENARACLQSHSISVDSSLSSLPSALTR RCMTGKACDSSRYEDYSELEDLPNSSIFULGSSEPDSALTR RCMTGKACDSSRYEDYSELEDLPNSSIFULGSSEPDSALTR RCMTGKACDSSRYEDYSELEDLPNSSIFULGSSEPDSALTR RCMTGKACHSTANDAMACLAGATST			i	LVTRKDLARYRLGKRGLEELSLAQT
OMCSVLOGILLPVSGRTSLACVRSILLSPASSPRIVGITVGGTGRA AGAAPAPEHGRVWHRRPSSARMTTTTGCLAGEGGGRGTGSP RSPESRTRGCCSASPACLP/CRSALIVANUCYINLLNYMDEPTV AGVUPDIEGPPWIGDSSSGLIGTVTTISSWVLAPVGGVLGRAVI RKYIMCGGIAFWSLVTLGSSPIPGEHFWLLLLTRGLIVGVGBAY STIAPTLIADLEVALORSMILSIPYTA PROSGIVATIAGSKVKO MAGDWHARLAVPFELGGVACKSSELSIPSTLTAPAFVGGLAVARGKVKO MAGDWHARLAVPFELGGVACKSSELSIPSTLTAPAFVGGLAVARPAFLL RSRVULGETPFELGGDCSSSSELSIPSTLTGLTGVLGVGLAVET SRRUHSHNPRADPILVCATGLGSAPFIFISLACARGSIVANYIF IFIGGTLLSMNNAVADILLVAVI PTRETSTAPAFVLSHLLOD AGSPYLIGLISDRIRRWPPSSLSEFFALQFSIMLCAFVGLAG AAFLGTAHLH ASSPYLIGLISDRIRRWPPSSLSEFFALQFSIMLCAFVGLAG AAFLGTAHLH SSPLIGLISDRIRRWPPSSLSEFFALQFSIMLCAFVGLAG AAFLGTAHLH ITSPLRCLFERKQKEHHIGEMKQTSQMAAENIGSLPPSALTR RLDMLNKKARSLTSSLSSILSGENARACLQSHSISVDSSLSSLPSALTR RLDMLNKKARSLTSSLSSILSGENARACLQSHSISVDSSLSSLPSALTR RLDMLNKKARSLTSSLSSILSGENARACLQSHSISVDSSLSSLPSALTR RLDMLNKKARSLTSSLSSILSGENARACLQSHSISVDSSLSSLPSALTR RLDMLNKKARSLTSSLSSILSGENARACLQSHSISVDSSLSSLPSALTR RCMTGKACDSSRYEDYSELEDLPNSSIFULGSSEPDSALTR RCMTGKACDSSRYEDYSELEDLPNSSIFULGSSEPDSALTR RCMTGKACDSSRYEDYSELEDLPNSSIFULGSSEPDSALTR RCMTGKACHSTANDAMACLAGATST	E414	2130	390	GVASAWDRALFSPLLSPTSRVPRTSPPRCVSTETGRRDRARVPS
AGAAPROHGRVRHERPSSARRWITETTGGCLAPRGCGGPRGTSP RSPRSTRTRGCASSAPACLP (CRSALIVANLINIAMDRETYLA AGVLPDIEOPPHIGDSSSGLQTVFISSWMLAPVGGVLGDRYN RKYLMCGGIAFWSLVTLGSSFIPGEHFWLLLITERGLVGVGASY STIAPTILADLFVADGRSMMSIFYFATPUSGGLGVIAGSKVKO MAGDWHNALRVTPGLGVVAVLLIFLVVREPPRGAVERRISDLPEL NPTSWMADLRALARNESPISLSGLGFTANFYTGSLALWAPFALL RSRVVLGETPPCLPGDSCSSDSLIFGLTCLTGVUGVGLGVEI SRRUKHENPRADPIVCATGLGSAPFIFLSTLACRRSIVATYFI FIGGTLLSRNWALVADILLYVVIPTRSTAGAGVIVJSHLGG AASPYLIGLISGRERWAPPSFLSEFRALQFSLMCCAFVGALGG AAFLGTAHLH 5415 693 2986 1PPKTKLEIQKH\LTTLT\NQBQATIFEVQKLRPRNEQRENEL ISPLACHEBERQKEHHIGENKQTSGMAAENIGSELPSATRF RLDMLKNKAKRSLTESLESILESRGNKARGLGEHSISVDLOSSLS STLSMTSKEPSVCKEALPISESSFKLLGGENSOLSSENSHIPS EPALSSPOGAFRRANTLSHFFIECOGPPOPARGS POVGOKLM RYHSUSTETPHERKDFSSKANHLGDSGGTPVKTRHSWQOIFT RVATPOKACDSSRYEDYSELGELDPRSPLEEVCEDGPFGPPP EKXRTSRELRELMOKATLQUILLLMRSKENGLASENDLANK LKLDYESITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMISAGG GFV,RHRRGEIKKFLASGPHLSHGPFSKQPEROFYVERHELKQLI SQGHAILIDLGHTFFTHFFYSAGLGAGGLSINTIKKASHLDG VGYCGLSFVAGILLLIMSEBEAFRMLKFLMFDMGIRKQYRPD IILGGMYGLSKLLIDHRHGLNKTINNIEHBEIGSTAPAPFITM ASGFFLGFVARVFDMIFLQGTZVIFKVALSLLGSHKRYLDGH LETTYDFIKSTLPDLIKGLMOKATLOUGKKTINOVFBMDTAKQLQAVEVEYY VLOESLIDSSPLSDNGNDRUKLBKTNSSLRKONLDLDEDLOVAN RIQSLRATIEKLLSSESKLKQAMLTLELERSALLQTVEETRRE ARPSBREPECTOPEPTGO VAPDDTGKGNTTIKKLINGKRKRSPUPCEPRFTTSGQGIGTSTESL LSSNSSDDNRQCHNFLIKARSJLRSGNFDTAWHLOHIERG RRPILASFGGMGTTSSLPSVUSGGMHPAKHQCNGYGGNGDY SYAPAPPTTSSMSSIRHISPLSSGSTFTVYTSMILLQHED LETTYDFIKSTSMSSIRHISPLSSGSTFTVYTSMILLQHED RRPILASFGGMGTTSSLPSVUSGGARRANGGTLYDFTTT ERRGLPPSSMSSIRHSPLSSGSTFTVYTSMILLQHED RRPILASFGGMGTTSSLPSVUSGLSKKVTDERRINGHUNGLER RSVAVGABEMMNDIVVYHRGSSSCGDAVGTLVERNKGVSVTT AMLGWMTERADGLSGGPCKNIVTYTAFRANGVGGNTT VENGSTGRITERFROL\TADHQALSGKCGUSGLENGMVTLANGVGSVTT AMLGWMTERADGLSGGPCKNIVTYTAFRANGVGGNTT VENGSTGRITERFROL\TADHQALSGKCGUSFLENGMVTLASGLGSGFC NUNGVFRANGSGENGGMGSNASGLSCOPECKNIVTGARSAGSGFC NUNGVFRANGSECGGCSVTVTVCSPECKASGRAGGSGFC NUNGVFRANGSGFCHANGVTAFRANGVGGSUFT NUNGVFRANGSGFCHANGVTAFRANGVGGSUFTAFRANGVGGNT MUNDTCVGTRRSVSMSGRGMGINSOLTSTESVINDLTLLK N	2414	2230	1	OWCSVI-OGKI-PVSGRTSLACVRSILLSPASSPRKVGIVGGTGAR
RSPESRTREGCSASPACLE/CREALLYANLCYINLINVANDETVY AGVUPDIEG/PRIGIOSSCILOTYTISSWINLAVERGILOTYAN RKYLMCGGIAFWSLVTLGSSPIPGEHFWILLLITEGLVGVGEASY STIAPTLIADIEVADGRSMMLSIFIPAIPVGGGLYAGSKVKD MAGDWRNALGYPEGLGVGVACULLEILVVREPRGAVERRISDIPPEL NTTSWHADLRALARNESFYLSSLEFTAVAFVTGSLALWAPAFLL RSRVVLGETPECLEGOSCSSSSLIFGLTGVAGVGGVGRISGLEPEL SRRUKHSNPRADPILVCATGLGSAPPIFFISLACARGSIVATYF IPIGETLLSMNATAVADILLYVAV PTRRSTAPOLVISHLLGD AGSPYLIGLISDRIRRWPPSFLSEFRALGFSLMLCAFVGALGG AAFLGTAHHH FIRENLEVERRYCKERAPPISESFRALGFSLMLCAFVGALGG AAFLGTAHHH FIRENLEVERRYCKERAPPISESFRALGESEDISSSSSHIPP FRALDMLKNKKARSLTESLSEISLEGROKRAGLGKHSISVDLDSSLS STILSTSKREPSVCEKRALPISESSFKLLGSSEDLSSDSSSHIPP ERAPLSPOOLARRANTLESSEISLEGROKRAGLGKHSISVDLDSSLS STILSTSKREPSVCEKRALPISESSFKLLGSSEDLSSDSSHIPP ERAPLSPOOLARRANTLESSESFRLLGSSEDLSSDSSHIPP ERAPLSPOOLARRANTLESFEIGEDEPDRESPERVERGERINGVAG RYHSVSTETPHERKOFESKANHLGDSGGTPVKTRRHSWGOIFF RVATFQGACDSSSKYEDYSELGELPRESPERVLEGREPORPOPPP EKKRTSRELERELWOKALLOGILLERMEKKONKOLGASENDLINKS LKLDYBEITPCLKEVTTVWEKMLSTFORSKLKPDMEKMBAVG GVP\RHRIGGENKFLAXOFFHENDENGLKGVARDON LKLUDYSEITPCLKEVTTVWEKMLSTFORSKLKPDMEKMBAVG GVP\RHRIGGENKFLAXOFFHENDENGLKGVARDON VOYCOGLSFVAGILLLIMMESKNIKADDMLKKVYRDD VOYCOGLSFVAGILLLIMMESKNIKADDMLKKVYRDD VOYCOGLSFVAGILLLIMMESKNIKADDMLKKVYRDD VOYCOGLSFVAGILLLIMMESKNIKADDMLKKVYRDD VOYCOGLSFVAGILLLIMMESKRIKADDMLKKVYRDD VOYCOGLSFVAGILLIMMESKRIKADDMLKKVYRDD VOYCOGLSFVAGILLIMMESKRIKADDMLKKVYRDD VOYCOGLSFVAGILLIMMESKRIKADDMLKKVYRDD VOYCOGLSFVAGILLIMMESKRIKADDMLKKVYRDD VOYCOGLSFVAGILLIMMESKRIKADDMLKKVYRDD VOYCOGLSFVAGILLIMMESKRIKADDMLKKVYRDD VOYCOGLSFVAGILLIMMENTALMERBELGGGATVOTTORELARGR ARPSDREPECTOPEPTGD KSOLFFTGGGGGTTSSLDSVOSGMNPAKHGLGONGVGGNOY VOYDIGKGNTIKKLNIQKREKSSVAGOGLSTARRASGGGLYTOTESLERA ARPSDREPECTOPEPTGD KSOLFFTGGGGGGTTSSLDSSVOSGMNPAKHGLGONGVGGNOY VOYCOGLSFVAGNAGATUTURENCOVSVT AMAGDWTEABAGERGGATDISGCGGGATSLEGGGGTYDTYBELGURG VORDAGRASKKVOKATHAQPLUTSENVAGNOSLA VORHUNGVAGRASKKVOKATHAQPLUTSENVALSANG MLAKEVESTAGGGSLSVAGNOGLOSSCAGASSLENGEN MLAVENTAGOGLOSSVATVAVVCYGEBLENGMINITURL VEHDRCAGRSVEMCOLSSPENTALSGGGGLYTOTLASHGGD VEH]	1	
AGVLPDIEGPFNIGDSSSGLIQTVFISSYMULAPVGSUGNYA RYYLMCGIAPHSUNTUGSSF PDERHWILLITEGLVGUGRAY STIAPTLIADLFVADQRSRMLSIPYPAIPVGSGLGYIAGSVKD MAGDMRMALRVTPGLGVVAVLLIFLVVREPPRGAVERHSDLPPL NPTSWADLRALARNSPFVISSLGFTAVAFVTGSLALARAFAIL RSRVVLGETPFCLPGDSCSSSDSLIFGLTGLTGLTGVGLGVEI SRRURHSNPRAPPLVCATGLGSAPFIFISLACARGSIVAFYTH IFIGETLLSNNNALVADILLYVVIPTRSTAGAFQTUSHLCAFVGLAGE ASFLTGHISISDRLRRWPPSFLSEFFALQFSIMLCAFVGLAGE AAFLGTAHLH 5415 693 2986 1PFKTKLELQKH\LTTLT\NQBQATIFESVQKLRPRNEGRENEI LISPLRCLEBBRQKEHHIGEMKQTSQMAAENIGSELPPSATRF RLDMLKNKAKRSLTESLESILSSCNKARGLGSEISSVDLSSLS STLSNTSKEPSVCEKALPISESSFKLLGSEBLSSDSSSHLPF EPALSSPQAFRRANTLSHFFIRCOFPPVARRHSWOOTH RYMSVSTETPHRRUFFSSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSKANILGDSGGTPVATRRHSWOOTH RYMSVSTETPHRRUFFSKANILGDSGGTPVATRANSPORT RYMDOTAGNTIKKLINGURKTINGVFENDURARCHAPPLITM ASGPLGFVANVFUNGTTHRHSMANILGDSGGTPVATRAGGGLOVAN RIOSILBATIEKSTANICHTERI			1	
REYLMCGGTAFWSLUTLGSSFIEGHFMILLLITRGLWOVGEANY STARPTLIADEPMADGRAMLSITYPTS USGLGYTAGSENVEN MAGDWHWALRVTPGLGVVAVLLLFLVVEEPPRGAVERISDLPPL NPTSWWADLRALARPSFVLSSLGFTAVAFVTGSLAUMAPAFIL RERVVLGETTP CLPGDSCSSSDSLITGLITCLTGVLGVGLGVEI SRRURISNNAIVADILLTVVIVTPRATAFAFQTULSHLLGD ASSPYLIGLISDRERNWPSPFLSEAPATLGFSIMLCAFVGALGG ASSPYLIGLISDRERNWPSPFLSEAPATLGFSIMLCAFVGALGG ASSPYLIGLISDRERNWPSPFLSEFRALQFSIMLCAFVGALGG ASSPYLIGLISDRERNWPSPFLSEFRALQFSIMLCAFVGALGG AFFLOTAHLH 5415 693 2986 TPFKTKLELQRH\LTTLT\NQEQATIFEEVQKLPRNEQREDEI ITSFLRCLFFBEKQKEHINIGEMGYTGVAARBNIGSELPSATRF RIDMLKWAKARRSLITSESISLISGNGKARGQERSISSVONGKLM RYHSVSTETPHREKDFSSKANHLGDSGTFVVKTRRISNQOIFT RVATFVKACADSSPREDVSELGGLPPGARGSGGVGGKLM RYHSVSTETPHREKDFSSKANHLGDSGTFVVKTRRISNQOIFT RVATFVKACADSSPREDVSELGGLPPGARGSGGVGGKLM RYHSVSTETPHREKDFSSKANHLGDSGTFVVKTRRISNQOIFT RVATFVKACADSSPREDVSELGGLPTSERVGEROPGPPPB EKKRTSRELRELWQKAILQQILLIRMEKENGKLQASSDESHLPS EKKRTSRELRELWQKAILQQILLIRMEKENGKLQASSDESHLPS RVATCHGSTVARFULDIGTFPTHPYFSAQLGALGGLSLYMILKAYSLLDG VGYCGLSFYAGILLHMSEBEAFRIKHFDFMGLRKYYRPD ILLOMYGLSRLLHDVIRDLYNHLEBEHIGGBLIXAPAFFLTM ASGPHJGFVARVFDMIFTCGTEVTFEVALSLLSHRPBLLDHEN LETTVDPIKSTLPNLGLVVQMEKTINQVFPMDIAKQLQAYEVEY VLQEBLIDSSFLARDGROMBKLEKTNISLRKGNLDLLDEQUVANW RTGSLEATTEKLLSSSSKIKGAMITLEBRSALLQTVEELRRE AKPSDREFBECTQFPTGD 5416 27 4074 **SSLDFFRGGKAGDILSGGODKSGNDFYFVETFYGYQLDLDFLI TRENGLPPPSSCLENNRANLGVTKTLBERSALLQTVEELRRE AKPSDREFBECTQFPTGD SKRATHSTSSMSSITRIBPLSSGGITTYNSSMHLQHIRGQ AIALKRLEELEGQVTTSSLDSFVGSGNINPAKIQLQNGYGNGDVS VXAPAAPTTSSMGSSITRIPLSSGGITTYNSSMHLQHIRGQ AIALKRLEELEGQVTTSSLDSFVGSGNINPAKIQLQNGYGNGDVS VXAPAAPTTSSMGSSITRIPLSSGGITTYNSSMHLQHIRGQ AIALKRLEELEGQVTTSSLCSSCKDAAVGTVBSMCNGSVST AMMGYMTEADKRIBPLSSGGCHYTVASSWUDLTLKK MLKBVSSIGCGGCSVGTVTSSLCSSRGWTDAVGYGRAGVSVT AMMGYMTEADKRIBPLSGGGCTTSSLCSSRGWTDAVGYGRAGVSVT AMMGYMTEADKRIBPLSGGGGTTTAVGTPROMGSSVT MAVPRTADQDTSTDLEQVHQPTNTSTATILESCTUTCLSTLDK TSTQTVETRTVAVGGGRVGDINSSTKTRSICGCTLLSGHSGFD PSAVKTKRSSLGCGGCSDATGMSGGGLISTISSINDGLLISTLSSINDGLLARGG BSAVKTKRSSLACAPGGMSMTAMSGYGAANA				
STIADITIADLEVADQRSRMLSITYATATVOSGLGYTAGSKVKU MAGDWHWALRVTPGLGVVAULLIFLUVEEPPGAVERSIGLEPEL NPTSWWADLRALARNPSFVLSSLGFTAVAFVTGSLALNAPAFLL RSRVVLGETFPCLPGDSCSSDSLIFGLITCLTGYLGYGLGVSI SRRUHENNFRAPIPLVCATGLLGSAPFLISLACARGSIVATYIF IFIGSTLLSNNNAIVADILLYVVIPTRSTAEAFQTVLSHLLGD AGSPYLIGLISDRLRNNPPSFLSEFRALQFSIMLCAFVGALGG AAFLGTAHLH 5415 693 2986 IPPKTKLEIQKH\LTTLT\NGQATIFEEVQKLRPRNEQRENEI IISPIRCLEPBRQKEHIHIGEMQGTSQMAARNIGSLEPPSATRF RLDMLKNKAKRSITESLESILSKGNKARGLQEHSISVDLDSSLS STLSNTSKEPSVCEKEABLFISSSFSLESDLSSDSSSSHLPB EPAPLSPQOAFRRANTLSHPPLEQEPPQPBAGSSPGVOKKM RYMSVSTETPHERKDFESKANHLGDGGTPVKTRRHSWRQOIFI RVATPQKACDSSRVEDYSELGSLPPRSPLEPVCEDGFPGPPB EKKRTSRELRELWGKAILQOILLIRNEKENGKLQASENDLINK LKLDVEEITPCLKEVTTVMERMISTGRSKKKPDMSKHBSAVG GVP\HHRIGGINKFLAEQFHLKHGPSKQQSKDVYKELLKQLI SQQHAILIDLIGHFPPPHYPSQLCAGGOLSLYNILKAYSLLDGB VGYCQGLSFVAGILLHMSEERAFKMLKFLMFDMSKHSAVG GVP\HHRIGGINKFLAEQFHLKHGPSKQQSKDVYKELLKQLI SQQHAILIDLIGGTFPTPHYPSQLCAGGOLSLYNILKAYSLLDGB VGYCQGLSFVAGILLHMSEERAFKMLKFLMFDMSKHRSAVG GVP\CHHRIGGINKFLAEQFHLKHGPSKQCKDVYKELLKQLI SQQHAILIDLIGGFTPPHYPSAQLCAGGOLSLYNILKAYSLLDGB VGYCQGLSFVAGILLHMSEERAFKMLKFLMFDMGLRKQYRPD IILQGMYGLSRLIHDYRRDLYNHLBEHEIGPSLYAAWHTIME ASQFFLGFVARVPDMHTFLQGTEVTFEVALISLLGSHKPLILQHE LETTUDFIKSTLDNLGLVQMSKTINQVFPMDIAKQQAVEVEYT VLQEELIDSSSLSDNDKALEXTNSSKKKQAMLTLELERSALLQTVEELRRS AKPSDEPECTQPEPTGD **KSSLZCFWGGKAGDILSGDOKEXGDPYFVSTYGYQLDLDFLI TSTQCFTGYGGKAGDILSGDOKEXGNPYFVSTYGYQLDLDFLI ENGOLPPSSPLDEHRHLHVTKTLMETRRLEGGERATUMTYDGE RRPKLLSSSNSDNNCQCNPTLARSGVTSTTSPPPDLETSLPFTTI ENGOLPPSSPLDEHRHLHVTKTLMETRRLEGGERATUMTYDGE RRPKLLSSSNSDNNCQCNPTLARSGVTSTSPPPDLETSLPFTTI ENGOLPPSSPLDEHRHLHVTKTLMETRRLEGGERATUMTYDGE RRPKLLSSSNSDNNCQCNPTLARSGVTSTSPPPDLETSLPFTTI ENGOLPPSSPLDEHRHLHVTKTLMETRRLEGGERTYDTVSEMRNCGVST **SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRGG SQINNCGVKRSYSAGNSGLGCLSSRRSGSELLENGVSUM **AKPSBLSCBGCSVGKNSVSVEVCTGSNTESSSLENGN MLUVDTCVGTSVETNSVGASGVEVASVEVCTGSNTESSSLENGN MLUVDTCVGTSVETNSVGASGVEVASVEVCTGSNTESSSUNDLTLLK **NANDARBERBERGGENNDTVVYYGHAGSSCKUNDLTLISCGTHLGGGNGVT **AMLGRERGENNDTVVYYHGSRSCKUNDARVITAGGPC]	1	
MAGDWHMALRVTPGIGVVAVLLIFLVVREPPRGAVERISDLPPL NPTSWANDLRALARNEPSVISSIGFTAVTSIALMAPAFIL RSRVVLGETPPCLPGDSCSSDSLIFGLITCLTGVLGVGLGVEL SRRURHNPRADPLVCATIGLISASPFLIFSLACARGSIVATYIF IFIGETLISMNMAIVADILLYVVIPTRESTARAFQIVUSHLLGD AGSPYLIGLISDRLERNMPPSFLSERALQPSIMLCAPVGALGG AAFLSTAHLH 5415 693 2986 1PRRVLEQKRLVTTITVNOEQATIFEEVGKLEPRNEQRENE LISPRCLFEBKQKEHINIGEMCOTSQMARANIGSELPPSATRR RLDMLKKKARRSLTSSLESISISRGNKARGLQEHSISVDLDSSLS STLSNTSKEPSVCEKEALPISSSFKLLGSSEDLSSDESSHLEP EPALSFOQAFRERANTISHFPIECQEPPOPARGSSGVGKLM RHSVSTETPHREKDFESKANHLGOSGTPVKTRRISMQQIFI RVASTOKACDSSRYEDVSELGGLIPPSEVGEDFGPPPP EKKRTSRELRELMGKALLQOILLIRMEKENGKLQASEDLINKE LKLDYBEITPCLKEVTTVWEKMLSTPGEDVCEDGPGPPP EKKRTSRELRELMGKALLQOILLIRMEKENGKLQASEDNLINKE LKLDYBEITPCLKEVTTVWEKMLSTPGENGCESSPLEVELGDFGPPP EKKRTSRELRELMGKALLQOILLIRMEKENGKLQASEDNLINKE LKLDYBEITPCLKEVTTVWEKMLSTPGENGCENSAVAG GVP\RHHRIGBINKFLAEGFHLKHQFPSKQQFKDVPYKELLKQLI SQQHAILLDLGRTFPTHPYFSAGLGGLSIYMILKAYSLLDG VGYCGLSFVAGILLHMYREDLYNHLEHEIGGBLYAPMFLTM ASGPELGFVAGILLHMSEERAFKUKFDMGKRKGYRPD IILGOMYGLSRLHHDYHRDLYNHLBEHSIGGBLYAPMFLTM ASGPELGFVAGILLHMSEERAFKUKFDMGKRKGYRPD LETTUDPIKSTLPNLGLVGMFKTINGVFFMDLAKGLQAVEVEYF VLQELIDSSPLSDNGMDKLEKTINGVFFMDLAKGLQAVEVEYF VLQELIDSSPLSDNGMDKLEKTINGVFFMDLAKGLQAVEVEYF VLQELIDSSPLSDNGMDKLEKTINGSRKKÜNLDLLEQLQVAN AKPSDREPECTQEPPTG AKSGNGTATSSLSSKLKQAMLTILELERSALLQTVEELARRA AKPSDREPECTQEPPTG AKSGNGTATSSLSSKLKQAMLTILELERSALLQTVEELARRA AKPSDREPECTQEPPTG AKSGNGTATSSLSSKLKQAMLTILELERSALLQTVEELARRA AKPSDREPECTQEPTG SCHAMMAURANDALGAVEVEYF VLQEKLARSSKLKGAMANAGALGAVEVEYF VLQEKLARSSKLKGAMANAGALGAVEVEYF VLQEKLARSSKLKGAMANAGALGAVEVEYF VLQEKLARSSKLKGAMANAGALGAVEVEYF VLQEKLARSSKLKGAMANAGALGAVEVEYF VLQEKLARSSKLKGAMANAGALGAVEVEYF VLQEKLARSSKLKGAMANAGALGAVEVEYF VLQEKLARSSKLKGAMANAGALGAVEVEYF VLQEKLARSSKLKGAMANAGALGAVEVEYF VLQEKLARSSKLKGAMANAGALGAVEVEYF VLQEKLARSSKLKGAMANAGALGAVEVEYF VLQEKLARSSKLKGAMANAGALGAVEVEYF VLQEKLARSSKLKGAMANAGALGAVEYF VLGAKAGAMANAGALGAVEYF VLGAKAGAMANAGALGAVEYF VLGAKAGAMANAGALGAVEYF VLGAKAGAMANAGALGAVAGAMAAAAAAAAAAAAAAAAAAAAAAAAAAAAA			!	
NPTSWMADLRALARNESFYLSSLOFTAVARVTGSLALMAPAFILL RSRVVLGETPPCLPGDSCSSDSLIFGLITCLTGYLGGGUSEI SRRUKHSNPRADPLVCATGLIGSAPFLFLSLACARGSIVATYIF IFIGETLLSNNWAIVADILLYVVIPTRESTARAFQIVLSHLLGD AGSPYLIGLISDBLRRWNPPSTLESFPALGFSIMLCAPVGLGG AAFLGTAHLH 5415 693 2986 IPPKYKLELQKH\LTTIT\NQEQATIFEEVGKLRPRNEQRENEL IISPLRCLFBEKGKEHIHIGEMKQTSQMAAENIGSELPPSATRF RLDMLKWKAKRSLTESLESILSRGMKARGLGBEISSVDESSESS STLSHTSKEPSVCEKEALPISESSFKLIGSSEDLSSDSSESHLP EPAPLSPQOAPRRANTLSHFFIECQEPPQPARGSGVGVKKK RYHSVSTTPHERKDESKANHLGDGTPVKTRRHSWRQDIFI RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCEDGPPGPPB EKKRTSRELBELWGKAILQQILLLIMEKERGKLASENDLINK LKLDVEELTPCLKEVTVVEKMLSTPGRSKIKRDMERWHSAVG GVP\RHHRGEIWKFLASQFHLKHQPPSKQQPKOVPYKELLKQLI SQQHALLDLGATTPTPYFSAQLGSLSINHILKAYSLDOG VGYCGGLSFVARGILLLIMESERAFKMLKFLMFINGLRKQYXPDW IILQIQMYQLSRLHDYHRDLYNHLEEHEIGPSLYAAPWFLTMI ASQPPIGFVARVPRMIFLGTSVTFRVALSLLGSHKPLILQHEN LETIVDFIKSTLPNLGLVOMEKTINQVFEMDIAKQLQAYEVEYY VLQEELISSSLISSNGMMKDLEKTRSIKQNIDLEGLQVAN RIQSLRATIEKLLSSESKLKQMLITLELERSALLQTVEELRRR AKSDREPECTOPPTOD 5416 27 4074 KSQLFCFWGGKAGDILSGDQDKBQXDPYFVETPYGYQLDLDFLI ENRQLPPPSPQLIPHNLHVYKTIMETRRELEGGRATMQNTOEB LSSSNSDDNKQCPMFLTARSQVTSTTSGQGGIWTSTENS SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRRG ATALKKLKELBEQVRTIPVLQVKISVLQEEKQLVSQLKNQRA SQINCGVKKSYSSAGNASGLECLSGRARSGGELY TDYEEEM TVRQSTQRIKBFRQL\TADMQALEQKIQDSSCRASSELEENGE RSVAVADREENNADLVVHRGSSSCKDAVGTLVEMNKGVSVT AMLGVMTEADKEIBLQQOTTESLKKKIVRLEVQLRETTIDERM KLKQELQAAGSRKKVDKATMAPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETINSVGISCQPECKNKVVGPBLPNNWITVKB VEMHDRCAGRSVEMCDKSVSVSVSVETGSNTESVNDLTLLK NILKEWSIGGGGCSVDVTVCSPERCASRGVNTEAVSQVEAA MAVPRRADQDTSTDLEQVHQFTNTETATLISSCTNTCLSTLUK VEMDRCAGRSVEMCDKSVSVSVSVETGSNTESVNDLTLIK NILKEWSIGGGGCSVDVTVCSPERCASRGVNTEAVSQVEAA MAVPRRADQDTSTDLEQVHQFTNTETATLISSCTNTCLSTLUK NILKEWSIGGGGCSVDVTVCSPERCASRGVNTEAVSQVEAA MAVPRRADQDTSTDLEQVHGYTNTETATLISSCTNTCLSTLUK TSTQTVETTVAVGGGRVKDINSSTKTRS LGVGTLLGGISGFD PSAVXKKBSGVQCININDNNIVGLKMRTIACGPPQLTVGLTAS RSVGVCDDPVGSSLENDQCQALGMMTGLDINTISTSLSSISVNKASS		ļ	1	
RSRVVLGETPPCLPGDSCSSSLIFGLITCLTGVLGVGLGVEY SRENHSNPRADPLVCATGLLGSAPFLFLSLACARGSIVATYTE IFIGSTLLSNNWAIVADILLEVUTPTRRSTAEAFQIVLSHLLGD AGSSYLIGLISDELRRNWPPSFLSEFFALQFSIMLCAFVGALGA AAFLSTAHLH 1ISPKRKLELQKH\LTTLT\NOBQATIFEEVGKLRPRNEQRENEL IISPKRKLELQKH\LTTLTT\NOBQATIFEEVGKLRPRNEQRENEL IISPKRKLELGKH\LTTLTT\NOBQATIFEEVGKLRPRNEQRENEL IISPKRKLELGKKEHIHIGEMKQTSQMAAENIGSELPPSATRF RLDMLKNKAKRSITESLESIISRGKKARGLQHBISTVDLDSSLS STLSNTSKEPSVCEKBALPISSSSFKLLGSSEDLSDSDESHLPF EPAPLSPQOAFRRANTLSHFPIECOPPDPARGSFSVGKLM RYHSVSTETPHERKDESKANHLGDSGGTPVKTRRHSWRQQIFT RVATPQKACDSSSYLEDYSSLGELPPRSPLEPVCEDGPFGPPB EKKRTSRELBELBUGKAILQOILLEMBKENCKLQASENDLINKR LKLDVEBITPCLKEVTTVWEKMLSTFGRSKIKKDMEKMHSAVGC GVP\RHHRGBIWKFLASOFHLKHPSKLEVMEKHMSAVGC GVP\RHHRGBIWKFLASOFHLKHPSKLEVMEKHMSAVGC GVP\RHHRGBIWKFLASOFHLKHPSKLEKDHEKMHSAVGC GVP\RHHRGBIWKFLASOFHLKHPSKLEKDFLKHPSKLIKQNI SQQHAILIDLGRTPPTHPYFSAQLGAGQLSLYNILKAYSLLDDE VGYCGGLSFVARILLHDYHRDLYNHLBEHEIGPSLYAAPWFITME ASGPFIGFVARVFPMIFLQGTSVIFKVALSLLGSHFPLILQHE LETTUDFIKSTLPHLGLVOMEKTINGVEMDIAVGHDIKQVAPUEYY VLQEELIDSSPLSDNORMSKLEKTNSSLRKGNILDLEQLGVANN RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS. ARPSDREPECTQPPPTGD KSQLFFFRGGKAGDILSGDDDKEQKDPYFVETFYGYQLDLDFL LSSNSDDNKQCPNFLIARSQVTSTPISKPPTTSQQGINTSTEL LSSNSDDNKQCPNFLIARSQVTSTPISKPPTTSQCGINTSTEL LSSNSDDNKQCPNFLIARSQVTSTPISKPPTTSQCGINTSTEL SSNSDDNKQCPNFLIARSQVTSTPISKPPDLETSLPFITTI ENRQLPPPSPQLEHNHLHVTKTLMTTRRLEQERATMQMTPGEI RRYLASFGGGKTTSSLPSFVGSGRHNPAKHQLQNGYQGNGDY SYAPAPTTSSMGSSIRHSPLSSGISTPVTNYSPMILQHIRRGV AALAKKEKELEQOATIESLKKRIVRLEVOLRETTHDERM KLKQELGAAGSRKKVUKARAMQDLEVSKVVSAVCATGELPMNWIVKE VEMHDRCAGRSVEMCDKSVSVSVCETGSNTVENSVGVETA MALVERTADQDTSTDLEQUHQFTTSTETATLISTCSTNTCLSTLUK KLKQELGAAGSRKKVAKARATMAPLYSERSVAVEAVOATTDGMVSS MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKE VEMHDRCAGRSVEMCDKSVSVSVSVCETGSNTESSVDDITLLK KLKGELGAAGSRKKVDKARTMAPLYFERVALVGLESGFGD PSAVKTKBSGVCDDPVCGSSLENDQCPGALGMMTGLDHYTESTVALSGISGFD PSAVKTKBSGVCDDPVGGSSLENDQCPGALGMMTGLDHYTESTVALSGISGFD PSAVKTKBSGVCDDPVGGSSLENDQCPGALGMMTGLDHYTERTQLLLAGE TLLA			1	
SRRLEHSNPRADPLVCATGLIGSAPFIFISLACARGSIVATISHLED AGSPYLIGHISDRIRRNWPPSFILSEFRATQFISIMLCAPVGALGG AAFLGTAHLH 1PSFKRLEJOKH\LITTLT\NOBQATIFEEVQKLRPRNEQRENEL 1ISPLRCLEBKQKEHIHIGEMKQTSQMAAENIGSELPPSATRF RIDMLKWKAKRSITESLESIISRGMKARGLQHSISVDLOSSLS STISMTSKEPSVCEKEALPISESSFFKLIGSSEDLSSDESHLPF ERAPLSPQQAPRRANTLSHFFIECQSPPQPARGSFGVSQKLK RYHSVSTETPHERKDFESKANILGDGTPVKTRRHSWRQIFI ERAPLSPQQAPRRANTLSHFFIECQSPPQPARGSFGVSQKLK RYHSVSTETPHERKDFESKANILGDGTPVKTRRHSWRQIFI EKKRTSRELRELWGKAILQQILLLEMBEKENGKLQASENDLINKT LKILDVEBLTPCLKEVTVVEKKLISTGRIKVFDMEKHSAVG GVP\RHHRGEIWKFLASQFHLHHQPPSKQOPKOVPYKELLKQIL SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQB VGYCQGLSFVAGILLHMSEBEAFKMLKFIMFUMGIRKQYRPDM IILQIQMYQLSRLHHDYHRDLVNHLBERIGIDSLYAADWFITM ASGPILGPVARVFDMIPLGQTSVIFKVALSLLGSKHKPLLQHER LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVETY VLQEELIDSSSLSDNORMDKLEKTMSSLRKQMLDLLEQLQVAN RIGSLEATIELLISSSEKULQAMLTLELERSALLQTVEELARRA AKPSDREPECTQPEPTGD \$Q\$PCFGWGKAGDILSGDQDKEQKDPYFVSTPYGYQLDLDFLI YVDDIQKGNTIKRINIQKRKRPSVPCFBPRTTSGQQGIWTSTES LSSSNSDDNKQCPMFLIARSQVTSTPISKPPDLETSLPFITTI ERNQLPPSPQDLFHNLHVYKTHMSTRRELGGERATMQNTTOGI RRPRLASFGGMGTTSSLPSPVGSGHNPARHQLQNGYQONGDY SYAPAPTTSSMSSIRHSPLSSGISTPVTNVSPMLQHIRGQ ATALKKELEEQVRTIPVLQVKISVLQEEKRQLNGYQONGDY SYAPAPTSSMSSIRHSPLSSGISTPVTNVSPMLQHIRGQ ATALKKELEEQVRTIPVLQVKISVLQEEKRQLNSQLKONGRA SQINVCGVKKRSYSAGNASGLEGLSRARSGGELYIDYEEEBM TVEQSTQRIKERSPLADAGALEKURJAPSGVLAPSTVNDSPMLQHIRGQ ATALKKELEEQVRTIPVLQVKISVLQEEKRGLVSQLKNORA SQINVCGVKKRSYSAGNASGLEGLSRARSGGELYIDYEEBEM TVEQSTQRIKERSLADAGVKINATAGQLVPSKVVSAVCYTDROMVGS MDLVDTCVGTSVETNSVGISGQPECKNKVVSPELPNNWIVKS KLKGELGAAAGSKKVARANTAGALVPSKVVSAVCYTDROMVGS MDLVDTCVGTSVETNSVGISGQPECKNKVVSPLPNNWIVKS VEMHDRCAGGRSVEMCDKSVSVEVSVCCTSSNTEESVNDLTLLK NLKKEVRSIGGGCSVDVTVCSPKECASRGVNTEAVSQVSRA MAVPRTADQDTSTDLEQVHQFTTTETATLISCTNTCLSTLDK TSTQTTVGTTTVAVGRGRKGUNGINSTKTRSIGVGTLLSGIGGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGSPDLTVGLTAGRISGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGSPDLTVGLTAGRISGFD TLAERTYSSLABAFOGPHSAMGMSLNSQLISTLSSINSVMKSAS				NPTSWWADLRALARNPSFVLSSLGFTAVAFVTGSLALWAPAFLL
SRRLEHSNPRADPLVCATGLIGSAPFIFISLACARGSIVATISHLED AGSPYLIGHISDRIRRNWPPSFILSEFRATQFISIMLCAPVGALGG AAFLGTAHLH 1PSFKRLEJOKH\LITTLT\NOBQATIFEEVQKLRPRNEQRENEL 1ISPLRCLEBKQKEHIHIGEMKQTSQMAAENIGSELPPSATRF RIDMLKWKAKRSITESLESIISRGMKARGLQHSISVDLOSSLS STISMTSKEPSVCEKEALPISESSFFKLIGSSEDLSSDESHLPF ERAPLSPQQAPRRANTLSHFFIECQSPPQPARGSFGVSQKLK RYHSVSTETPHERKDFESKANILGDGTPVKTRRHSWRQIFI ERAPLSPQQAPRRANTLSHFFIECQSPPQPARGSFGVSQKLK RYHSVSTETPHERKDFESKANILGDGTPVKTRRHSWRQIFI EKKRTSRELRELWGKAILQQILLLEMBEKENGKLQASENDLINKT LKILDVEBLTPCLKEVTVVEKKLISTGRIKVFDMEKHSAVG GVP\RHHRGEIWKFLASQFHLHHQPPSKQOPKOVPYKELLKQIL SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQB VGYCQGLSFVAGILLHMSEBEAFKMLKFIMFUMGIRKQYRPDM IILQIQMYQLSRLHHDYHRDLVNHLBERIGIDSLYAADWFITM ASGPILGPVARVFDMIPLGQTSVIFKVALSLLGSKHKPLLQHER LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVETY VLQEELIDSSSLSDNORMDKLEKTMSSLRKQMLDLLEQLQVAN RIGSLEATIELLISSSEKULQAMLTLELERSALLQTVEELARRA AKPSDREPECTQPEPTGD \$Q\$PCFGWGKAGDILSGDQDKEQKDPYFVSTPYGYQLDLDFLI YVDDIQKGNTIKRINIQKRKRPSVPCFBPRTTSGQQGIWTSTES LSSSNSDDNKQCPMFLIARSQVTSTPISKPPDLETSLPFITTI ERNQLPPSPQDLFHNLHVYKTHMSTRRELGGERATMQNTTOGI RRPRLASFGGMGTTSSLPSPVGSGHNPARHQLQNGYQONGDY SYAPAPTTSSMSSIRHSPLSSGISTPVTNVSPMLQHIRGQ ATALKKELEEQVRTIPVLQVKISVLQEEKRQLNGYQONGDY SYAPAPTSSMSSIRHSPLSSGISTPVTNVSPMLQHIRGQ ATALKKELEEQVRTIPVLQVKISVLQEEKRQLNSQLKONGRA SQINVCGVKKRSYSAGNASGLEGLSRARSGGELYIDYEEEBM TVEQSTQRIKERSPLADAGALEKURJAPSGVLAPSTVNDSPMLQHIRGQ ATALKKELEEQVRTIPVLQVKISVLQEEKRGLVSQLKNORA SQINVCGVKKRSYSAGNASGLEGLSRARSGGELYIDYEEBEM TVEQSTQRIKERSLADAGVKINATAGQLVPSKVVSAVCYTDROMVGS MDLVDTCVGTSVETNSVGISGQPECKNKVVSPELPNNWIVKS KLKGELGAAAGSKKVARANTAGALVPSKVVSAVCYTDROMVGS MDLVDTCVGTSVETNSVGISGQPECKNKVVSPLPNNWIVKS VEMHDRCAGGRSVEMCDKSVSVEVSVCCTSSNTEESVNDLTLLK NLKKEVRSIGGGCSVDVTVCSPKECASRGVNTEAVSQVSRA MAVPRTADQDTSTDLEQVHQFTTTETATLISCTNTCLSTLDK TSTQTTVGTTTVAVGRGRKGUNGINSTKTRSIGVGTLLSGIGGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGSPDLTVGLTAGRISGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGSPDLTVGLTAGRISGFD TLAERTYSSLABAFOGPHSAMGMSLNSQLISTLSSINSVMKSAS				RSRVVLGETPPCLPGDSCSSSDSLIFGLITCLTGVLGVGLGVEI
IFIGETLLISNIMAIVADILLYVU PTRESTABAFQIVUSHLLED AGSPYLIGLISDRERNWPPSFLSEFRALQFSLMLCAFVGALGG AAFLGTAHLH 5415 693 2986 IFPKYKLELQKH LITTLT\NDEQATI FEEVQKLEPRINGERENEL ITSPLECLFEBKQKEHHI GEMKOTSOMAAENIGSELPFSATRE RLDMLKNKAKRSJESESELLSEGNKARGLQHEISISVDLOSSLE STLENTEKEPSVCEKBALPISESSFKLLGSSEDLSSDSSSHLPE EPAPLSPQQAFRERANTLSHFPIECQEPPQPARGSPGVSOKKLM RYHSVSTTFTPHERKDESSKANILGDSGGTPVKTRRHSWRQQIFT RVATPQKACDSSSRYEDYSELGELPSPLEPPCGEDGPGPPP EKKRTSRELRELWQKAILQQILLLRMEKENCKLQASERDLINKE LKIDVEBETTPCLKEVTTVUEWRISTPGRSKIKFDMEKMHSAVG GVP\HHHHGBEWKFLAEQFHLHKQPPBCKQQFKUVPY KELLKQLI SQQHAILLDLGRTFPTHFYFSAQLGAGGLSLYNILKAYSLLDQS VGYCQGLSFVAGILLHMSEEBERHKIMFMGMIRGKYRPDM ASQPPLGFVARVFDMIFLGGTEVIFKVALSLIGSKFLILQHE LETTUDFIKSTLPNICLVOMENTINQVERMDIAKQLAYEVEYY VLQEELIDSSPLSDNORMDKLEKTNSSLRKQNLDLLEQLQVAN RQUSLANTIEKLLSSBEKLKQAMLTLELERSALLQTVEELRRE AKPSDREPECTQPEPTGD KSQLFFKGGKGGILSGDDDKEDKDPYFVETFYGYQLDLDFLI SQUKATIEKLLSSBEKLKQAMLTLELERSALLQTVEELRRE AKPSDREPECTQPEPTGD KSQLFFKGGKGGILSGDDDKEDKDPYFVETFYGYQLDLDFLI ENRQLPPPSPQLPKHNLHVYKTLMETRERLEGSERAWQMTOGEI ENROLLSSRSDDDNKQCPMFLIARSQVTSTBISKPPPPLETSLPFITTIL ENRQLPPPSPQLPKHNLHVYKTLMETRERLEGSERAWQMTOGEI SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLGHIRKGY SYAPAAPTTSSMGSIRHSPLSSGISTPVTNVSPMHLGHIRKGY ALALKEKLEEQOVATTPVLQVKISVLGEERGLVSDLKINGRA SQINVCGVEKRSYSAGNASOLEGLSRARRSGGELYIDYEERBM KLKQELQAAGSRKKVDLATHAQUVLYHRSSSCKDAAVGTLVEMRNCGVSVTI AMLGVWTEADKSIELQQQTIESLKEKIYRLEVGLRETTHDERW KLKQELQAAGSRKKVDKATMAQDLYPSKVVBAVOGTRODMVSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKE VEMDRCAAGSRVEMCDKSVEVSVCETGSNTEESVNDLTLLK NILKEWRSIGGGDCSVDVTVCSPKCASRGVNTEAVSVCBAA MAVPRTADODTSTDLEQVHOFTNTETATLISTCNTCLSTLLKK NILKEWRSIGGGDCSVDVTVCSPKCASRGVNTEAVSVCBAA MAVPRTADODTSTDLEQVHOFTNTETATLISTCNTCLSTLLKK TSTQTVCTTTVAVGERSCROPHISMGSINSTRISTGSIGVSLLGSGGFD PSAVXTKESGVGQININDNLVGLKMRTIACGPPQLTVGLTAS RSVGVCDDDVGSSLENDQDQAALGMRTCLBUTJERIQKLLAEQ FSAVXTKESGVGQININDNLVGLKMRTIACGPPQLTVGLTAS RSVGVCDDDVGSSLENDQDQAALGMRTCLBUTJERIQKLLAEQ FLAVYTESSLAAEDGEPHSGMGSINSQLISTSSISSISTVSNKASS	j	1	1	SRRLRHSNPRADPLVCATGLLGSAPFLFLSLACARGSIVATYIF
AGSPYLIGLISDRIRRNWPPSFLSEPRALQFSLMLCAFVGALGG AAFLGTAHLH 1FPKRKLELQKH\LTTLT\NQEQATIFEEVQKLRPRNEQRENEL 1ISFLRCLFBEKQKEHLHIGEMKQT5QMAABRIGSELPPSATKF RLDMLKNKAKRSLTSLESLESLESNARAGLQHBISTVDLDSSLS STLENTSKEPSVCEKEALPISESSFKLLGSSEDLSSDSESHLPF EPAPLSPQQAFRRANTLSHFPIEQQEPPQDARGSFGVSGRKLM RHSVSTTPHERENDFSKANHLDGSGGTPVKTRHSNRQOIFI RVATPQKACDSSSRYEDYSELGELPPSCPLEDGCPGPPPP EKKRTSRELRELWGKAILQQILLLRMEKENQKLQASENDLLNK LKLDYEETTPCLKEVTTVWEKMLSTBGRSKIKFDMEKMHSAVGC GVP\RHHRGETWKFLAEGFHKLGPSKQOPKOVPYKELLKQLI SQQHAILDLGRTPPTHFYPSQLGAGQISLVNILKAYSLLDGD VQYCQGLSFVAGILLLHMSEEEAFKMLKFLMFDMGLRKQYRPOM 1ILQIQMYQLSFLLHDYHRDLYNHLEHBIGSLYAAPMFLTME ASGPFJGFVARKYPMIFLQGTEVTFKVALSLLGSIKFPLIQHER LETTVDFIKSTLPNLGLLOMEKTTNQYFFRDTAKQLQAYEVEYY VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEDLQVAM RIQSLEATIEKLLSSESKLKQAMLTIELERSALLQTVEELRRS AKPSDREPECTQPBPTGD \$5416 27 4074 \$SQLFFWGGKAGDILSGDOKEQKDPYFVETPYGYQLDLFFLI URQULFFFWGGKAGDILSGDOKEQKDPYFVETPYGYQLDLFFLI VYDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSQQGTWTSTES LSSSNSDDNKQCPNFLIARGGVTSTISKPPPDLETSLPFLTI ERRQLPPPSPQDLPKHLHVTTLTMETRRLEGERATMQMTFGEI RRPRLASFGGMTTTSSLPSFVGSGNNHPAKHQLQNGYQGNGYY SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRGQI AIALKELEEQVRTIPVLQVKISVLQEEKRRQLVSQLKNGRA SQINVCGVKRSYSAGNASQLEQLSRARRSGGELYIDTEERBM TVPQSTQRIKERFROL\TADMQLAEQKTQDSSCERASELRENGE RSVAVQAEENMNDIVVYHRGSRSCKDAVGTLVEMENCUSVT AMLGVWTEADKSELLQQTIESLEKKIYRLEVQLRETTHDREM KLKQELQAAGSKKKVDKATMAQPLVFSKVVEAVVQTRDMMCSVT AMLGVWTEADKSELGGDCSVDVTVCSFKKVEAVVQTRDMMCSVT MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNNIVKE VEMHDRCAGRSVEMCDKSVSVEVSVCTGGSNTEESVNDLTLKK NLLKEVRSIGGGDCSVDVTVCSFKRCASRGWTEAVSQVEAA MAVPRTADQDTSTETTAURGRUWCDINSTRISTIOTSTLDKGTSTLDK TSTQTVETTTVAUGRGRVWCDINSTRISTIOTSTLSTLKSKITS.	Į		1	TETGETILISMNWATVADILLYVVIPTRRSTAEAFOIVLSHLLGD
5415 5415 693 2986 IPPKTKLELQKH\LTTLT\NQEQATIFEEVQKLRPRNEQRENEL IISPLRCLFBEKQKEHHHIGEMKQTSQMAAEMIGSELPFSATKF RLDMLKNTAKRSLTESLESILSRGNTARGLQBHSISVDLDSSLS STLSNTSKEPSVCEKEALPISESSFILGSSEDLSSDESHLIPE EPAPLSPQQAFRRANTLSHFPIECQEPPQPARGSPGVSQRKLM RYHSVSTETPHERKDFSSKANHLGDSGGTPVKTRRHSNRQQIFI PVATFQKACDSSSKYEDYSSLGELPRSPLEPVCEDGFPGPPB EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLINKI LKLDVEETIPCLKEVTTVWEMMLSTBGRSKIKFDMEKHHSAVG GUP\RHRINGEIWKFLAEGFHIKHGPSKQQPKDVYYKELLKQII SQQHAILLDLGRTPPTHEYYSQLGAGQLSLYNILKAYSLLDGB VGYCGGLSFVAGILLLHMSEEBEAFKMLKFLMFDMSLRKQYRDDW IILQIQMYQLSRLHHDVHRDLYNHLEHBIGESLYAAPWEITMI ASGPPLGFVARVFDMIFLGGTEVIFKVALSLLGSKKPLILDHEN LETIVDFIKSTLPNGLYQMEKTINQVFEMDLAKQLQAYEVEYT VLQEELIDSSILSDNQRMDKLEKTNSLRQQLDLLEQLQVANM RIGSLBATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS AKPSDREPECTQPEPTGD 5416 27 4074 KSQLFCFWGGKAGDILSGDQDKEQXDPYFVETPYGYQLDLDFLI SSNSDDNXQCPNFLILARSQYTEISKPPPLTSLPFLTIFL ENRQLPPPSPQLPKHNLHVTKTLMETRRLEGERATMOMTFGEI RRPRLASFGGMTTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDV SVAPPAAPTTSSMGSIRHSPLSSGISTPVTNVSPHHLGHIREQ AIALKRLKELERQVRTIFVLQVKISVLQBEKKRQLVSQLKNORA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEBEMI TVEQSTQRIKEFRQL\TADMAALEQKTQDSSCEASSELREMGEW RKVAGAEERMMDIVVYHRGSRSCKDAAVGTLVEMENGUSVT AMLGVMTEADKEIELQQQTIESLKEKIYRLEQVLRETTHDERM KLKQELQAAGSKKVDKATMAQPLVPSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETRSVGISCQPECKNKVVGPELPMNWIVKE VEMHDRCAGRSVBMCDKSVSVESVCTGSNTEESVNDLTLK.K VEMHDRCAGRSVBMCDKSVSVESVCTGSNTEESVNDLTLK.K VEMHDRCAGRSVBMCDKSVSVESVCTGSNTEESVNDLTLK.K TSTQTVETRTVAVGRGCNKGINSTKRISIGVSTLISGEBER PSAVKTKESGVGQININDNYLVGLKMRTIAGGPPQLTVGLTAS. RSVGVCDDPVGESLENPQPQAFLGMMTGGLDHYIERTIKLLEGL TLLAEMYSSLAARAFGEPHSGMSSLNSQLISSLISSINSVMXSAS RSVGVCDDPVGBSLENPQPQAFLGMMTGGLDHYIERIKMLAEG TLLAEMYSSLAARAFGEPHSGMSSLNSQLISINSSINSVMXSAS RSVGVCDDPVGBSLENPQPQAFLGMMTGGLDHYIERIKMLAEG TLLAEMYSSLAARAFGEPHSGMSSLNSQLISINSLISSINSVMXSAS TLLAEMYSSLAARAFGEPHSGMSSLNSQLISINSLISSINSVMXSAS STANDARAFGEPHSGMSSLNSQLISINSLISSINSVMXSAS RSVGVCDDPVGBSLENPQQSALGMNTGGLDHYIERIGKLLAEQ	ſ			ACCEVITGE TODE DONNED SET SEPRALOFSEM CAPVGALGG
5415 693 2986 IPPKTKLELQKH\LTTLT\NQEQATIFEEVQKLRPRNEQRENEI IISPLRCLFBEKQKEHHHIGEMKQTSQMAAENIGSELPSATRF RLDMKKNAKKSLESLESLISENGNARGLQBHSISVDLDSSUS STLSKTSKEPSVCEKEALPISESSFILLGSSBDLSSDESSHLPE EPAPLSPQQAFRRANTLSHFPIECQCEPPOPARAS GPUSQRKKM RYHSVSTETPHERKDFSSKANHGDSGGTPVKTRRHSWRQOIFL RVATFQKACDSSSYEDYSELGELPPRSPLEVVCEDGPFGPPB EKKTTSRELRELWOKATLQOILLIAMEKENOKLQASENDLINK LKLDYEEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKHBAVG GVP\RHHRGETWKFLASGFHLKHGFPSKQOPKDVPYKELKKQLI SQQHAILDLGRTFPTHFYFSADLGAGQISLINILKAYSLLDGD VGYCQGLSFVAGILLIAMSEEAFKMLKFIMFDMGLRKQYRPDM IILQIGMYQLSRLLHDYHRDLYNHLBHEIGFBSKQOPKDVPYKELKKQLI ASGPFIGFVARVFDMIFLQGTEVTFKVALSLLGSHKPLILQHEN LETTUDFIKSTLPNLGLVQMEKTINQVFBUDLAKQLQAYEVEYY VLQEELIDSSPLSDNONNDKLKEKTNSSLRKQNLDLLEQLQVAN RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS AKPSDREPECTQPEPTGD \$5416 27 4074 \$\$\text{SQLFCYWGKKGDILSGDQDKSQKDPYFVETPYGYQLDLDFLI} YVDDIQKGMTIKRANIQKRKPSVPCPEPRTTSGQOGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPJSKPPPDLETSLPFLTII ENRQLPPPSPGLPKHNLHVTTLMETRRLEGERATMQMTFGEI RRPRLASFGGMTTTSSLSFYGSGNHPARHQLQNGYQGNDY SYAPAAPTTSSMSSIRHSPLSSTPYNNVSPHLGHTRGD RRPRLASFGGMTTTSSLSFYGSGNHPARHQLQNGYQGNDY SYAPAAPTTSSMSSIRHSPLSSTPYNNVSPHLGHTRGD AIALKELKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNORAI SQINVCGVKRSYSAGNASQLEGLSRARRSGGELYIDTEEBEM TVRQSYORIKERGROLTDATERSHVTLYGLYGDSCCBASELERNGE RSVAVGAEENMNDIVVYHRGSRSCKDAVGTLVEMENCUSVT AMLGVWTEADKBILQQTIESLKKHYPLEVQLRETTHDREM KLKQELQAAGSKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGFBLPNNWIVKE VEMHDRCAGRSVEMCDKSVSVEVSVETGSNTESSVNDLTLKK NLMLKEVRSIGGGCDSVDVTVCSPKRCASRGVNTEAVSQVEAN MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDK TTGTVETTTVAUGRGRVEDINSKINSGLISTLISSINSVMKSAS RSVGVGDDDVGBSLENPQQAPLGMMTIAGSLNSGLISTLDSSINSVMKSAS RSVGVGDDDVGBSLENPQQAPLGMMTIAGSLNSGLISTLLASGNSGDP PSAVKTKESGVQOININDNYLVGLKMRTIACGPPQLTVGLTAS. RSVGVCDDDVGBSLENPQQAPLGMMTIAGSLNSGLISTLUSSINSVMKSAS RSVGVCDDDVGBSLENPQQAPLGMMTIAGSLNSGLISTLUSSINSVMLSAS	i	1	1	I .
IISPLRCLEBERQKEHIHIGENKOTSQNARENIGSELPSATER RIDMIKNKAKRSLTESLESILSGRONARENIGSELPSATER STISNTSKEPSVCEREALP ISESSFKLLGSSESHLEP EPAPLSPQQAFRRANTISHTPIECQBPQDARGSPGVGRKIM RYHSVSTETPHERKDFESKANHLGDSGTPVKTRHSWRQQIFI RVATPQKACDSSRYEDYSELGELPPRSPLEPVCEDGPFGPPB EKKRTISRELRELWQKAILQQILLLIMERENQKLQASENDLINIX LKLDYBEITPCLKEVTTYWERMLSTPGRSKIKFDMEKHSAVG GVP\RHRIGEIWKFLAEQFHLKHQPPSKQQPKDVPYKELLKQLI SQQHAILIDLGRTFPTHPYFSAQLGAGGLSYNILKAYSLLDGD VGYCQGLSEVAGILLIHMSEERAFKMLKFLWFDMGLRKQYRPD IILQIQMYQLSRLLHDYHRDLYNHLBEHEIGPSLYAAPWFLTMI ASGPFLGFVARVFDMIFTQGTEVIFKVALISLIGSHKPLILQHEB LETIVDFIKSTLIPNLGLVQWERTIQNYERMDIAKQLQAYEVEYY VLQEELIDSSPLSDNORMMKLEKTNSSLRKQNLDLLEGLQVANK RIQSLEATIEKLLSSESKLKQAMLITLELERSALLQTVEELRRE AKPSDREPECTQPEPTGD 5416 27 4074 KSQLFCFWGGKAGDILSGDDDKEQKDPYFVETPYGYQLDLDFLI LSSSNSDDNKQCPNFILARSQVTSTPISKPPPHETSLPFLTTI ENRQLPPPSFOLPKHAILHVTKTIMETRRIEGERATMQMTFGEI RRPRLASFGGMGTTSSLPSFVGSGNINPAKHQLQNGYGONGDY SYAPAAPTTSSMGSSTRHBPLSSGISTPVTNVSPMHLQHIRQQ RYDROGVRKRSYSAGNASOLEQLSRARSGGELYIDVEEREM TVEQSTQRIKEFRQL\TAMQALEQKIQDSSCEASSELRENGE RSVAVGABENMNDIVVYHRGSSSCKDARGGLYIDTGEREM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTRSTETBLGQCGCKNVVGFELBMNNIVKE VEMHDRCAGRSVSMCDKSVSVEVSVCETGSNTESSWDITLILK NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA MAVPRTADQDTSTDLEQVHQFTNTETATLIBECTRUTCUSTLING NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA MAVPRTADQDTSTDLEQVHQFTNTETATLIBECTRUTCUSTLING TSTQTVETTTVAVGVGRKVKD INSTKTRSIGVGTLLSGRSGFD PSAVKTKESGVGQININDNYLVGLKWRTLGCBPQLTVGLTASS				
RIDMLKNYAKRSLTESLESILGRCMKARGLQBHSISVDLDSSUS STISNTSKEPSVCEKEALPISESSPKLLGSSEDLSDDESHLPB EPAPLSPQQAFRERNNTLSHFPIEQGEPQPARGSPGVSQKLM RYHSVSTETPHERKDFESKANHLGDSGTFVKTRHSWRQOIFI RVATPQKACDSSRYEDYSELGELPPRSPLEPVCEDGPFGPPPB EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLINK LKLDYEBITPCLKEVTTWEKMLSTPGRSKIKFDMEKMHSAVG GVP\RHHRGEIWKFLAEQFHLKKUPPSKQQPKDVPYKELLKQLI SQQHAILIDLGRTFPTHYFYSAQLGAGQLSIYNILKAYSLLDGE VGYCQGLSFVAGILLLHMSEERAFKMLKFLMFDMSLRGVRPDM IILQIQMYQLSRLHDYHRDLYNHLBEHEIGPSLYAAPWFLTMH ASGFPIGFVARVFDMIFTQGTSVIFKVALSLLGSHKPLLIQHEN LETIVDPIKSTLPNLGLVQMEKTINQVFBMDTAKQLQAYEVEYY VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLEATIEKKLLSSESKLKQMLTLELERSALLQTVEELRRRK AKPSREPBETQPEPTGD ***SQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLI** YVDDIQKGNTIKKLNIQKRRKPSVPCPBPRITSGQQGIWTSTE** LSSSNSDDMKQCPNFLIARSQVTSTFISKPPPPLETSLPFLTTI ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMQMTPGSI** RRPRLASFGGMGTTSSLPSFYVGSGNINPAKHQLONGYGGNGDY** SYAPAAPTTSSMGSIKHBPLSSGISTPYTNVSPMHLQHIREQI** ATALKRLKELEEQVRTTPVLQVKISVLQEEKRQLVSQLKNORA** SQINVGGVKRSYSAGNASQLEQLSRARRSGGELYIDVEEBEM** TVEQSTQRIKEFRQL\TADMQALEQKIQDSCEASSELREMGE** RSVAVGABENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI** AMLGVMTEADKBTELQQQTITESLKERIYLBEVQLRETTHDREM** KLKQELQAAGSRKKVNKATMAQDLVPSKVVEAVVOTRDQMVGSI** MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKE** VEMHDRCAGRSVEMCNKSVSVEVSVCETGSNTEESVNDLTILK** NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA** MAVPRTADQDTSTDLEQVHQFTNTTETATLIESCTNTCLSTLDK** TSTQTVETTETVAVGRGRVKD INSTKTRSIGYGTLLSCHSGFD-* PSAVKKESGVGQININDNJLVGLKWRTLACGPQLTVGLTAS** RSVGVGBDPVGESLENPQQAPLGMNTLANSQVEAA** MAVPRTADQDTSTDLEQVHQFTNTTETATLIESCTNTCLSTLDK** TSTQTVETTETVAVGRGRVKD INSTKTRSIGYGTLLSCHSGFD-* PSAVKKESGVGQININDNJLVGLKWRTLACGPQLTVGLTAS** RSVGVGBDPVGESLENPQQAPAGLGNNSLUSTISSINSVNKSAS** SINSUNGDPVGESLENPQQAPAGLGNNSLUSTISSINSVNKSAS**	5415	693	2986	TPPKTKLEDQKH\LTTDT\NQEQATTTEEVQABARANEQAENED
STLSNTSKEPSVCEKEALPISESSFILLGSSEDLSDSESHLER EPAPLSPQQAFRRRANTLSHFPIECQEPPQPARGSPGVSQKILM RYHSVSTETPHERKDEFSKANHLGDSGTFVKTRRHSWRQQIFI RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCEDGPFGPPP EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLINKR LKLDYESITPCLKEVTTVWEKMLSTPGRSKIKPDMERMHSAVGC GVP\RHHRGEIWFLAEQFHLKHQFPSKQQFKDVPYKELLKQIT SQQHAILIDLGRTFPTHYPFSAQLGAGQLSLYNILKAYSLLDQD VGYCQGLSFVAGILLHDWHRDLYNHLBEHEIGPSLYAAPWFLTME ASQPPLGFVARVFDMIFLQGTEVTFKVALSLLGSHKPLILQHEN LETIVDFIKSTLDNLGLVQMEKTINQVFEMDIAKQLQAYEVEYF VLQEELIDSSPLSDNQRMDKLEKTNSLRKQNLDLLEQLQVANK RIQSLBATIEKLLSSESKLQAMLTLELERSALLQTVEELRRR AKRSDREPBECTQPEPTGD **SQLFCFWGGKAGDILSGDQDKEQKDPFVETPYGYQLDLDFLI- LSSSNSDDMKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTII ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQEBATMQMTFGEI RPRPLASFGGGMCTTSSLPYGSGNHHPAKHQLQNGYGGNGDY SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRRQI AIALKRLKELEEQWRTIPVLQVKISVLQEEKRQLVSQLKNGRA- SQLNVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDVEEEMI TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGE RSVAVGAEEMNNDIVVYHRGSRSCKDAAVGTLVEERMICKSUL AMLGVMTEAAKEIELQQOTISSLKKHIYRLEVQLRETTHDREM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMYGSI MDLVDTCVGTSVETINSVGISCQPECKNKVVGPELPMNWIVVE VEMHDRCAGRSVEMCDRSVUSVSVCSTGSNTESSVNDLTLLK NLNLKEVRS IGCGDCSVDVTVCSPKECASRGVNTEAVSQVZRA- MAVPRTADQDTSTDLEQVHQFTNTFATTLIESCTNTCLSTLDK TSTQTVETRTVAVGERGVKDINSSTKKTSSIGVGTLLSCHSGFD PSAVKTKESGYGQLNINDNYLVGLKMRTIACGPPQLTVGLTALSQ TLLAENSELAEAGCEINPQPQAPLGMMTGLDHYIERIQKLAEQ TLLAENSELAEAGCEINPQPGANLGLDHYIERIQKLAEQ TLLAENSELAEAGCEINPQPGANLSUNSOLISTLSSINSVMKSAS	}	1		
EPAPLSPQQAFRRRAWTLSHFPIECQEPDQPARGSSPAVSQRIM RYHSVETPHERKDFESKANHLGDSGGTPVKTRRHSWRQQIFI RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCEDGPFOPPP EKKRTSRELRELWQKAILQQILLLRMSKENQKLQASENDLINK: LKLDYEEITPCLKEVTTVEKKMLSTPGRSKIKFDMEKMHSAVG GVP\RHRGEIMKFLABOGFHLKHQFPSKQQFKDVPYKELLKQIJ SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDGS VGYCQGLSFVAGILLHMMSEEBAFKMLKFLMFDMGLRKQYRPDM IILQIQMYQLSRLHDYMRDLYNHLBEHEIGPSLYAAPMFLTMI ASQFPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLHLQHEN LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYF VLQEELIDSSPLSNORMDKLEKTNSSLRKÖNLDLLEGLQVANN RIQSLBATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS: AKPSDREPECTQPEPTGD YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCDNFLLARSQVTSTPISKOPPPDLETSLPFLTTI ENRQLPPPSDQLPKHNLHVTKTLMETRRRLEGERATMQMTGGEI RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDY SYAPAAPTTSSMGSSIRHSPLSSGISTPVTTNVSFMHLQHIREQ RRPRLASFGCMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDY SYAPAAPTTSSMGSSIRHSPLSSGISTPVTTNVSFMHLQHIREQ AIALKRLKELEGQVRTTPUQKISVLQEERRQLVSQLKNGRA SQINVCGVRKSYSAGNASQLEQLSRRARSGGELYIDYEEEMI TVEQSTGRIKEFRGL\TADMQALBQKIQDSSCEASSELRENGE RSVAVGAEENMNDIVVYHGSRSCKDAAVGTLVEMNGGVSVT AMM_GVMTEADKEIBLQQQTIESLKEKIYRLEVQLRETTHDREM KLKQELQAAGSRKKVDKATMAQPLVFSKVVBAVVQTRDQMYGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKISL VEMHDRCAGRSVEMCDKSVSVEVSUCETGSNTEBSVNDLTLLK NLNLKEVRSIGGGCSVDVTVCSPKECASRGVNTEAVSQVBAA MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVCEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTRESGGGQLNINDNYLVGLKMRTIACGPPQLTVGLTASA RSVGVGDDPVGSSLENDQQDAFLGMNTGLDHYIERIQKLLABQQ TLLAENSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS	}	1		
RYHSVSTETPHERKDFSSKANHLGDSGGTPVATRRENKQQIFI RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCEDGPFGPPPE EKKRTSRELELWQKATLQQILLLKHMEKENQKLQASENDLINKI LKLDYEEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGC GVP\RHHRGBIWKIAEGFHLKHQFPSKQOPKDVPYKELLKQLT SQQHAILIDLGRTFPTHPYFSAQLGAGQUSLYNILKAYSLLDGS VGYCQGLSFVAGILLHMSEBEAFKMLKFLMFDMGLRKQYRPDM IILQIQMYGLSRLHDYHRDLYHHLBEHBIGBSLYAAPWPLTMI ASQFPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLILQHE LETIVDPIKSTLPHNLGLVQMEKTINQVFSMDTAKQLQAYEVEYF VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANK RIQSLBATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS. ARPSDREPECTQPEBTGD 5416 27 4074 KSQLFCFWGGKAGDILSGDQDKBQKDPYFVETPYGYQLDLDFLI YVDDIQKGNTIKRLNIQKRKRSVPCPEPPRTTSQQGIWTSTES LSSSNSDDNKQCPMFLIARSQVTSTPISKPPPPLETSLPFLTTI ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMQMTPGEI RRPRLASFGGMSTTSSLPSFVGSGNINPAKHQLQNGYQGNGDYX SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSFMHLQHIRRQI RSPLASFGGMSTTSSLPSFVGSGNINPAKHQLQNGYQGNGDYX SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSFMHLQHIRRQI AIALKRIKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAI SQLNVCGVRKSYSAGNASOLEGLSRARRSGGELYIDYEEBEMI TVEQSTQRIKEFRQL\TADMQALEQKIQDSCEASSELRENGE RSVAVGAEENNNDIVVYHRGSSSCKDAAVGTLUEMRNGGVSVTI AMLGVMTEADKBIBLQQQTIESLKEKIYRLEVQLRETTHDREM KLKQELQAAGSRKKVDKATMAQPLVFSKVVAVQTELPMNWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK NLNIKEVRSIGGGDCSVDVTVCSPKECASRGVNTEAVSQUEAA MAVPRTADQDTSTDLEQVHOFTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGRGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKWRTIAGGPPQLTVGLTASS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ PSAVKTKESGVGQININDNYLVGLKWRTIAGGPPQLTVGLTASS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS				STLSNTSKEPSVCEKEALPISESSFKLLGSSEDLSSDSESHLPE
RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCENGPFGPPPE EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLLNKE LKLDYBEITPCLKEVTTVWEKMLSTIGRSKIKFDMEKMISAVGC GVP\RHHRGEIWKFLAEQFHLKHQFPSKQPKDVPYKELLKQLT SQQHAILIDLGRTFPTHEYFSALCAGQLSLYNILKAYSLLDGE VGYCQGLSFVAGILLHMSEEAFKMLKFIMFDMGLRKQYRPDW IILQIQMYQLSRLLHDYHRDLYNHLBEHEIGPSLYAAPWFLTME ASGFPLGFVARVFFMIFTQGTEVJFKVALSLLGSHKPLILIQHEN LETTVDPIKSTIPNLGLVQMEKTINQVFEMDIAKQLQAYBVEYT VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIGSLBATIEKILSSESKLKQAMLTLELERSALLQTVEELRRK AKPSDREPECTQPEPTGD 5416 27 4074 KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLI YVDDIOKGNTIKRINIQKRRKPSVPCPBPRTTSGQQGIWTSTES LSSSNSDDNKQPFFLIARSQVTSTPJSKPPPPLETSLPFLTII ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMQMTFGEI RRPLASFGGMGTTSSLPSFVGSGNINPAKHQLQNGYQGNGDY SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRBQI RRPLASFGGMGTTSSLPSFVGSGNINPAKHQLQNGYQGNGDY SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRBQI AIALKRIKELEEQVRTIPVLQVKISVLQEEKRQLVSOLKNORA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEBEMI TVEQSTQRIKSFRQL\TADMQALEQKIQDSCEASSELRENGEI RSVAVGABENNNDIVVYHRGSRSCKDAAVGTLUEMRNGGVSUTI AMLGVMTEADKEIBLQQQTIESLKEKIYRLEVQLRETTHDREM KLKQELQAAGSRKKVDKATMAQPLVPSKVVAPAUVGTRDQMVGSI MDLVDTCVGTSVETTNSVGISCQPECKNKVVGPELPMNWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK NLNILKEVRSIGGGDCSVDVTVCSPKECASRGVNTEAVSQVBAA MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGRGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIAAGGPQLTVGLTASS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ PSAVKTKESGVGQININDNYLVGLKMRTIAAGGPQLTVGLTASS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAENVSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS	ł	i .		EPAPLSPQQAFRRRANTLSHFPIECQEPPQPARGSPGVSQRKLM
RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCENGPFGPPPE EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLLNKE LKLDYBEITPCLKEVTTVWEKMLSTIGRSKIKFDMEKMISAVGC GVP\RHHRGEIWKFLAEQFHLKHQFPSKQPKDVPYKELLKQLT SQQHAILIDLGRTFPTHEYFSALCAGQLSLYNILKAYSLLDGE VGYCQGLSFVAGILLHMSEEAFKMLKFIMFDMGLRKQYRPDW IILQIQMYQLSRLLHDYHRDLYNHLBEHEIGPSLYAAPWFLTME ASGFPLGFVARVFFMIFTQGTEVJFKVALSLLGSHKPLILIQHEN LETTVDPIKSTIPNLGLVQMEKTINQVFEMDIAKQLQAYBVEYT VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIGSLBATIEKILSSESKLKQAMLTLELERSALLQTVEELRRK AKPSDREPECTQPEPTGD 5416 27 4074 KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLI YVDDIOKGNTIKRINIQKRRKPSVPCPBPRTTSGQQGIWTSTES LSSSNSDDNKQPFFLIARSQVTSTPJSKPPPPLETSLPFLTII ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMQMTFGEI RRPLASFGGMGTTSSLPSFVGSGNINPAKHQLQNGYQGNGDY SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRBQI RRPLASFGGMGTTSSLPSFVGSGNINPAKHQLQNGYQGNGDY SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRBQI AIALKRIKELEEQVRTIPVLQVKISVLQEEKRQLVSOLKNORA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEBEMI TVEQSTQRIKSFRQL\TADMQALEQKIQDSCEASSELRENGEI RSVAVGABENNNDIVVYHRGSRSCKDAAVGTLUEMRNGGVSUTI AMLGVMTEADKEIBLQQQTIESLKEKIYRLEVQLRETTHDREM KLKQELQAAGSRKKVDKATMAQPLVPSKVVAPAUVGTRDQMVGSI MDLVDTCVGTSVETTNSVGISCQPECKNKVVGPELPMNWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK NLNILKEVRSIGGGDCSVDVTVCSPKECASRGVNTEAVSQVBAA MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGRGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIAAGGPQLTVGLTASS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ PSAVKTKESGVGQININDNYLVGLKMRTIAAGGPQLTVGLTASS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAENVSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS	ļ	1	i	RYHSVSTETPHERKDFESKANHLGDSGGTPVKTRRHSWRQQIFL
EKKRTSRELRELWQKAILQQILLLRMEKENQKAGASENDLINKE LKLDYESITPELKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGC GVP\RHHRGETWKFLAEQFHLKHGFPSKQQPKDVPYKELLKQLT SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQE VGYCQGLSFVAGILLHMSEEBEFAKMLKFLMFDMGLRKQYRPDW IILQIQMYQLSRLLHDYHRDLYNHLBEHEIGESLYAAPWPLTME ASGFPLGFVARVFDMTFLQGTEVTFKVALSLLGSHKPLILQHEN LETIVDPIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYP VLQEELIDSSPLSDNQMEKLEKTNSSLRKQNLDLLEQLQVANC RIGSLBATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRKE AKPSDREPECTQPEPTGD SSQLFCFWGGKAGDILSGDQDKEQXDPYFVETPYGYQLDLDFLI YVDDIQKGNTIKRLNIQKRRKPSVPCPBFRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTI ENRQLPPPSPQLPKHNLHVYNTTLMETRRLEQERATMQMTGGEI RRPRLASFGGMCTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDY SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQI AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNGRA SQINVCGVRKRSYSAGNASQLEQJSRARSGGELYIDYEEEMI TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGE RSVAVGAEENNNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKBIELQQQTIESLKEKIYRLEVQLRETTHDREM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPSLPMNWIVKBI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK' NLNLKEVRS IGGGDCSVDVTVCSPKECASRGNTEESVNDLTLLK' NLNLKEVRS IGGGDCSVDVTVCSPKECASRGVNTEAVSQVEAA' MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGRGRVKDINSSTKTRS IGVGTLLSGHSGFD PSAVKTKBSGVGGIN INDNYLVGLKMRTLACGPPQLTVGLTASS RSVGVGDDPVGESLENDPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTISSINSVMKSAS	l	1	l	RVATPOKACDSSSRYEDYSELGELPPRSPLEPVCEDGPFGPPPE
LKLDYEEITPCLKEVTTVWEKMLSTPGRSKIKPDMEKMHSAVG GVP\RHHRGEIWKFLAEQFHLHG\(\text{PF}\) SKQ\(\text{PK}\) SQ\(\text{PK}\) HILL\(\text{LIKQ}\) TS\(\text{QPK}\) VP\(\text{RELIKQ}\) TS\(\text{QPK}\) VP\(\text{RELIKQ}\) TS\(\text{QPK}\) VP\(\text{RELIKQ}\) TU\(\text{LILD}\) G\(\text{QGLSFVAGILL}\) HMSEERAFKMLKFLMFDMGLRK\(\text{QYPDM}\) UG\(\text{QCISFVAGILL}\) HMSEERAFKMLKFLMFDMGLRK\(\text{QYPDM}\) IILQ\(\text{QMYQLSFLLHDYHRDLYNHLBEHEIGFSLYAAPWFLTMF\) ASQFPLGFVARVFDMIFLQWTEVIFKVALSLLGSHKPLILQHE LETTVDFIKSTL\(\text{PMIFLQUMEKTINQVFEMDIAK\(\text{QLQAVEVEYY}\) VL\(\text{QEELIDSSPLSDN\(\text{QPMM}\) MRIGSLBATIEKLLSSESKL\(\text{QAMLITLELERSALL\(\text{QTVEELRRK}\) AKPSDREPECTQPEPTGD\(\text{PMGGKAGDILGOD\(\text{DDMEQKDPYFVETPYGYQLDLDFLI\) YVDDIQKG\(\text{MISTIKLLNIQKRRK\(\text{PSVPCPEPRTTSQQQGI\) WTSTES LSS\(\text{SSNSDDNK\(\text{QCPMFILARS\(\text{QYTSPULETSLPFLTI\) ENR\(\text{QPPSPQLIKMINLYTKTLMETRRLE\(\text{QERATM\(\text{MYPGEI}\) BRPLASFGG\(\text{MSTTYTL\(\text{MSTTSLPSETY\) MSSGISTPYTNVSPMHL\(\text{QHTQPULYS\(\text{LIKQ}\) MTSTTSSMGSSIRHSPLSSGISTPYTNVSPMHL\(\text{QHTQPULYS\(\text{LIKQ}\) MTSTTSMGSSIRHSPLSSGISTPYTNVSPMHL\(\text{QHTQPULYS\(\text{LIKQ}\) MTSTTST\(\text{LIKELEEQVRTIPULYKIS\(\text{LIKEL\(\text{LIKQ}\) MTSTT\(LIKEL\(\text{LIKELEEQVRTIPULYKIS\(\text{LIKE\(\text{LIKEL\(\text{LIKEL\(\text{LIKE\	}		ł	EKKPTSPELBELWOKATLOOTIJJERMEKENOKLOASENDLLNKR
GVP\RHHRGEIWKFLAEQFHLKHQPPSKQQFKDVPYKELLKQLI SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQE VGYCQGLSFVAGILLLHMSEEEAFKMLKFLMFDMGLKGVGYPDM IILQIQMYQLSRLLHDVHRDLYNHLBEHEIGPSLYAAPWFLTMI ASQFPLGFVARVPDMIFLQGTEVIFKVALSLLGSHKPLLLQHEB LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYH VLQSELIDSSPLSDOQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLBATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS AKPEDREPECTQPEPTGD \$4074 KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLI YVDDIQKGMTIKKLNIQKRRKPSVPCPEPRITSGQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTISKPPPPLETSLPFLTII ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEI RRPRLASFGGMGTTSSLPSFVGSGNIMPAKHQLQNGYQGNGDY SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQI AIALKRLKELEEQVRTIPVLQVKISVLQEERRQLVSQLKNQRAX SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEMI TVEGSTQRIKEFRGL\TADMQALEQKTQDSSCEASSELRENGES RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKEITELQQTIESLKEKIYRLEVQLRETTHDREM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTILK NLMLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA MAVPRTADQDTSTDLEQVHQFTMTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGGEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKBSGVGQININDNYLVCLKMRTIACGPPQLTVGLTAS. RSVGVGDDPVGESLENPQGAGLMSJOLISTLSSINSVMKSAS	1	1	1	
SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDGE VGYCQGLSFVAGILLLIMSEERAFKNLKFLMFDMGLRKGYPDG IILQIQMYQLSRLLHDYHRDLYHRDLKHLKFLMFDMGLRKGYPDG ASGPPLGFVARVPDMIFLQGTEVIFKVALSLLGSHKPLILQHEN LETIVDFIKSTLPNLGLVQMEKTINQVFEMDLAKQLQAVEVEYV VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLBATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS AKPSDRSPECTQPEPTGD 5416 27 4074 KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLI LSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTII ENRQLPPPSPQDLPKHNLHVTKTLMETRRRLEQERATMQMTPGEI RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDY SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPHHLQHLRGY AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNORA SQINVCGVRKRSVSAGNASQLEQLSRARRSGGELYIDYEEEMM TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGE RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVRENCCGVSVI AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKEI VEMHDRCAGRSVENCDKSVSVEVSVCETGSNTEESVNDLTLIK NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGBGRVKDINSSTKTRSIGGGTLLSGHSGFD PSAVKTKESGVGQININDNYLVCLKMRTIACGPPQDLTVGLTASL RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TSLAENYSELAERAFGEPHSQMGSLNSQLISTLSSINSVMKSAS			ļ	
VGYCQGLSFVAGILLLHMSEERAFKMLKFIMFDMGLRKQYRPDM IIIQIQMYQLSRLLHDYHRDLYNHLBEHBIGBSLYAADWFLTME ASQFPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLILQHEM LETTUDFIKSTLPMIGLVQMEKTINQVFEMDIAKQLQAVEVETY- VLQEELIDSSPLSDNQRMDKLEKTINSSLRKQNLDLLEQLQVANG RIQSLBATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRES AKPSDREPECTQPEPTGD KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLI- YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTII ENRQLPPBSPQLPKHNLHVTKTLMETRRLLEQERATMQMTPGEI RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSSMHLQHIREQG AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRA- SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEBMI TVEGSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEG RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVERRNCGYSVTI AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREM- KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETTNSVGISCQPECKNKVVGPELPMNWNIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK- NLNLKEVRSIGCGDCSVDVTVCSPRECASRGVNTEAVSQVEAA- MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDL PSAVKTKESGVGQININDNIVLGKMRTIACGPPQLTVGLTAS: RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQG TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS	1		[
IIIQIQMYQLSRLLHDYHRDLYNHLBEHEIGBSLYAAPMFLTME ASGPPLGFVARVFFMIFLQGTEVIFKVALSLLGSHKPLILQHEN LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYY VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRES AKPBDREPECTQPEPTGD SKQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLI YVDDIQKGMTIKRINIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTII ENRQLPPPSPQLPKINLHVTKTLMETRRILEQERATMQMTPGEI RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGTSTPVTNVSPMHLQHTREQD RSVAPAAPTTSSMGSSIRHSPLSSGTSTPVTNVSPMHLQHTREQD SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEMI TVEGSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEN RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGYMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETTNSVGISCQPECKNKVVGPELPMNWUTVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTILK* NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA* MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERTQKLLAEQ	\			SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLINILKAISLDDQL
ASQFPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLILQHEN LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYF VLQELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLEATI EKLLSSESKLKQAMLTLELERSALLQTVEELRRES AKPSDREPECTQPEPTGD 5416 27 4074 KSQLFCFWGGKAGDILSGDQDKEQXDPYFVETPYGYQLDLDFLI YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRITSGQQGIWTSTES LSSSNSDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTII ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMOMTPGEI RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQI AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAX SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEMI TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEG RSVAVGAEEMNNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMG KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTILKG NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAMAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD. PSAVKTKESGVGQINDNYLVGLKMRTIACGPPQLTVGLTASS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TSLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS	i		1	VGYCQGLSFVAGILLLHMSEEKAFKMLKFLMFDMGLRKQIRPDM
LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYY VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLBATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS AKPSDREPECTQPEPTGD 5416 27 4074 KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLI YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTI ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMQMTPGBI RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRBQI AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEMM TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEG RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMM KLKQELQAAGSRKKVDKATMAQPLVPSKVVEAVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGLSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTAS: RSVGVGDDPVGESLENPQPQAPLGMMTGLDHY1ERIQKLLAEQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS	i	1		IILQIQMYQLSRLLHDYHRDLYNHLBEHEIGPSLYAAPWFLTMF
VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLBATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDREPECTQPEPTGD 5416 27 4074 KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLI YVDDIQKGNTIKKLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTII ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEI RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQI AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRA SQINVCGVKKRSYSAGNASQLEQLSRARRSGGELYIDYEEEBMI TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEG RSVAVGAEENMNDIVVYHRGSRSCKDAVGTLVEMRNCGVSVTI AMLGVMTEADKRIBLQQQTIESLKEKIYRLEVQLRETTHDREM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKGINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTAS: RSVGVGDDDYGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ	j	j	1	ASQFPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLILQHEN
VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLBATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDREPECTQPEPTGD 5416 27 4074 KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLI YVDDIQKGNTIKKLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTII ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEI RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQI AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRA SQINVCGVKKRSYSAGNASQLEQLSRARRSGGELYIDYEEEBMI TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEG RSVAVGAEENMNDIVVYHRGSRSCKDAVGTLVEMRNCGVSVTI AMLGVMTEADKRIBLQQQTIESLKEKIYRLEVQLRETTHDREM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKGINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTAS: RSVGVGDDDYGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ	}		j	LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYH
RIQSLBATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDREPECTQPEPTGD 5416 27 4074 KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLI YVDDIQKGNTIKKLNIQKRRKPSVPCPEPRTTSQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTII ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEI RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQI AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAI SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEBMI TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEG RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMI KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKG NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASG RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAERYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS				VLOEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG
AKPSDREPECTQPEPTGD 5416 27 4074 KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLY YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTII ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMQMTPGEI RRPRLASFGGMGTTSSLPSFVGSGNINPAKHQLQNGYQGNGDY SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQI AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAI SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEBMI TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGE RSVAVQABEENMNDIVVYHRGSRSCKDAAVGTLVERMRCGVSVTI AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKBI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTAS: RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS			ļ	
5416 27 4074 KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLITYDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTII ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEDY RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDY SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQN AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAM SQINVCGVKKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEM TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEM RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTM AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWNIVKEN VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKM NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAM MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGBGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQU TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS	1		}	
YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTII ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMQMTPGEI RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQI AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAM SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEMI TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEM RSVAVGAEENNNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWMIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKM NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAM MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKM TSTQTVETRTVAVGRGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQU TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSASS	F		4034	KSOLECEWCCKACDII SCHODKEOKDPY EVETPYCYOLDI DELK
LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTII ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMQMTPGEI RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQN AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAN SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEMI TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEG RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKEIBLQQQTIESLKEKIYRLEVQLRETTHDREMI KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWNIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA' MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTAS: RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ	5416	27	40/4	AMDIOACHLIADITOODANIACHTI IIII TOLANIACHEC
ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMQMTPGET RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQN AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAG SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEMN TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEG RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKEIBLQQQTIESLKEKIYRLEVQLRETTHDREMS KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKEN VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS	i	ļ		I ADDITOVOM I TUKUM TOVOKU PO CENEKI 1900 ORI MILI
RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQI AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAI SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEMI TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEG RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSJ MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKM NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAM MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDKM TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASSINSVMKSAST	1			LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP
SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQN AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAM SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEMM TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEM RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMM KLKQELQAAGSRKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKEN VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKM NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAM MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDKM TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQM TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS			i	ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF
AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAM SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEMM TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEG RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKM NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAM MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKM TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQU TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS	j	1	}	RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG
AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAM SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEMM TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEG RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKM NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAM MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKM TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQU TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS		1		
SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEMI TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEG RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMI KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKBI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKI NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAI MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKI TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDI PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASI RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQI TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSASI	1			AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA
TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEG RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREM KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA* MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKNRTIACGPPQLTVGLTAS: RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS*		1		SOINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME
RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTI AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREM' KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQFECKNKVVGPELPMNWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK' NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA' MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD' PSAVKTKESGVGQININDNYLVGLKNRTIACGPPQLTVGLTAS: RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ' TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS'	1			TVEOSTORIKEFROL\TADMOALEOKIODSSCEASSELRENGEC
AMLGVMTEADKEIBLQQQTIESLKEKIYRLEVQLRETTHDREMS KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKS NLINLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAS MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDI PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTAS: RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQU TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSASS	1	1		PSVAVGA EENMNDT VVYHRGSRSCKDAAVGTI.VEMRNCGVSVTE
KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSI MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK* NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA* MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDK* TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD* PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTAS* RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ* TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS*	1	1		
MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKEI VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTAS RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS				MINOALOS SCODAMIDAS MAYODI (IECAMIES MODEDO MICOLE)
VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLK' NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA' MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD: PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTAS: RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS'		[KLKQELQAAGSKKKVDKATMAQPDVFSKVVEAVVQTRDQMVGSH
NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAA' MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDKI TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDI PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASI RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQI TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSASI	1			MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER
MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTAS: RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS				
MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTAS: RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS	[NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV
TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFD: PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTAS: RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS	i			MAVPRTADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDKQ
PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTAS: RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS	1]	}	TSTOTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR
RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQ TLLAENYSBLAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS	1			DSAVKTKESGVGOININDNYLVGLKMRTIACGPPOLTVGLTASR
TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAS'			-	DOUGLODDINGEST BADODOS DE CAMPOLORYTES TOKELS AEOO
TELAENYSELAEAFGEPHSQWGSENSQHISINSVINGAS EELRNPDFOKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQP	}		Í	MILY PERMEDITY DE PORDITO MOST MOST TOUT CETTICAMENTA
	}			There was the transmission of the property of
	<u> </u>	L		RETRUBUL Ó KLADAKTLES AT GALCKO GET Ó PASA ET 29 Ó L2 Ó SE

SEO	Predicted	Predicted end	Amino acid coment containing cional martida
ID	beginning	nucleotide	Amino acid segment containing signal peptide
			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	sequence	
<u> </u>	sequence		\=possible nucleotide insertion)
	[QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN
1	1 .	1	ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD
	Į	Į	ESSSSESDDECDVIEYPLEBEEEEEDEDTRGMAEGHHAVNIEGL
1	{	1	KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND
	ļ	J	PKALTSKDMRFCLNTLOHEWFRVSSOKSAIPAMVGDYIAAFRAI
1	i	}	SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD
1	l	ļ	HONKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASOAG
ŀ	\	Į	
İ	t	i	QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG
]	HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA
	<u> </u>		HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD
5417	27	4074	KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK
1			YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES
	İ	1	LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP
J			ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMOMTPGEF
			RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHOLONGYOGNGDYG
1	!		SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLOHIREOM
Ī			AIALKELKELEEOVRTIPVLOVKISVLOEEKROLVSOLKNORAA
1			
1			SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME
1			TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC
}			RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE
1			AMLGVMTBADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT
ţ	•		KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH
1		,	MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER
1			VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT
1 .			NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV
			MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ
1			
}			TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR
ļ			PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR
ł			RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ
1			TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAST
1	['	EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE
Į,			QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN
			ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD
1	1 .		ESSSSESDDECDVIEYPLEEEEEEEDEDTRGMAEGHHAVNIEGL
			KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND
		•	1
1			PKALTSKOMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI
			SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD
1 .			HQNKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG
			QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG
			HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA
1			HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD
5418	24	1133	SVPRAGGDMETGAAELYDOALLGILOHVGNVQDFLRVLFGFLYR
[[KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR
j l			ROELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL
1			"
1			DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI
<u> </u>			LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK
1 1			GKQVSVALSSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL
]			EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE
			EEQAVLDRLTFDYHQKLQGKPQSHBLKVHEMLKKGWDAEGSPFR
j i			GQRFDPAMFNISPGAVQF
5419	1395	259	GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG
			SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA
} J			KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL
, ,			
1 1			PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH
		•	ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR
1			VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT
, ,			YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK
1			RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN
1			RAGLLALMLHQTIQHDPLTTDLRSSADR
5420	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG
1 1	İ		GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR
	<u></u>		·

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
!	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
1	corresponding	to first	P-Proline, Q-Glutamine, R-Arginine,
	to first	amino acid	p-proline, Q=Giutamine, K=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, A=Unknown, "=SLOP
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<u></u>	\=possible nucleotide insertion)
			ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
1	 	{	LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS
1			LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV
}		}	YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP
i	ł	ł	YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE
i			QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL
1		ļ	LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID
J	1		EAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGF
ļ			YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
Í	1		TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
ł			RAELIRAFGERE
5421	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG
			GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR
			ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
1	į		LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS
1	i i	1	LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV
i			YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP
	1		YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE
1			QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL
)	j		LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID
		j	EAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGF
j			YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
		İ	TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
1	}	İ	RABLIRAFGERE
5422	3	1263	SCGESLPTWLAGASRPGIGRKGGAWGGRGGSSPAQVLLSPGPVF
1	İ	1	KAGCNWWHLSRDQAGVQRCDLGSSQPPPLGFKRFSCLSLPSSWD
1		Ĭ	YRSTVLCVSKMEADLSGFNIDAPRWDQRTFLGRVKHFLNITDPR
1			TVFVSERELDWAKVMVEKSRMGVVPPGTQVEQLLYAKKLYDSAF
	1		HPDTGEKMNVIGRMSFQLPGGMIITGFMLQFYRTMPAVIFWQWV
1	i		NQSFNALVNYTNRNAASPTSVRQMALSYFTATTTAVATAVGMNM
} .	ł		LTKKAPPLVGRWVPFAAVAAANCVNIPMMRQQELIKGICVKDRN
			ENEIGHSRRAAAIGITQVVISRITMSAPGMILLPVIMERLEKLH
	ľ		FMQKVKVL/SAPLQVMLSGCFLIFMVPVACGLFPQKCELPVSYL
İ	1		EPKLQDTIKAKYGELEPYVYFNKGL
5423	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ
			PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD
1		}	ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE
1			EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG
	,		LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQERAEPRG
			GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL
			GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT
1			YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP
1			TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW
1			SOLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL
			RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
1			LALPARLTOVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
1		1	PASFPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
1		1	EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
			GGEOGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
			SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
]		NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
			DKKPMAAMEHPCEGV
5424	3186	905	GVSMALGEEKAEABASEDTKAQSYGRGSCRERELDIPGPMSGEQ
2424	3.20		PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD
1			ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE
			EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG
	1		LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQERAEPRG
1			GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL
		•	GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT
1		}	YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP
	[TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW
1	l		THASEMOLEUMUNDEL GOLUCEUM DULL SUSSELLOTTEN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
)	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
·	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence		\=possible nucleotide insertion)
		 	SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPOL
ļ			RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
			LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
ļ	ł		PASFPSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
j	J	1	
			EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
			GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
1 .	1	ļ	SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
1		1	NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
L	<u> </u>		DKKPMAAMEHPCEGV
5425	1086	115	GFCPSPSLGHQPPRVLHPTMSMAVETFGFFMATVGLLMLGVTLP
			NSYWRVSTVHGNVITTNTIFENLWFSCATDSLGVYNCWEFPSML
1		[ALSGYIQACRALMITAILLGFLGLLLGIAGLRCTNIGGLELSRK
1	1	1	AKLAATAGAPH\ILPGICGMVAI\SWYAFNITR\DFSDPLYPGT
I			KYELGPALYLGWSASLISILGGLCLCSACCCGSDEDPAASARRP
1			YQAPVSVMPVATSDQEGDSSFGKYGRNALRVAALCRGPRCLPTA
1 '	1	}	PKKRGPGRGPFPYSNLRGRPRPVPVAPPRPRPRVLHSHGPSOAK
)	J.		NCSWEVAYLPSEAGSLIF
5426	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDOPSAPSDPTDOP
	1 ""	1	PAAHAKPDPGSGGOPAGPGAAGBALAVLTSFGRRLLVLIPVYLA
1	1		GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAAROLLDDEEOL
	i .		
			TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
1 .	}		LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR
1			KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
1			EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD
1			TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
ļ			LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
			PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV
1	1	·	LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
1			VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
	1		MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQBLDVQV
l	4		KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
	<u>"</u> .		KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
			PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
			VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF
:	 		DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL
			ERLTPRPTAABLEEVLOVNSLIOTOKSAELAAALLSIYMERAED
1			LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
ł			RKPHTESLELOVRGEGTGVLGSLSLPLSELLVADOLCLDRWFTL
			SSGOGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
	}		GGPPHITSSAPEV\RORLTHVDSPLEAPAGPLGOVKLTLWYYSE
	[
1	ļ.		ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
			KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
E433			LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
5427	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
1			PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA
1	[•	GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL
1			TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
}			LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR
	ĺ		KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
	ł		EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD
			TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
			LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
			PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV
			LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
			VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
	•	ı	MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV
			KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
		,	KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
	}	i	PCHTTPDSQFGTBHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
			VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF
			DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
1		Sequence	\=possible nucleotide insertion)
	sequence		ERLTPRPTAAELEEVLQVNSLIQTQKSAELAAALLSIYMERAED
			LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
	i	ĺ	
	ł		RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
1	[İ	SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
ł	t	ì	GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE
1		1	ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
1		į.	KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
}	1	}	LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
5428	3	1839	SSRSERLSACAIAPPWLVSSRPARPAQLQRPGKMVEDGAEELED
3420	1	1	LVHFSVSELPSRGYGVMEEIRRQGKLCDVTLKIGDHKFSAHRIV
1	1	1	LAASIPYFHAMFTNDMMECKQDEIVMQGMDPSALEALINFAYNG
1			17
1	1		NLAIDQQNVQSLLMGASFLQLQSIKDACCTFLRERLHPKNCLGV
1			RQFAETMMCAVLYDAANSFIHQHFVEVSMSEEFLALPLEDVLEL
1			VSRDELNVKSEEQVFEAALAWVRYDREQRGTFL\RNLQSNIRLL
1	1		FCRPQFLSDRVQQDDLVRCCHKCRDLVDEAKDYLLMPERRPHLP
1			AFRTRPRCCTSIAGLIYAVGGLNSAGDSLNVVEVFDPIANCWER
1			CRPMTTARSRVGVAVVNGLLYAIGGYDGQLRLSTVQAYNTETDT
1			WTRVGSMNSKRSAMGTVVLDGQIYVCGGYDGNSSLSSVETYSPE
i			TDKWTVVTSMSSNRSAA\GVTVFEGRIYVSGGHDGLQIFSSVEH
1	1	1	YNHHTATWHPAAGMLNKRCRHGAASLGSKMFVCGGYDGSGFLSI
			AEMYSSV\ADQWCLIVPM\HTRR\SRVSLGGPAVGRLYAVWGVT
			TGQSNL\SSVGDVLTPETDCWTFM\APMACHEGGVGVGCIPLLT
1	}	ł	I
	<u> </u>		RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPF
5429	828	202	
}	l .	1	AQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQ
Ì			LRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNS
1	-	1	GISATCYGSGGRMEGPPP\TYSEVIGHYPGSSFQHQQSSGPPSL
			LEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL
5430	441	1507	QKRRKRRKKIMKTIQPKMHNSISWAIFTGLAALCLFQGVPVRS
	1		GDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYA
ŀ	1	<u> </u>	GNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDN
İ	1		HPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEP
		}	TVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDV\A
i	1		APV\VRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSA
	1	Ì	APV (VKKVKVI VNIPPI I JEAKGIGVE VOQUGI EQEMENVE IX
1			EFQWYKDDKRLI/EGKKGVKVENRPFLSKLIFFNVSEHDYGNYT
1	•		CVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVL
l	1		HLLLKF
5431	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
į.	1		LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ
1	1		KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
1	1	1	GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY
1			SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA
1		1	YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
1			FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP
	1	1	DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
ĺ			AMAIFELLDYIVNRPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
L	1		DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
5432	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
1			LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ
			KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
			GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY
	1		SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA
1			YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
1		1	FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP
1	ļ		DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
Į.			DAKELEAT FGREVVDGEEGEENS 15 PKEKEPEGKEVSGREFDSRE
1			AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
-	_ l		DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
5433	360	1885	SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV
ł			LFGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF
1			SLIFTLGSFMNNFMTFPTGYIFDRFKTTVARLIAIFFYTTATLI
<u> </u>	_ 		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
""	location		Glucamic Acid, Fernenylatanine, GeGlycine,
- [corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence		\=possible nucleotide insertion)
			IAFTSAGSAVLLFLAMPMLTIGGILFLITNLQIGNLFGQHRSTI
1	1.		ITLYNGAFDSSSAVFLIIKLLYEKGISLR/VLLHLHLCLOYLAC
j		ļ	STHFPPDAPGAHPIPTAPQLQLWPVPWEWHHKGREG/QQLSMKT
			, ·
Ì			GSYSQRSSFQRRKRPQGQGRSRNSAPSGATL/CSRRFAWHLVWL
			SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTQFGVL
			CAPWNGLLMDRLKQKYQKEARKTGSSTLAVALCSTVPSLALTSL
	j		LCLGFALCASVPILPLQYLTFILQVISRSFLYGSNAAFLTLAFP
			SEHFGKLFGLVMALSAVVSLLQFPIFTLIKGSLQNDPFYVNVMF
	<u> </u>		MLAILLTFFHPFLVYRECRTWKESPSAIA
5434	66	652	RYAALIISLIQHKLLWRNQHCSRCVIMSPAQSAGLNWLF/GSGK
			HGPFLGCSQYPACDYVRPLKSSADGHIVKVLEGQVCPACGANLV
1			LRQGRFGMFIGCINYPECEHTBLIDKPDETAITCPQCRTGHLVQ
1			RRSRYGKTFHSCDRYPECQFAINFKPIAGECPECHYPLLIEKKT
1	Į.		AQGVKHFCASKQCGKPVSAE
5435	4704	1597	PGDSSQRLAEMSNAKERKHAKKMRNQPTNVTLSSGFVADRGVKH
		13,7	HSGGEKPFQAQKQEPHPGTSRQRQTRVNPHSLPDPEVNEQSSK
Į.	1		
ſ			GMFRKKGGWKAGPEGTSQEIPKYITASTFAQARAAEISAMLKAV
1	1		TQKSSNSLVFQTLPRHMRRRAMSHNVKRLPRRLQEIAQKEAEKA
			VHQKKEHSKNKCHKARRCHMNRTLEFNRRQKKNIWLETHIWHAK
1	1		RFHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLQDLSYYCCLE
]		LKGKEEEILKALSGMCNIDTGLTFAAVHCLSGKRQGSLVLYRVN
}	1		KYPREMLGPVTFIWKSQRTPGDPSESRQLWIWLHPTLKQDILEE
1	1		IKAACQCVEPIKSAVCIADPLPTPSQEKSQTELPDEKIGKKRKR
1	!		KDDGENAKPIKKIIGDGTRDPCLPYSWISPTTGIIISDLTMEMN
1	1		RPRLIGPLSHSILTEAIKAASVHTVGEDTEETPHRWWIETCKKP
	1		DSVSLHCRQEAIFELLGGITSPAEIPAGTILGLTVGDPRINLPO
ł	1 .		KKSKALPNPEKCQDNEKVRQLLLEGVPVECTHSFIWNODICKSV
1	1 1		TENKISDQDLNRMRSELLVPGSQLILGPHESKIPILLIQQPGKV
1	i l		TGEDRLGWGSGWDVLLPKGWGMAFWIPFIYRGVRVGGLKBSAVH
	1		SQYKRSPNVPGDFPDCPAGMLFAEEQAKNLLEKYKRRPPAKRPN
}]		
			YVKLGTLAPFCCPWEQLTQDWESRVQAYEEPSVASSPNGKESDL
1	ł 1		RRSEVPCAPMPKKTHQPSDEVGTSIEHPREAEBVMDAGCQESAG
			PERITDQEASENHVAATGSHLCVLRSRKLLKQLSAWCGPSSEDS
1	1		RGGRRAPGRGQQGLTREACLSILGHFPRALVWVSLSLLSKGSPE
1] .]		PHTMICVPAKEDFLQLHEDWHYCGPQESKHSDPFRSKILKQKEK
1	ļ . l		KKREKRQKF\GRASSDGPAGEEPVAGQEALTLGLWSGPLPRVTL
1	·		HCSRTLLGFVTQGDFSMAVGCGEALGFVSLTGLLDMLSSQPAAQ
L	L ·		RGLVLLRPPASLQYRFARIAIEV
5436	· 1781	635	ASDSIPWSEARTTRKLAQRGCQWSLPERMPLVVFCGLPYSGKSR
1	:		RAEELRVALAAEGRAVYVVDDAAVLGAEDPAVYGDSAREKALRG
]		ALRASVERRLSRHDVVILDSLNYIKGFRYELY\CLARAARTPLC
1	1		LVYCVRPGGPIAGPQVAGANENPGRNVSVSWRPRAEEDGRAOAA
]]		GSSVLRELHTADSVVNGSAQADVPKELEREESGAAESPALVTPD
1 .	}		SEKSAKHGSGAFYSPELLEALTLRFEAPDSRNRWDRPLFTLVGL
'			EEPLPLAGIRSALFENRAPPPHQSTQSQPLASGSFLHQLDQVTS
1 1			QVLAGLMEAQKSAVPGDLLTLPGTTEHLRFTRPLTMAELSRLRR
 			QFISYTKMHPNNENLPQLANMFLQYLSQSLH
5437	739	1672	CQEAASEFGGPLHTPAMFLRRLGGWLPRPWGRRKPMRPDPPYPE
1 1	1		PRRVDSSSENSGSDWDSAPETMEDVGHPKTKDSGALRVSRAASE
1			PSKEBPQVEQLGSKRMDSLKWDQPISSTQESGRLEAGGASPKLR
1 1	ŀ		WDHVDSGGTRRPGVSPEGGL\GVPGPGAPLEKPGRREKLLGWLR
])			GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR
1 1	ľ	•	AALDTLGLRGPLGLWLHGLLSFLAALHGLHAVLSLLTAHPLHFA
1 1	}		
1			CLFGLLQALVLAVSLREPNGDEAATDWESEGLEREGEEQRGDPG
- E432			KGL
5438	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
1 1		1	LAPPSLRRPMMCQSEARQGPBLRAAKWLHFPQLALRRRLGQLSC
]]		ļ	MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
			VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
1 1		•	.DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK
ļ			NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	\=possible nucleotide insertion)
	sequence		REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP
ļ	l		
ĺ	l		GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY
Į.	1]	FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS
1		l	FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL
5439	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
1	}	1	LAPPSLRRPMMCQSEARQGPELRAAKWLHFPQLALRRRLGQLSC
ł		1	MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
1	1		VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
1			DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK
l .]	NCEVEOVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT
-			
Į.	1	1	REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP
1			GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY
l			FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS
1			FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL
5440	693	253	EPIPVTPDHRLVTMTHIV\QTFSPVNS\GQPPNYEMLKEEQEVA
1	1		MLGAPHNPAPPMSTVIHIRSETSVPDHVVWSLFNTLFMNTCCLG
1			FIAFAYSVKSRDRKMVGDVTGAQAYASTAKCLNIWALILGIFMT
1	1	1	ILLIIIPVLVVQAQR
5441	2	2054	CRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSFIN
2441	1 2	2034	NSDLWVANIETGEERRLTFCHOGLSNVLDDPKSAGVATFVIQEE
1		j	
ſ	{	ļ	FDRFTGYWWCPTASWEGSEGLKTLRILYEEVDESEVEVIHVPSP
1	j	1	ALEERKTDSYRYPRTGSKNPKIALKLAEFQTDSQGKIVSTQEKE
I	1	1	LVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLL
İ	1	1	PPALFIPSTENEEQ\RLASARAVPRNVQPYVVYEBVTNVWINVH
Į.	1	1	DIFYPFPQSEGEDELCFLRANECKTGFCHLYKVTAVLKSQGYDW
İ	•	1	SEPFSPGEGEQSLTNAIWVNEETKLVYFQGTKDTPLEHHLYVVS
Į.		1	YEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHYSSVSTPPCVHVY
1	1		KLSGPDDDPLHKOPRFWASMMEAAKIFHFHTRSDVRLYGMIYKP
1	Į	ì	HALOPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGY
	1		AVVVIDGRGSCORGLRFEGALKNOMGOVEIEDQVEGLQFVAEKY
ł	1	İ	
1	1	1	GFIDLSRVAIHGWSYGGFLSLMGLIHKPQVFKVAIAGAPVTVWM
ł	Ī	F.	AYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLILH
ļ	1	}	GFLDENVHFFHTNFLVSQLIRAGKPYQLQVALPPVSPQIYPNER
1		į.	HSIRCPESGEHYEVTLLHFLQEYL
5442	1	3474	CGQRSRRRSPDMPEAKPAAKKAPKGKDAPKGAPKEAPPKEAPAB
1		<u> </u>	APKEAPPEDQSPTAEEPTGVFLKKPDSVSVETGKDAVVVAKVNG
1		-	KELPDKPTIKWFKGKWLELGSKSGARFSFKESHNSASNVYTVEL
1		1	HIGKVVLGDRGYYRLEVKAKDTCDSCGFNIDVEAPRQDASGQSL
1			ESFKRTSEKKSDTAGELDFSGLLKKREVVEEEKKKKKKDDDDLG
1			IPPEIWELLKGAKKSEYEKIAFQYGITDLRGMLKRLKKAKVEVK
1	1		KSAAFTKKLDPAYQVDRGNKIKLMVEISDPDLTLKWFKNGQEIK
1	1		PSSKYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCFTELFV
1	1		KEPPVLIVTPLEDOOVFVGDRVEMAVEVSBEGAQVMWMKDGVEL
i			
1			TREDSFKARYRFKKDGKRHILIFSDVVQEDRGRYQVITNGGQCE
1			AELIVEEKQLEVLQDIADLTVKASEQAVFKCEVSDEKVTGKWYK
1			NGVEVRPSKRITISHVGRFHKLVIDDVRPEDEGDYTFVPDGYAL
1			GSLSAKLNFLEIKVEYVPKQ\EPPKIPLGFASGGKTSENAD/IV
i			VVAGNKLRLDV\SITGEAPSPFAT\WLKG\DEVFTTTEGRTRIE
1	}		KRVDCSSFVIESAQREDEGRYTIKVTNPIGEDVASIFLQVVDVP
Į.			DPPEAVRITSVGEDWAILVWEPPMYDGGKPVTGYLVERKKKGSQ
1			RWMKLNFEVFTETTYESTKMIEGILYEMRVFAVNAIGVSQPSMN
1			TKPFMPIAPTSEPLHLIVEDVTDTTTTLKWRPPNRIGAGGIDGY
1			LVEYCLEGSEEWVPANTEPVERCGFTVKNLPTGARILFRVVGVN
1			
1	1		IAGRSEPATLAQPVTIREIAEPPKIRLPRHLRQTYIRKVGEQLN
j	}	1	LVVPFQGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVRQAA
1		1	RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT
1	1	}	NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSC
1			TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK
1			PFEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV
}			VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV
1			NELGEALAECKLEVRVPQ
L			

SEQ	Predicted	Predicted end	Amino acid coment containing circul acatida
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
-	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
]	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
5443	66	1003	SRGQLDAGQSSEQHGGNRQPEQSRSRSSSSSSSSPRRSRSAAEPA
	}		MALSMPLNGLKEEDKEPLIELFVKAGSDGESIGNCPFSQRLFMI
1]		LWLKGVVFSVTTVDLKRKPADLQNLAPGTHPPFITFNSEVKTDV
ĺ			NKIEEFLBEVLCPPKYLKLSPKHPESNTAGMDIFAKFSAYIKNS
l			RPEANEALERGLLKTLQKLDEYLNSPLPDEIDENSMEDIKFSTR
			KFLDGNEMTLADCNLLPKLHIVKVVAKKYRNFDIPKEMTGIWRY
ļ			LTNAYSRDEFTNTCPSDKEVEI\AYSDVAKRLHQVKSRLLKEVS
Ĺ			FMSSP
5444	2	344	SGPIGVTGAQMAKWLRDYLSFGGRRPPPQPPTPDYTESDILRAY
1			RAQKNLDFEDPY*DSESRLEPDPAGPGDSKNPGDAKYGSPKHRL
1			IKVEAADMARAKALLGGPGEELEADTEYLDPFDAQPHPAPPDDG
[!		YMEPYDAQWVMSELPGRGVQLYDTPYEEQDPETADGPPSGQKPR
			QSRMPQEDERPADEYDQPWEWKKDHISRAFAVQFDSPEWERTPG
			SAKELRRPPPRSPQPAERVDPALPLEKQPWFHGPLNRADAESLL
].]		SLCKEGSYLVRLSETNPQDCSLSLRSSQGFLHLKFARTRENQVV LGQHSGPFPSVPELVLHYSSRPLPVQGAEHLALLYPVVTOTP*O
			· - · · · · · · · · · · · · · · · · · ·
	[*PDWGDRRPNGQVATGLPELWGAEAPSAAAHPGLHRERHPEGLP RAEKPGLRGPLLGLREPLGAGPRGPWGLOEPRRCOVWFSOAPAH
1			QGGGCGYGOSQGPSGRPRGGAGSRH
5445	2364	486	ILSRGFLGSVEICIQLPLPASEPVLLLTWARRRWRETRSRREPT
			TLRAQSVCPWWI*ETRMNRSIPVEVDESEPYPSQLLKPIPEYSP
İ			EEESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSQAHSTLKLANH
1			QRPVSRQVTCLRTQVLEDSEDSFCRRHPGLGKAFPSGCSAVSEP
1			ASESVVGALPAEHQFSFMEKRNQWLVSQLSAASPDTGHDSDKSD
1			QSLPNASADSLGGSQEMVQRPQPHRNRAGLDLPTIDTGYDSQPQ
1			DVLGIRQLERPLPLTSVCYPQDLPRPLRSREFPQFEPQRYPACA
1			QMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDYPRAAYQQVIQP
1			ALPGQPLPGASVRGLHPVQKVILNYPSPWDQEERPAQRDCSFPG
1	1		LPRHQDQPHHQPPNRAGAPGESLECPAELRPQVPQPPSPAAVPR
			PPSNPPARGTLKTSNLPEELRKVFITYSMDTAMEVVKFVNFLLV
ł			NGFQTAIDIFEDRIRGIDIIKWMERYLRDKTVMIIVAISPKYKQ
.	ļ.		DVEGAESQLDEDEHGLHTKYIHRMMQIEFIKQGSMNFRFIPVLF
1	<u> </u>		PNAKKEHVPTWLQNTHVYSWPKNKKNILLRLLREEEYVAPPRGP
		·	LPTLQVVPL
5446	972	161	SSWSWCTGRMRKTRLWGLLWMLFVSELRAATKLTEEKYELKEGQ
			TLDVKCDYTLEKFASSQKAWQIIRDGEMPKTLACTERPSKNSHP
			VQVGRIILEDYHDHGLLRVRMVNLQVEDSGLYQCVIYQPPKEPH MLFDRIRLVVTKGFSGTPGSNENSTONVYKIPPTTTKALCPLYT
			TPRTVTQAPPKSTADVSTPDSEINLTNVTDIIRVPVFNIVILLA
			GGFLSKSLVFSVLFAVTLRSFVP*AHEPTRMSSDFQPHPSGSCA
1	ļ.		KGGGRR
5447	207	617	MTARTLSLMASLVAYDDSDSEAETEHAGSFNATGOOKDTSGVAR
1		 -	PPGQDFASGTLDVPKAGAQPTKHGSCEDPGGYRLPLAQLGRSDR
			GSCPSQRLQWPGKEPQVTFPIKEPSCSSLWTSHVPASHMPLAAA
			RFKQVKLSRNFPKSSFHAQSESETVGKNGSSFQKKKCEDCVVPY
1			TPRRLRQRQALSTETGKGKDVEPQGPPAGRAPAPLYVGPGVSEF
			IQPYLNSHYKETTVPRKVLFHLRGHRGPVNTIQWCPVLSKSHML
			LSTSMDKTFKVWNAVDSGHCLQTYSLHTEAVRAARWAPCGRRIL
			SGGFDFALHLTDLETGTQLFSGRSDFRITTLKFHPKDHNIFLCG
1			GFSSEMKAWDIRTGKVMRSYKATIQQTLDILFLREGSEFLSSTD
			ASTRDSADRTIIAWDFRTSAKISNQIFHERFTCPSLALHPREPV
			FLAQTNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECSPG
	[GDLLVTGSADGRVLMYSFRTASRACTLQGHTQACVGTTYHPVLP
			SVLATCSWGGDMKIWH*AFHWLSLGEAIGDLAPARGYSGPGRSL
L			KSPSPSKSLLVLLCGRAMFQPATCPWQLPALSK
5448	194	1833	MASKVTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA
			HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF
	}		RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
			GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRKLRKAAHLEV
	j		HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCET
L			COMMENCE TO TO TO TO TO TO TO TO TO TO TO TO TO

AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSN SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGH PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYC TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTN LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWH TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQC SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASH YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMM SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAM RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSOEAVDTGRVLYHLSRPEAWSDAFSLDVASGLGAP				
No. location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence Serine, P-Proline, Q-Gultamine, R-Argainine, P-Proline, Sequence P-Proline, Q-Gultamine, R-Argainine, P-Proline, Sequence Serine, T-Threonine, V-Valline, W-Trystophan, Y-Trystoph	SEQ	Predicted		Amino acid segment containing signal peptide
corresponding to first amino acid amino acid residue of amino acid amino acid sequence February	ID	beginning		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first anino acid anino acid residue of anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid sequence Selection Testiculor of anino acid sequence Selection Testiculor of anino acid sequence Selection Testiculor of anino acid sequence Selection Testiculor of anino acid sequence Testiculor of acid sequence Testiculor of acid sequence Testiculor of acid sequence Testiculor of acid sequence Testiculor of acid sequence Testicu	NO:	nucleotide		Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid am	}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first mino acid residue of mino acid residue of mino acid sequence S-Serine, T-Threenine, V-Valline, S-Serine, T-Threenine, V-Valline, S-Serine, T-Threenine, V-Valline, S-Serine, T-Threenine, V-Valline, S-Serine, T-Threenine, V-Valline, S-Serine, T-Threenine, V-Valline, S-Serine, T-Threenine, V-Valline, W-Tryptophan, Y-Trytosine, X-Unknown, *-Stop Codon, I-possible nucleotide insertion) Index		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
amino acid residue of amino acid sequence Sequence Sequence TEREPTANNYGTILANGPSKDTQGTT ITVSDEWSSEGGEFTGYSIL REPUTANNYGTILANGPSKDTQGTT ITVSDEWSSEGGEFTGYSIL REPUTANNYGTILANGPSKDTQGTT ITVSDEWSSEGGEFTGYSIL REPUTANNYGTILANGPSKDTQGTT ITVSDEWSSEGGEFTGYSIL REPUTANNYGTILANGPSKDTQGTT ITVSDEWSSEGGEFTGYSIL REPUTANNYGTILANGPSKDTQGTT ITVSDEWSSEGGEFTGYSIL REPUTANNYGTILANGPSKDTQGTGTASTVERGNCKAPME VIKENTDEWSTANGSEGGEFTGYSILANGPSKDTGTGSSCGSSSS QDSSCARPESETEDVIMEDLHIGAGCHSSCTSSTTDVENNQING TEREQUTANSASELVITAGSSNEDVITAGSTVENGTICKAPME VIKENTDEWSTANGSSCGSTGGSSSARPSSTETDVIMEDLICHGEGERSC SETDVENNQING CVKENTDDFTGGALDHIGSTSCGSCGSSSS SETDVENNQING CVKENTDDFTGGALDHIGSTSCGSCGSSSS SETDVENNQING CVKENTDDFTGGALDHIGSTSCGSCGSSSS SETDVENNQING CVKENTDDFTGGALDHIGSTSCGSCGSSSS SETDVENNQING CVKENTDDFTGGALDHIGSTSCGSTGGSSS SETDVENNQING CVKENTDDFTGGALDHIGSTSCGSTGGSSS SETDVENNQING CVKENTDDFTGGALDHIGSTSCGSTGGSSS SETDVENNQING CVKENTDDFTGGALDHIGSTSCGSTGGSSS SETDVENNQING CVKENTDDFTGGALDHIGSTGGALDHIG	}			P=Proline, Q=Glutamine, R=Arginine,
residue of anino acid sequence (Codon, 'possible nucleotide deletion, 'sslop (Codon, 'possible nucleotide deletion) (-possible nucleotide deletion) (-possible nucleotide deletion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide) (-possib				S=Serine, T=Threonine, V=Valine,
amino acid sequence Codon. /=possible nucleotide disertion) INFERTANTIGHIANGESIDIUM (INFERTANTIGHIANGESIDIUM) REPETANTIGHIANGESIDIUM (INFERTANTIGHIANGESIDIUM) REPETANTIGHIANGESIDIUM (INFERTANTIGHIANGESIDIUM) REPETANTIGHIANGESIDIUM (INFERTANTIGHIANGESIDIUM) PROPERTIGHIANGESIDIUM (INFERTANTIGHIANGESIDIUM) PROPERTIGHIANGESIDIUM (INFERTANTIGHIANGESIDIUM) PROPERTIGHIANGESIDIUM (INFERTANTIGHIANGESIDIUM) REPETANTIGHIANGESIDIUM (INFERTANTIGHIANGESIDIUM) PROPERTIGHIANGESIDIUM (INFERTANTIGHIANGESIDIUM) PROPERTIGHIANGESIDIUM (INFERTANTIGHIANGESIDIUM) PROPERTIGHIANGESIDIUM (INFERTANTICHIANGESIDIUM) PROPERTIGHIANGESIDIUM (INFERTANTICHIANGESIDIUM) PROPERTIGHIANGESIDIUM (INFERTANTICHIANGESIDIUM) RESPONSANCE (INFERTANTICHIANGESIDIUM) PROPERTIGHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPETANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPOTANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPOTANTICHIANGESIDIUM (INFERTANTICHIANGESIDIUM) REPOTANTICHIANGESIDIUM (INFE		***************************************		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Neposible nuclectide insertion				Codon /=possible nucleotide deletion.
I IR PERTAMNITIANGIS KONTOPTITIM VISION SS EEGPET VOYS. RHYDYDTSEGUL IMINSHIP KANTY PERDAPKSOTT CSSECSSAS ODS SSARPESET EDULHEDLIH CARCHES CTSST TURNING INVEYOR VEX YES TO THE CONTROL OF THE CONTROL O			sequence	\-nocsible nucleotide insertion)
RRHUDRTSBOULENRISHBYKKHYPHEDAPKSGTSCSSRCSSRC OSSEARPRESETEDU/WEGLIKCSGTSCTSTUSMIQING VEKSTRODPFKQSHLPMLBSSHCOLEKISATWERNDCKKADM VLBISGMINNEVSHIGHT OF THE VERSIC STETUS OF TOLEGULTARISASELYVIA PGSMEDVIVLSMVII S PVURVSLUM T PEPLLCVARRTY KOVIM THE SEVURVSLUM PFELLCVARRTY KOVIM THE SEVURVSLUM PFELLCVARRTY KOVIM THE SEVURVSLUM PFELLCVARRTY KOVIM THE SEVURVSLUM THE SEVURVSLUM THE SEVURVSLUM THE PROBLEKT SATURE OF THE VERSIC SETUS OF THE VERSIC SETU		sequence		TODORNAL DICOLOGICA TRANSPORTATION OF THE TOTAL OF THE TO
OSSEARPESETEDVIMEDLIHCAECHSSCTSSTTVENRIQINVE VKEYEDDPFROSHIPMISSISPICIEKISAITWEGNEKKADME VLEISGMIMMINVASHIPGIGYGIFGMAVSLIJGLIFFEVERLSON TILEGULTHARSASILVATAFOSMEDVIVLSMVIIS FYVEYLSVAN TEPETLUCHAERIS STEUSTENGGINDE VKENTERSGULENRESHEKKEHYENDAPPE SGTSCSSCSSSCROSSSARPESSTEDVIMMISSIPGIGYGIPGMAVSLIJGLIFFEVERLSON STOURNIGHD VKENTERSGULENRESHEKKEHYENDAPPE SGTSCSSCSSSCOSSSARPESSTEDVIMMISSIPGIGHERISAIT WERDENCKKADMENT STEUTHMINGHASHPELEKISAIT WERDENCKKADMENT STEUTHMINGHASHPELEKISAIT WERDENCKKADMENT STEUTHMINGHASHPELEKISAIT LISEFVENSVAN THE PELLUCHARTYKOVIM INSPECTION OF THE PERLUCHARTYKOVIM STEUTHMINGHASHPEL		•		PRINCIPAGE AND TO THE PROPERTY OF THE PROPERTY
VIKESYEDDPEPGSHLEVELBSSEPGLEKESALVWERNDCKKADM VLBISGMIMMRVSBILEGIOTOT GENEVALVILSWULTSPVURSLUM TDLEQUITAHSASELVYLAFGSNEDVILSWULTSPVURSLUM FFELCVAREPTYKOVIM THESGULBINKSHINKYKHYKHYPRIDAP SGTSCSSRCSSRCOSSARPESETEDVILWEDLLICAECHSSCI SETDVERNIGINE OVIKES PRODPETGISELWKSHINKYKHYPRIDAP SGTSCSSRCSSRCOSSARPESETEDVILWEDLLICAECHSSCI VWEGNDCKKADMSVLEIGORIMNTWISHIPOLOTYCIRGNAVSLI LGITPFVERLSQATDLEQUITAHSSAELYVILAFSSNEDVILVISM LGITPFVERLSQATDLEQUITAHSSAELYVILAFSSNEDVILVISM LGITPFVERLSQATDLEQUITAHSSAELYVILAFSSNEDVILVISM ILSVURVSLWWITFFLLCVARETYKOVGIN MASKYTDALVWYCKKIGATDOQTHEKSVEPETKGERRKKHYKKYPKTD RWMLQVTSKVIFFNLLOVILLUQAAUTUFCSTSS PHSTEITTKY GIVHAMLLGTVISCOVITYSTREVERPSTGERRRKKHKAAHLEE HREGDGSSTTDNTOGRAVQRHGTSTSHSVGTVERLUMBAFFLE GSKAKANSIDKSTETINONYSLOKATVVISGESEG JOHNEOCE: IPPEETAMNTGTLRNOPSKUTGRTITINVSDEVSSEEGFETGYSI RHYDRTSSGVLIKRKSSHYKKHYPRODAPHSTSCSSRCSSSI QOSSSARPSSTSDVLWBDLLICAECHSSCTSSTDVENHGINDV VKEYEDDPFIGGSHLWMISSHPELGERISALVWENDCKKADM VLEIGONINNWSNIHPOLOVILSWMIISFVVVSLOW FEYLLCVARPTYKOVOIN*TSSGVLRANSLHIKKKHYNNEDDP SGTSCSSRCSSRGOBESARPSSETEDVLWBDLHAGACKKADM VLEIGONINNWSNIHPOLOVILSWMIISFVVVSLOW FEYLLCVARPTYKOVIN*TSSGVLRANSLHYKKKYNNEDDP SGTSCSSRCSSRGDBESARPSSETEDVLWBDLHAGACKKADM VLEIGONINNWSNIHPOLOVILSWMIISFVVVSLOW FEYLLCVARPTYKOVIN*TSSGVLRANSHYKKKYNNEDDP SGTSCSSRCSSRGDBESARPSSETEDVLWBDLHAGACKKADM VLEIGONINNWSNIHPOLOVILSWMIISFVVVSLOW FEYLLCVARPTYKOVIN*TSSGVLRANSHYKKKYNNEDDP SGTSCSSRCSSRGDBESARPSSETEDVLWBDLHAGACKKADM VLEIGONINNWSNIHPOLOVILSWMIISFVVVSLOW FEYLLCVARPTYKOVIN*TSSGVLRANSHYKKKYNNEDDP SGTSCSSRCSSRGDBESARPSSETEDVLWBDLHAGACKKADM VLEIGONINNWSNIHPOLOVILSWMIISFVVVSLOW FEYLLCVARPTYKOVIN*THEOLOVILSWMIISFVVVSLOW FEYLLCVARPTYKOVINNSHYDFOLOVILSWMIISFVCHADCHADA SGTSCSRCSSRGDBESARPSSETEDVLWBDLHAGACKGCGGGGGTGAALTLANG VLEIGNAMSHAANTANSLIGGEBLAGATVANSHIPOLOVILSMMIISFVCHADCHADA TURVERSPENDARTHANSHYNDACHADHAGACHADA FEYNANTOLUTAHAGACHADA FEYNANTOLUTAHAGACHADACHADACHADACHADACHADACHADACHADA				RRHVDRTSEGVLRNRKSHHIKKHIPNEDAPRSGISCSSRCSSSR
VLBISGMINNRVSHIPGIGYQIFGNAVSLIGJUTPFVFRISQUIN TDLEQUITAHASSELVYLIAGSNEDVIVLSMVI IS FVORVSLVMI FFFILLCVARRTYKQVGINM*TSEGVLRMRKSHHYKKHYPNEDAP SGTGCSSRCSSSGOSSARPSEFTEOVLMEDLIAGCHSSCI SETDVRNHQINPCVKKEYRDDPFHQSHLPMLHSSHPGLEKITA VWEGNDCKKADMWYLGISGMINMRVNSHIPGIGYGYGIGNAVSLI LGLPFPYPELGQATDLEQLTAHASAELYVLAGGNEDVIVLSM IS FVVAVSLAWF FFFILLCVARSTYKQVGIN MASKYTDALVMYQKKIGAYDQQUWESSVEGREIKGLANKYKAL LGLPFPYPELGQATQLEQLTAHASAELYVLAGGNEDVIVLSM IS FVVAVSLAWF FFFILLCVARSPYTKACUTR WARDALVMYQKKIGAYDQQUWESSVEGREIKGLANKYKAL HOURDLADVALOMASAPAKATPURDLATVAGNET KALLANKYKAL GENIMMLQYTSKVIFPULLVILLQVARITYHDLAGNETURVYPPPPF RWWLQYTSKVIFPULLVILLQVARITYHDLAGNETURVAGNET GENIMMLGATHQQUYSTFFYHDLAGNETURKALHAF GSKKARNSIDKSTETINGTYSLLQKKTYKAGEDGIOHAHAPFIL GSKKARNSIDKSTETINGTYSLLQKKTYKAGEDGIOHAHAPFIL GSKKARNSIDKSTETINGTYSLLQKKTYKAGEDGIOHAHAPFIL GSKKARNSIDKSTETINGTYSLLQKKTYKAGEDGIOHAHAPFIL GSKKARNSIDKSTETINGTYSLLQKKTYKAGEDGIOHAHAPFIL GSKKARNSIDKSTETINGTYSLLQKKTYKAGEDGIOHAHAPFIL GSKKARNSIDKSTETINGTYSLLQKKTYKAGEDGIOHAHAPFIL GSKARNSIDKSTETINGTYSLLQKKTYKYGEDGIOHAHAPFIL GSKARNSIDKSTETINGTYSLLQKKTYKYGEDGIOHAPPICTSCI RHYDRTSEGVLRRRKSHHYKKTYNEDDAYGSSSEGPETOYIS RHYDRTSEGVLRRRKSHHYKKTYNEDDAYGSSSEGPETOYIS GNESAPPSSETEDVLWEDLLAGKGNISTSTYDKRIGINFP VKKEYRDDFHQSILLPHLRSHSHGILEKISAITWRKNIGHTAPPICLAGENAS STISCSSRCSSSRQDESSARPSSETEDVLWEDLLAGCRESTSABO VKEYRDDFHQSARDVAKTYNOVIMTSSERPICHEKISA VWEGNDCKKADMSVLEISGMIMNRVSSHIPGIGYQIFGRUSLL LGHIPFYFYTANACHYDDLQQFSMAPPICHYDLAGCAR VKEYRDDFHQSARDVAKTYDDLQQFGSMAPPICHSBUSHTYLLS LGHIPFYFYTANACHYDDLQQFGSMAPPICHSBUSHTYLLS LGHIPFYFTYAGATTAKGSSLLTPLTTDUHGGCAEFFASAB VALGFSGPHALAAFPAMCTODEGILFFTLTTGSAFEDVIVLSM LGHIPFYTYAGATTAKGSSLLTPLTTDUHGGCAEFFASAB VALGFSGPHALAAFPAMCTODEGILFFTLTTGSAFEDVIVLSM LGHIPFYTTALVEKCQGTVLLIHNSVEVADGGPHEV HIAMBRLEISVDAYFTAGSLEDATGHAFRYNDAMSRAPH GSEDTSDDLVLEVSTYGGAPATHIAGSSLLTPLTDUHGGCAEFFASAB VALGFSGPHATGATAGSSLATARGSAFATAGARHYCPPTLDLHEAER SQUASSFFTANACHYTAGAGAAFMTILAGGAMPHIA GRENDLYBAGAAFMTATAGAGAAFMTILAGGAMPHIA GSEDTSDDLVLEVSTYDQHAFATAGAGAAFMTILAGGAMPHIA GSEDTSDDLVLEVSTYGGAPATAGAGAAFMTALAGAGAMPHIA GSEDTSDLVL				QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC
TDLEQUITARISASELYVILAFGSNEDVITLISWVITSTYVRVSUVAL FEPLLCUARRYTYKOVOIN **SEGULVERKENHIKKHYPREDAPP SGTGCSSRCGSSRQDSESARPESETEDVLWEDLLHCACCHSSCT SETDVENHIGH POCKKEYRDDPFOSILPHLLISK PLEKKISA VWEGNDCKKADMSVLETGGMINNEVNSHIPGIOYOI FGRAVEL LLUIPPFYFELSQATDLEQUITARISASELYVITAFGNEDVIVISM LLUIPPFYFELSQATDLEQUITARISASELYVITAFGNEDVIVISM LISPFVALOVAGENDCKADMSVLETSGMINNEVNSHIPGIOYOI FROM THE SEVERGRET KGLENKOKKTY RYKODLIDUDLYRGSAFAKARPESPWTSLITKGIVRVVFPFFF RWWLQVTSKVIFFFHLOVASETYKQUTM HEROGOGSTTDNTQCGAVQNNGTSTSHSVOTVFRDAPPH PROMINDLYRGSAFAKARPESPWTSLITKGIVRVVFPFFF RWWLQVTSKVIFFFHLOVASETTHOPESTGCARRACHARMISM HEROGOGSTTDNTQCGAVQNNGTSTSHSVOTVFRDAMHARD KARRAMISM HEROGOGSTTDNTQCGAVQNNGTSTSHSVOTVFRDAMHARD KARRAMISM HEROGOGSTTDNTQCGAVQNNGTSTSHSVOTVFRDAMHARD KARRAMISM HEROGOGSTTDNTQCGAVQNNGTSTSHSVOTVFRDAMHARD VKKERDDFFNGSKLIVMLASSHCHEVNIFNEDAPKSTGCSSRCSSSI QOSSASAPESETEDVLWENGKKTVKSGEDGT QNHED QUE IRPETAMNTOTLENOFS KOTQCTTTMVSDEVSSEEGPFTVG SRRAMINDRINGSHSTRINGVRAMHARD VKKERDDFFNGSKLIVMLASSHCHEKISATIVENDAMKSTGCSSRCSSST QOSSASAPESETEDVLWENGENGKAMM VKERTODFNGSKLIVMLASSHCHEKISATIVENDAMKSHCHEVAND VKKERDDFFNGSKLIVMLASSHCHEKISATIVENDAMKSHCHEVAND VKKERDDFFNGSKLIVMLASSHCHIVKHAYPNDED KARDAMISM STORGASSACSST SETDVENHOLD CVKKYKDDDFFNGSKLIVMLASSHCHIKKHYPNDEAD KARDAMISM STORGASSACSST SETDVENHOLD CVKKYKDDDFFNGSKLIVMLASSHCIVTAFGSNEDVITLISM LLUITPFVFRLSQATOLGCTAHARSSLLVVIAGGSNEDVITLISM LLUITPFVFRLSQATOLGCTAHARSSLLVVIAGGSNEDVITLISM LLUITPFVFRLSQATOLGCTAHARSSLLVVIAGGSNEDVITLISM LLUITPFVFRLSQATOLGCTAHARSSLLVVIAGGSNEDVITLISM LLUITPFVFRLSQATOLGCTAHARSSLLVATAFGSNEDVITLISM LLUITPFVFRLSQATOLGCTAHARSSLLARLITPDUHGGCALEFSAGAVANDAM AKRADAMISM SACRAMIS		ì	İ	VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
FFFLLCVARRITYKQUZINH*TSEQULRNKKSHHYKKHYPREDS SGTSCSSRCSSRQDESARPESTEPOUMEDLLHCAECHSSCT SETUVRNHQINPCVKKEYRDDPPHQSHLPMLHSBHPGLEKIS SETUVRNHQINPCVKKEYRDDPPHQSHLPMLHSBHPGLEKIS VWEGNDCKKADMWSLRIGGMINMRVSHIPGIGVTQYTGRAVSLI LGIPPPYPELSQATDLEQLTAHSASELYVTAFGSNEDVIVLSM 11SPVVRVSLWHIPPLLCVLSHEVTYROGTH MSKVTDALIVWTQKKIGAYDQQIMEKSVEQREIKGLRNKOKKTI HVKDPLIDVDLVRGSAFAKAPPSSWTSLTTKGIVRVVPPFPFP RWLQVTSKVIPTFLLVYLLEQVANIVLFSTSSBHSIDLTKU GPIMMLLGTYHQIVSTRTPKPPLSTSSBKSTLTKGIVRVVPPFPFP RWLQVTSKVIPTFLAVILVSLUQVANIVLFSTSSBHSIDLTKU GPIMMLLGTYHQIVSTRTPKPPLSTSGKRRKLKRAAHLEE HREGGGSSTIDNTGGAQOMIGTSTSHSVTYKRAHHAAFFLL GSKKARNSIDKSTTINNGVSLDGKKTVKSGEDGIQNHEPGCF IRPESTANNTGILRNGPSENDGYSTINNSVSLSSEGPFTGYSI RRHUDRTSGGVLRNRKSHYKKHYPNEDAPKGGTSCSSRCSSS QOSSSAPPSSTEDVLWBDLLHGAGKSSTSTSSTVSTNHQIND VKKEYRDDPFHQSILDWLLSSHGGLEKISAIWEGNDCKKHOW TULEQGMINRVSSHTYKHYPNEDAPKGGTSCSSRCSSS QOSSSAPPSSTEDVLWBDLLHGAGHSSGTSSTVSNHQIND VKKEYRDDPFHQSILDWLHSSHGGLEKISAIWEGNDCKKHOW TULEQGMINRVSSHTJOFFHGSHLDWLHSSHGGLEKISAI VEGNDCKARDWSTHJOFFHGSHLDWLHSSHGGLEKISAI VEGNDCKARDWSTLJSGMINNKVSSHIFGIGTGYIPANNVSL LGITPFYFRISQATDLEQUTAHSASELYVLAGGSNEDVIVLS STINCSRCSSSRCSSSRCDGSARPSSETEDVLWBDLLHCABCKSC SETDVENHQINPCVKKEYRDDPFHGSHLDWLHSSHGCIEKISTQ TORANVSL LGITPFYFRISQATDLEQUTAHSASSLIVTLRGSNEDVIVLI LTVVKGWATLSVOGFINASSAVPQAPLEVPFYGGFTQTFTGNAVSL LGITPFYFRISQATDLEQUTAHSASSLIVTLRGSNEDVIVLI LTVVKGWATLSVOGFINASSAVPQAPLEVPFYGGFTQTFTSHANAL LGITPFYBLISQATDLEQUTAHSASSLIVTLRGGNEDAPKHLLLLLA RRGDFFTGHTANSLIGGCGFTLLHSDSIPHT LTVVKGWATLSVOGFINASSAVPQAPLEVPFYGGFTQTFTGNAVSL AGGSTSDGDLVLEVSTTARVPHSCLLRRDFTDFTLSGGDAPAGAPKH HIGHRLGTPRATASLIGGCGTTLLHSDSTPTTLSGGDAPAGAPKH HIGHRLGTPRATASLIGGCGTTLLHSDSTPTTLSGGDAPAGAPKH HIGHRLGTPRATASLIGGCGTTLLHSDSTPTTLSGGDAPAGAPKH AGGREGGEREEDDAYGGFTATASLGGCGTTLLHDOLAGARKY VSGGLAPBATTLABLIGGCATALTANDLAGGAPKYTTLAGGAPAGAPKH LSVETNAVGGDAVLSTDTQHARATARVTAHLLAGGAPATLT VSGGLAPBATTLKVALRFATLGTHSGGSTAVVCGGPAQLGAR PPPTHYEVQAAGGAPKTTLAVLATRATARTYCHLIGGTDADAGARTYT VSGGLAPBATTLATLENGARAFTTATHLEATTLERGG PPPTHYEVQAAGGAPKTALTAVTROLIGGDAPTATALLBOTAGGRE TODAAFSGGAPGAAGAATALSVAGGAPATALLBOTA		1	1	VLBISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
SSTECSSRCSSSRQDSESARPSESTEDULMEDLLHCAECHSCT SETDYRNHQIN PUCKKERNDDPHQSILPHALISEDIKATSA VUERONCKKADMSYLEIGEMINNEVNSHIPGIGYQIFGRAVSI LICHTPYPRISQATDLEQUTHASABELYVITASSREDVIVISM IISVVRYSLWWIFFFLLCVAERTYXQVGIM MASKYTDAIVWYGKKIGAYDQIWEKSYGRBIKGIRKOKAPKTY HYKPDLIDVDLVRGSAFAKAKPBSPWTSLTTKGIRVWYFFFFF RWWLQVTSKVIFFMLUVIYLLQVAAITU-CSTSSPHSIPLTKGIRVWYFFFFF RWWLQVTSKVIFFMLUVIYLLQVAAITU-CSTSSPHSIPLTKGIRVWYFFFFF RWWLQVTSKVIFFMLUVIYLLQVAAITU-CSTSSPHSIPLTKGIRVWYFFFFF RWWLQVTSKVIFFMLUVIYLLQVAAITU-CSTSSPHSIPLTKGIRVWYFFFFFF RWWLQVTSKVIFFMLUVIYLLQVAAITU-CSTSSPHSIPLTW-CSTSSPHSIPLTW-CSTSSPHSIPLTW-CSTSSPHSIPLTW-CSTSSPHSIPLTW-CSTSSPHSIPLTW-CSTSSPHSIPLTW-CSTSSPHSIPLTW-CSTSSPHSIPLTW-CSTSSPHSIPLTW-CSTSST-CSTSCSSRGSSISSISSISSISSISSISSISSISSISSISSISSISSI				TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
SETUVENHOINPCVKKEYRDDPFHQSHLPMLHSSHPGLEKEYS VWEGNDCKKADMSVLEISGMINKRVNSHIFGIGVGYGTGNAVSLI LGLIPPFYPELGOATDLEGLTHASAGELYVTAFGGNEDVIVLSM ISPVAVSLUMF FFILLCVARGETYKYQGUM SETVAVSLUMF FFILLCVARGETYKYQGUM WASKYTDAIVWYQKKIGAYDQQUMEESVEGREIKGLENKPKAD HVKDDLIDVDLVRGSAPAKAYDGSPWTSLTKKGUTVAVPPPPFI HVKDDLIDVDLVRGSAPAKAYDGSPWTSLTKKGUTVAVPPPPFI HVKDDLIDVDLVRGSAPAKAYDGSPWTSLTKKGUTVAVPPPPFI HVKDDLIDVDLVRGSAPAKAYDGSPWTSLTKKGUTVAVPPPPFI HVKDDLIDVDLVRGSAPAKAYDGSPWTSLTKKGUTVAVPPPPFI HVKDDLIDVDLVRGSAPAKAYDGSPWTSLTKKGUTVAUHPPPFFI GSKKAKNSIDKSTETNOVYSLDGKKTVKSGEDGIGNHEGOG IRPEGTAMNTGILKNOPSKDTQATITNYSDEVSSEGOPETGYSI RHIVDRTSEGVLRRIKSHYKKHYNEDDAPKGGTSCSSRCSSS ODSSSAPPSSTEDVLMEDLLHGAGRGSGTSSSETDVENHGIND VKKEYRDDPFHQSILDWLHSSHPGLEKISAIVWEGNDCKKAND VLEIGGMINRVNSHIPGIGGVGFGAVSLLIGLTPFVFFLSQ TOLEGLTAHSABELYVIARGSNEDVIVUSHULIPPVFFLSQ STISCSSRCSSSRQDSSSARPSSTEDVLMEDLLHCAGETSCSS STEDVEHHQINPCVKGEYRDDPFHQSHLPWLHSHPGLEKISA VWEGNDCKKADDWSVLEISGMINKRNNSHIPGIGTQIFGNAVSLL LGHTPFYFRLSQATDLEGUTHASASSLTVIARGSNEDVIVIG SCTSCSSRCSSSRQDSSARPSSTEDVLWEDLLHCAGETSCS STEDVEHHQINPCVKGEYRDDPFHQSHLPWLHSSHPGILEKISA VWEGNDCKADDWSVLEISGMINKRNNSHIPGIGTQIFGNAVSL LGHTPFYRLSQATDLEGUTHASASSLTVIARGSNEDVIVIG SCTSCSSRCSSRQSSGARPSSTEDVLWEDLLHCHCEKISA VWEGNDCKADDWSVLEISGMINKRNNSHIPGIGTQIFGNAVSL LGHTPFYRLSQATDLEGUTHASASSLTVIARGSNEDVIVIG TLYVZGWATLSVOGFINASSAVPGAPLEVPYGLFYGGGTGLILLIDA ISFVAVSULWHIPFFLLCVAGCGTLLHSDBIPHTY LTVVZGWATLSVOGFINASSAVPGAPLEVPYGLFYGGGTGLILLIDA TLYVZGWATLSVOGFINASSAVPGAPLEVPYGLFYGGGTGLILLIDA TLYVZGWATLSVOGFINASSAVPGAPLEVPYGLFYGGGTGLILLIDA HLGHTSFTANASLIGGGEGLAURPATLIDABSIPHTY LTVVZGWATLSVOFFINASSAVPGAPLERPYDLGGAPEFSASD VALGFSGRGHLAAPTANASLIGGEBLAWDQGGALREALLTRIM AGCRLBEBEYEDDAYGHYRAPSTLABEAMPAMLIPPCVPEPB PPYFANFTQLITTISPLVVABGGTAHLBWRHVDGAGERFALDTRIM AGCRLBEESYEDDAYGHYRAPSTLABEAMPAMLIPPCVPEPB PPYFANFTQLITTISPLVVABGGTAHLBWRHVDLAGGGPHEW SSCLVPURRDQGGGATATLAURVAGGAARAFTILLDVANRARFTH LSVETNAWGGDEVATLSTDOGFTDATAGLEGALTATAN AFRIGDRYGGGWATLSTDOFHATAVDTVENLLAURGGBEN TDDAWFSBADAFRANALURARDAYVENLLAURGGRAUFT LLVVPGGGGGGLAGARANTTROLLIGGTDAGATALLBURDLANG SSCDMMBEVRG			ļ	FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAPK
SETUVENHOINPCVKKEYRDDPFHQSHLPMLHSSHPGLEKEYS VWEGNDCKKADMSVLEISGMINKRVNSHIFGIGVGYGTGNAVSLI LGLIPPFYPELGOATDLEGLTHASAGELYVTAFGGNEDVIVLSM ISPVAVSLUMF FFILLCVARGETYKYQGUM SETVAVSLUMF FFILLCVARGETYKYQGUM WASKYTDAIVWYQKKIGAYDQQUMEESVEGREIKGLENKPKAD HVKDDLIDVDLVRGSAPAKAYDGSPWTSLTKKGUTVAVPPPPFI HVKDDLIDVDLVRGSAPAKAYDGSPWTSLTKKGUTVAVPPPPFI HVKDDLIDVDLVRGSAPAKAYDGSPWTSLTKKGUTVAVPPPPFI HVKDDLIDVDLVRGSAPAKAYDGSPWTSLTKKGUTVAVPPPPFI HVKDDLIDVDLVRGSAPAKAYDGSPWTSLTKKGUTVAVPPPPFI HVKDDLIDVDLVRGSAPAKAYDGSPWTSLTKKGUTVAUHPPPFFI GSKKAKNSIDKSTETNOVYSLDGKKTVKSGEDGIGNHEGOG IRPEGTAMNTGILKNOPSKDTQATITNYSDEVSSEGOPETGYSI RHIVDRTSEGVLRRIKSHYKKHYNEDDAPKGGTSCSSRCSSS ODSSSAPPSSTEDVLMEDLLHGAGRGSGTSSSETDVENHGIND VKKEYRDDPFHQSILDWLHSSHPGLEKISAIVWEGNDCKKAND VLEIGGMINRVNSHIPGIGGVGFGAVSLLIGLTPFVFFLSQ TOLEGLTAHSABELYVIARGSNEDVIVUSHULIPPVFFLSQ STISCSSRCSSSRQDSSSARPSSTEDVLMEDLLHCAGETSCSS STEDVEHHQINPCVKGEYRDDPFHQSHLPWLHSHPGLEKISA VWEGNDCKKADDWSVLEISGMINKRNNSHIPGIGTQIFGNAVSLL LGHTPFYFRLSQATDLEGUTHASASSLTVIARGSNEDVIVIG SCTSCSSRCSSSRQDSSARPSSTEDVLWEDLLHCAGETSCS STEDVEHHQINPCVKGEYRDDPFHQSHLPWLHSSHPGILEKISA VWEGNDCKADDWSVLEISGMINKRNNSHIPGIGTQIFGNAVSL LGHTPFYRLSQATDLEGUTHASASSLTVIARGSNEDVIVIG SCTSCSSRCSSRQSSGARPSSTEDVLWEDLLHCHCEKISA VWEGNDCKADDWSVLEISGMINKRNNSHIPGIGTQIFGNAVSL LGHTPFYRLSQATDLEGUTHASASSLTVIARGSNEDVIVIG TLYVZGWATLSVOGFINASSAVPGAPLEVPYGLFYGGGTGLILLIDA ISFVAVSULWHIPFFLLCVAGCGTLLHSDBIPHTY LTVVZGWATLSVOGFINASSAVPGAPLEVPYGLFYGGGTGLILLIDA TLYVZGWATLSVOGFINASSAVPGAPLEVPYGLFYGGGTGLILLIDA TLYVZGWATLSVOGFINASSAVPGAPLEVPYGLFYGGGTGLILLIDA HLGHTSFTANASLIGGGEGLAURPATLIDABSIPHTY LTVVZGWATLSVOFFINASSAVPGAPLERPYDLGGAPEFSASD VALGFSGRGHLAAPTANASLIGGEBLAWDQGGALREALLTRIM AGCRLBEBEYEDDAYGHYRAPSTLABEAMPAMLIPPCVPEPB PPYFANFTQLITTISPLVVABGGTAHLBWRHVDGAGERFALDTRIM AGCRLBEESYEDDAYGHYRAPSTLABEAMPAMLIPPCVPEPB PPYFANFTQLITTISPLVVABGGTAHLBWRHVDLAGGGPHEW SSCLVPURRDQGGGATATLAURVAGGAARAFTILLDVANRARFTH LSVETNAWGGDEVATLSTDOGFTDATAGLEGALTATAN AFRIGDRYGGGWATLSTDOFHATAVDTVENLLAURGGBEN TDDAWFSBADAFRANALURARDAYVENLLAURGGRAUFT LLVVPGGGGGGLAGARANTTROLLIGGTDAGATALLBURDLANG SSCDMMBEVRG		ļ		SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
WEENDCKKADMSVLEISGMINNTVINSHIPGIGVGIFGANASL LIGHPFYFELGANTARGASHEVIJARGANEV				SETDVENHOINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
LILIPPYPELSQATDLEQUTAHSASELYVIAFGSNEDYTVISM 1159YWYSKIGAYDQQIMEKSVEQREIKGLENKPKKT HVKDDLIDVIDVRGSAPAKAXPESPWTSLTTKG UTRWYPPYPEY RWMLQVTSKVIFFHLLVILLQVAAIVLFCSTSSPHSIPLTEV; GFIMMLLGTHCQIVSTRTEKPPLSTGSKRRKLRKAALEN HREGOSSTIDNTOGGAVGMTSTSHSWYGTYFRDUMHAAFFL GSKAKNSIDKSTETDNGYVSLDCKKTVKSGEDGIOMHPQCE: IRPETAMNTGTLRNGPSKJOTGRT ITAVSDEVSSEEGPTGYSI RRHVDRTSGAVLRNKSHHYKKHYPBDAPKSGTGSSKGSSS QOSSSARRESTETDVLWEDLLCARCHSSTSTETDVENNOINP VKKEYRDDPFHQSHLPWLHSSHPCLEKISALVWGONDCKKADM VLEISGMIMRRVMSHIPCIGYGIFGNAVSLILGLTPPVFRLSQ TOLGCUTAHSASELVLTAFGSNEDVIVLBWAISIFVYRGUN FPFLLCVARETYKQVGIM*TSSGVLRRKKHHYKKHYPBDAP FFFLLCVARETYKQVGIM*TSSGVLRRKKHHYKHYPBDAP SGTSGSGRGSSSRQDSSSARPSETEDVLWEDLLHCAECHSSC SETDVENNOINPCVKKEYRDDPFHQSHLPWLHSSEPDVIVLSM LIGHTPVFRLSQATDLEQUTAHSASELYVLAGGSNEDVIVLSM LIGHTPVFRLSQATDLEQUTAHSASELYVLAGGSNEDVIVLSM LIGHTPVFRLSQATDLEQUTAHSASELYVLAGGSNEDVIVLSM LIGHTPVFRLSQATDLEQUTAHSASELYVLAGGSSEDVIVLSM LIGHTPVFRLSQATDLEQUTAHSASELYVLAGGSSEDVIVLSM LIGHTPVFRLSQATDLEQUTAHSASELYVLAGGSSEDVIVLSM LIGHTPVFRLSQATDLEQUTAHSASELYVLAGGSSEDVIVLSM LIGHTPVFRLSQATDLEQUTAHSASELYVLAGGSSEDVIVLSM LIGHTPVFRLSQATDLEQUTAHSASELYVLAGGSSEDVIVLSM LIGHTPVFRLSQATDLEQUTAHSASELYVLAGGSSEDVIVLSM LIGHTPVFRLSQATDLEQUTAHSASELYVLAGGSSEDVIVLSM LIGHTPVFRLSQATGHANALTDLDLQLQFSMSQBEALLLLAA PADHLLLQLYSGHGLVRLVLGGGSELQTFASTLDLAA PADHLLLQLYSGHGLVRLVLGGGSTULLHNSVPVALDGQHEVS HINAHELBISTDOPPTHSRGVLSVLERPSGAPLAPGADELPGFLFFOYLG RRGDF1YDDFECHLRAVVEKGGGTVLLHNSVPVALDGQHEVS HINAHELBISTDOPPTHSRGVLSVLERPSGLAFLAGGADAPLAF AGGRLEEESTEDDOPPTHSRGVLSVLERPSGLAGGAPLAFPAGA HLQSHRLULFUNSTATARVFRSCLLRGGTGTLDLMCARAFT GSGDTSDQLVLESVYTARVFRSCLRGGGTCDDLAGGAPLFOYLG SGLDFVERDCDGFATLSTVARGGAPADAPLTRATALAGLAGSAMPLIP LSVETNAVGQDVSVLPRVTGALPGGTALLFPCVLGGGPGDLTTGVLG SSGLPVERDCDGFATLSTVALGGFTCDDLTGARPTYT TARASSAVEDTFRFSVTAPPYFSCLRGGGTLAGGAPADAPLTT TARASSAVEDTFRFSVTAPPYFSCLRGGGTCDDLTGARPTYT TARASSAVEDTFRFSVTAPPYFSCLRGGGTCDDLTGARPTYT TARASSAVEDTFRFSVTAPPYFSCLRGGTVAGGPGADAPLTT TARASSAVEDTFRFSVTAPPYFSCLRGGTVAGGPGATALLEVAGG SSCMMMERVGGVFAVAGGGGGTLDTAVLLLTATLLATLAGGEVYHYH AGFRMGUVRAGGFATAFGGAPADALLTVRINGSTSVA		{	1	VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYOIFGNAVSLI
115FYVRVSLWVIFFFLLCVARRTYKQVJIM MASKYTDAJVWYQKKIGATVQQIMEKSVEQRBIKGLENKPKKY HVKPDLIDVDLVRGSAPAKAXPESPWTSLITKG IVRVVFPFFF RWWQVTSKVIFFHLUTLLLQVAAIVFCSTSS PHSIPLTEV; GPIMMLLIGTHOLTVTSKTPSFTSGKRRKKRAALBEI HREGGGSTTDNTOBGAVQNHGTSTSBSVGTVFRDLWHAAFFL GSKKAKNSIDKTVTSKOSEGDIQNHEPQCS; IRPETANNTG'LRNGESKDTQRTITMVSBGEDIQNHEPQCS; IRPETANNTG'LRNGESKDTQRTITMVSBGSGBGIQNHEPQCS; RRHVDRTSBCVLRNRSKHHYKKHYPNGDAPKSGTSCSSKCSS; QUSBSARPESETEDVLWEDLLHCABCUSSCTSETDVENHQINP VKKEYRDDFFHGSHLDWILSSHPGLEKISAIVWEGNDCKKADM; VLEISGMINMRVNSHIFGIGYQIFGNAVSLILIGUTPFVFRLSQ; TDLEQLTAHSABELYVIAPGSNEDVIVLSMVIISFVVRSUW PFFLLCVARETYKQVGIM*PSSGVLRNKSHHYKKHYPNEDAP; SGTSCSSRCSSSRODSSARPSSETEDVLWEDLLHCABCHSSC SETDVENHQINPOVKKEYRDDFPHOSHLDWISHGELHCABCHSSC SETDVENHQINPOVKKEYRDDPFHOSHLDWSHIPGIGYQIFGNAVSL LGITFFVFRLSQATDLEQLTAHSASELYVIAPGSNEDVIVLSM LGITFFVFRLSQATDLEQLTAHSASELYVIAPGSNEDVIVLSM LGITFFVFRLSQATDLEQLTAHSASELYVIAPGSNEDVIVLSM LGITFFVFRLSQATDLEQLTAHSASELYVIAPGSNEDVIVLSM LGITFFVFRLSQATDLEQLTAHSASELYVIAPGSNEDVIVLSM LGITFFVFRLSQATDLEQLTAHSASELYVIAPGCABFSASD VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAPQAG RGDBTIYODTFEGHLRAVVERGGETVLHNSVYPAGQQHEVS HINARELE ISVOQYFHITSRGVLLAFERGABFSLLDGLABASA HLQEHRIGLTPEATMASLLCCMEDLSVNGQRRGLERALITRIM AGCRLEEEEVEDDAYGHHAFSTLAFERAPMELEPECVPERG PPFAMFTQLLTTSPLVVARGGTARLBKRRVQTTLDJUNRABFIR GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLDTQVIACAFA GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLDTQVIACAFAQLA HILGPRIGHTGWHAFLAFELAFACAGA GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLDTQVIACAFAQLA HILGPRIGHVGLLGSTGLAGGGSAMPILAP LSVETNANGGQDVSUFBYTGALDFGCRAFAGABFLATAMA AFIQRDVEQGRAYTLSTDPGHAYDTVENLALEEVGABBMILAP HILFPGSLAVILBLETGVPURDLAGTLARAGERGLTPQVLG SSCLPVERGYQGVSUFBYTGALPGGSAMPILAP LSVETNANGGQCUSVLFTALDFGCGAFTGLDGTQAGATTTATALEATLERAGE PPTTHRVVWALREBELHTAMVULTAHLDTALEATLERAGE PPTTHYTORTWHALREBELHTAMVULTAHLGTAHLBATLERAGE PPTTHYTORTWHALREBELHTAMVULTAHLGTAHLBATLERAGE PPTTHYTORTWHALLBELHTAMVULTAHLGTAHLBATLERAGE PPTTHYTORTWHALLBELHTAMVULTAHLGTAHLBATLERAGE PPTTHYTORTWHALLBELHTAMVULTAHLGTAHLBATLERAGE TTDDVAFSORGGVATALLBVQASICAPTHYTYTHALBATLERAGE TTDDVAFSORGGVATALLBVQASICAPTHYTHA				LGLTDEVERLSOATDLEOLTAHSASELYVTAFGSNEDVIVLSMV
194 1833 MASKYTDALYWYOKKIGAYDQGINEKSVEQREIGURNYFKPFINUKPDLIDULDURGSAPAKARDESPWSILTGURVYFFPFIR RWLQVTSKVIFFHLULVILLQVAAIVIFCSTSG PHSILTEV. GPIHMILLGTVHCQIVSTRTPKPPLSTGKRRRKLRKAAHLES HREGOGSSTIDNTDEGGVONNETSTSISVGTVFROLMHAAFFLE GSKAKAKSIDKSTETDOKYVSJOCKKTVKSGEDGIONHBQCE: IRPETAMNTGTLRINGSKJOTRITTNYSDEVSSEEGPETGYSI RRHUDRTSEGVLRNNKSHHYKKHYPNDAPKSGTSCSSRGSSI QUSSSARPESFTEDVLWEDLLGARCHSSTSTETDVSNNQIND- VKKEYRDDPFIGSHLPWILSSPECLEKISAIVWEGNOCKADM. VLEISCMIMNRVNSHIPCIOKQTDENVSLILGITPFVFLSGG TOLGQUTAHBASELYVLAPGSNEDVIVLSMVIISFVVVSUVM PFFLLCVAERTYKQVGIM*TSSGVLRNRKSHHYKKHYPSDAP SOTSCSSRGSSSRQDSSSARPESFTEDVLWEDLLHCAECHSSC STETUBHNQIND*CVKKEYRDDPFHGSHLPWILSSPHDLEKISA VWEGNDCKKADMSVLEISGHNRVNSHIP IEGGVQIFGNAVSL LGITPFVFRISQATDLEGUTAHSASELYVLAPGSNEDVIVLSM 15FVVRSVLSWMFFFLLCVAERTYKQVGITFGNAVSL LGITPFVFRISQATDLEGUTAHSASELYVLAPGSNEDVIVLSM 11FFVVRSVLSWMFFFLLCVAERTYKQVGITFGNAVSL LGITPFVFRISQATDLEGUTAHSASELYVLAPGSNEDVIVLSM 11FFVVRSVLSWMFFFLLCVAERTYKQVGITFGNAVSL VALGTSGFBLALGLARPAMYCDDETLEFILTTDSRQAPLAPQAG RRGDFIYDDLFEGHLARVNKRGGGTVLLHNSVVLADGQPHEVS HINARIELISUDOYPTHYSRGVLSVLEPSFSADD VALGTSGFBLAAFPAMYCDDETLEFILTTDSRQAPLAPQAG RRGDFIYDDLFEGHLARVNKRGGGTVLLHNSVVLADGQPHEVS HINARIELISUDOYPTHYSRGVLSVLEPSGLIGGIDABAS HLOBHRULLFBRATVASLLCGMBDLSVNGGRRGKLRELITGNM AGCRLEEEEYEDDAVGHYBFSTLAFERSTLERGELIGGIDABAS HLOBHRULLFBRATVASLLCGMBDLSVNGGRRGKLRELITGNM AGCRLEEEEYEDDAVGHYBFSTLAFERSTLERGVLYVRCGGPAQDLTF USDGLQASPPATLKVVATRPAIQIHRSTGLRAGGSANPILPP LSVETNAVGQUSVLFSVTACHAPFSTLAFERSTGVFQVAEGTVGVLG SSGLPVERRODGEPATSFCRLARGSLVYVRCGGPAQDLTF VSDGLQASPPATLKVVATRPAIQIHRSTGLRAGGSANPILPP LSVETNAVGQUSVLFSVTACHAPFSCLRAGGVTLODAGRAFTYT TARASSAVEDTFFRYTAPFYFSPLTTPFHLIGGDDAPVITT TARASSAVEDTFFRYTAPFYFSPLTTPFHLIGGDAPVITT TARASSAVEDTFRYTTSFTTBLLRAGGSAVPTLERAGG PFTFHYEVYGAPRKONLOLGOTRLSFTGGTGVAGEMMAN TODKTTMTTSFTNEDLLEGRIVVQHDSETTEDDITFRITYT TODVAFSTANDLSFTHVSFTSFTTTPTHTAGGDEVTYPT TODVAFSTANDLSFTHVSFTSFTTTPTHTAGGDEVTYPT TODVAFSDANGGLARGROUNDLAVITSRUGGSTVANDERPRIYT TODVAFSDANGGAFADAGLULTSRUGLFGSTVANDEPRIYT TODVAFSDANGGAFADAGLULTSRUGLFGSTVANDEPRIYT TODVAFSDANGGAFADAGLUL			1	TTCPWPVCTAWTFRETT.CVARPTVKOVCTM
HUKPDLIDVILVIRGSAPAKARPSPWTSLITKGLYRVFPFPF RWHLOYTSKVI FFWILLYLLQWAALVLCGTSS PHIS PLTEV. GPIWHMLLGTVCQIVSTRTPKP PLSTGGRRRKLRKAHLER HREGGGSTTDMTQSGAVQWRIGTSTSHVGVTFRDLWHAAFFL GSKKAKNS INKSTETDNOYVSLOKKTVKSGEDG IQMHEPQCE IRPESTAWNTGTLRNGPS KDTQRTITNVSDEVSS ERGPTGYSI RRHVDRTSEGVLRNRKSHYKKHYNDDAPKSGTSCSSKCSSI QUSESARPESETBULWEDLLHCAECHSSCTSETPURNIQINP VKKEYRDDPFRQSHLDWHLSSHDGLER ISA IVWBGNDCKKADM VLEISGMIMNRVNSHIPGIGYQIFGNAVSLIJGLTPPVFRLSQ TDLEQLTAHSASILVIAFGSNEDVIVLSMYIIS FVVRVSLVW FPFILCVABERTYNQVGIM*TSEGVLRNKSHYKKKHYPEDAP SGTSCSRCSSSRODSESARPESETBULWEDLHFWLHSSHPGLEKISA VMEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSL LGLTPFVFRLSQATDLEQLTAHSASILVIAFGSNEDVIVLSM LISFVRVSLWHIFFFLLCVAERTYKQVGIM SGTSCSRCSSSRODSEGARPESETBULWEDLHFWLHSSHPGLEKISA VMEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYGIFGNAVSL LGLTPFVFRLSQATDLEQLTAHSASILVIAFGSNEDVIVLSM LISFVRVSLWHIFFFLLCVAERTYKQVGIM SGTSCSRCSSSRODSEGARPESETBULWEDLHVALGENELSEN VMEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYGIFGNAVSL LGLTPFVFRLSQATDLEQLTAHSASILVIAFGSNEDVIVLSM LISFVRVSLWHIFFFLLCVAERTYKQVGIM LTSFVRVSLWHIFFFLLCVAERTYKQVGIM LTSFVRVSLWHIFFFLLCVAERTYKQVGIM STAGNAPALAFON VALGTSGFHELAAFPAWGTODEGTLEFTLITGSRCAPLAFONA RRODFIYDJIFGHLAVALGQEELKLQTPAETLLSDS IPHTV LTVVSGWATLSVOOFINASSAVPGAPLEVPYGLFVGGTGTIGA VALGTSGFHELAAFPAWGTODEGTLEFTLITGSRCAPLAFONA RRODFIYDJIFGHLAVUKGQGTLUKSVARQARQLAROAA RRODFIYDJIFGHLAVATKQGGTLEVPUKGQGTGLABAA HLQEHRLGITPEATNASLIGCMEDLSVNQCRGLEALITRIM AGCRLEEEEEYEDDAYVHXAFSTLAFASHAPAMELDECVPERG PPYFANFTQLLTISPLVVABGGTAWLEWRRIVQTILDMEAER SQULFSVTRGANYGLEDLIJGAQARMTILLDVVNNKARFIH GSEDTSDQLVLEVSVTRAVPBMSCLRRGOTYLLDIAMEAER SQULFSVTRGANYGLUSTARAFTLLDVVNNKARFI GSEDTSDQLVLEVSVTRAVPBMSCLRRGOTYLLDIAMEAER SQULFSVTRGANYGLUSTARAFTLLDVVNNKARFI GSEDTSDQLVLEVSVTRAVPBMSCLRRGOTYLLDIAMEAER SGLEVERRDQDFERPATRICVALRAPATLICHTAHLEATLERGG PPTFHYEVVQAPRKGNLOLOGTRLSDEGGFTODDIAGACVTX TARASEAVEDTFRRVTAPPTFSPLYTFP HITGGDDDAPULT TARASEAVEDTFRRVTAPPTFSPLYTFP LYTFP HITGGDDDAPULT TORATTWMSFTINDLLRGRLVYQGDDSETTEDD PPVATRQ SSGMMAGNEVRSVFRVLYQUMDHAPQTIST FFUXAGGRR TTDDVAFSDADAGRADAAVLQVMDHAPQTIST FFUXAGGRR TTDDVAFSDADAGRAD				TIBE A AKABRA TIMANAKATUN ADOUTHIDAGA DEL AGLI DAKARAMAN
ROMILOYTSKVI FFNILLVLYLLQVAATVEPCETSSPHSIPLITEN; GPINLMILLGTVHCQIVSTRPPKPDLSTOGGRRRKLKRAAHLEN HREGGGSTTDNTQSGAVQNHGTSTSHSVGTVFRDLMHAAFFL GSKKAKNSINKSTETDNOTYSLJOKKTVKSGEGG JONNEPQCE: IRPETTAMTGTLRNEPS KDTQRTITNYSDEVSSERGPETGYSI RRHVDRTSEGVLRNKKSHHYKKIPPEDDPKSGTSCSSCSSSI QNGSSARPSESTEDVLWEDLLHCACRECTSTEDVENNIQINF VKKEYRDDPFHQSHLPWLHSSHPOLEKISATVMSGRDCKKADM VLEISGMIMMRVNSHPOIGTGNAVSLIJGLTPPVFRLSQ TOLEQLITHAGASELVVLAFGSNEDVLVLSMVIISFVVRNSLW FPFLLCVAERTYKQVGIM*TSEGVLRNKSHHYKKHYPHEDAP SGTSCSSCSSSCROBESARPESTEDVLMEDLHCACCHSSC SETDVENNQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISA VWEGNDCKKADMSVLEISGMIMMRVNSHTPGIGVOIFGNAVSLIJGLTPPVFRLSQ SGTSCSSCSSROBESARPESTEDVLMEDLHCACCHSSC SETDVENNQINPFFLLCVAERTYKQVGIM FFFLLCVAERTYKQVGIM*TSEGVLRNKSHHYKKHYPHEDAP GOGFASFFG*MHPEVYVARNANTDIDLQLGFSNSQPEALLLAA VWEGNDCKKADMSVLEISGMIMMRVNSHTPGIGVOIFGNAVSL LGITFFVFRLSQATOLEQLTHABASSLIVVLAFGSNEDVIVLSM IISFVVRNSLWHIFFFLLCVAERTYKQVGIM GOGFASFFG*MHPEVYVARANTDTDLQLGFSNSQPEALLLLAA VALGGGFASLAFARATOLEGGLAFPAWTSNGHPEVYGAGGAFAFAAV LTVURGWATLLVOGFILANSAVPCABLEPVYGLFVGGTOTLGL YKRGTSRPLRGCLHAATLNGRSLLRPLTPTDVHEGCAEEFSASD VALGFSGFHSLAAFPAWTODEGTLEFTLTTTSRAPLAFDAGARPAWGL RRGDFIYVDIFEGHLRAVVLKGQGTVLLLHNSVPVADGQPHEVS HINARRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEAS HLQERHALGTPEANNALGGMEDLSVALLHNSVPADGQPHEVS HINARRLEISVDQYPTHTSNRGVLSYLEPRGSLLLIGGLDAEAS HLQERHALGTPEANNALGGMEDLSVALLGGLDAEAS HLQERHALGTPEANVLRGGGTVLLDFURVNDD AGCRLEEEBYEDDAYGHYRAPSTLAPEAMPAMELPEPCVEPG PPYFANFTQLLTISPLVVARGGTRALLERTUQPTLDLMEAELR SQVLFSVTGAHYBAYBAYBAYBAYBAYBAYBAYBAYBAYBAYBAYBAYBAY	5449	194	1833	MASKAIDAT AM IÖKVIRAIDÄÄTMEVS AEÄKET VRIKAKAKKIN
GPIMMILLGTYHCQIVSTRTPKPPLSTGGRRRKLRKAMHLER HREGGGSTTDNTYGSBAUQNGHGTSTHSVTYFRDLMHAAFFLE GSKKAKNSIDKSTETDNTYGSBAUQNGHGTSTHSVTYFRDLMHAAFFLE GSKKAKNSIDKSTETDNTYSBAUQNGHGTSTHSVGTYFRDLMHAAFFLE GSKKAKNSIDKSTETDNGTVSLDGKKTVKSGEDGIOMHEPQCE: IRPEETAWNTGTLRNGFSKDTGTTTNYDDEVSSEEGPETGYSI RRHVDRTSEGVLENKKSHYKKHYRNEDAPKSGTSCSSKCSSI QUSSSARPESETEDVLWEDLLHCAECHSSCTSETDVENNIQINP VKKEVRDDPFPQSHLGWHLSSHPCLEKKSALVWEGNDCKKADM VLEISCMIMMRVUSSHTPGIGVOTFGRAVSLLIGLTPVFVRLSQ TDLEQLTAHSASELYVLAFGSNEDVLYLGWTISFVVRLSQ TDLEQLTAHSASELYVLAFGSNEDVLWEDLHFVKKHYPNEDAP SGTSCSGSCSSSRODSESARPESETEDVLWEDLHFVKKHYPNEDAP SGTSCSGSCSSSRODSESARPESETEDVLWEDLHFVKKHYPNEDAP SGTSCSGSCSSSRODSESARPESETEDVLWEDLHFVKKHYPNEDAP SGTSCSGSCSSSRODSESARPESETEDVLWEDLHFVKKHYPNEDAP SGTSCSGSCSSSRODSESARPESETEDVLWEDLHFVKKHYPNEDAP SGTSCSGSCSSSRODSESARPESETEDVLWEDLHFVKKHYPNEDAP SGTSCSGSCSSSRODSESARPESETEDVLWEDLHFVKKHYPNEDAP SGTSCSGSCSSSRODSESARPESETEDVLWEDLHFVKKHYPNEDAP SGTSCSGSCSSSRODSESARPESETEDVLWEDLHFVKKHYPNEDAP SGTSCSGSCSSRODSESARPESETEDVLWEDLHFVKKHYPNEDAP SGTDVENDLYNFCLSCHTUNGTVALFFULHFUNDLACEKISA VBEGNDCHTLAGGLAFVALFTULGVALFTULHGACHEKIST LUGHTPVRSSLUHTHSPHTVANALTDIDLQCFSMSOPPERLLLLAA LUGHTPVRSSLUHTHSPHTVANALTDIDLQCFSMSOPPERLLLLAA VBEGNDCHTLAGGSCHTALTSTULGHADEACH LUGHTLGLTPAHTAGSLLCHTPATLLINSVPVADGOPHEVS HINAHRLEISVDQYPTHTSNRGVLSVLEPRGGLLLLAA AGCRLEEERFYNDDAYHVERAGGTAWLENWRIVOPTLUMFAELE SGULFSVTRAGAVGHSTANALLGCMEDLSVNGQRRGLREALLTRIM AGCRLEEERFYNDDAYHVERAGGTAWLENWRIVOPTLUMFAELE SGULFSVTRAGAVGHSTANALLGCMEDLSVNGARGGLERETOVL GSBOTSDOLVLEVSVTARVPMSCLARGGTVLLDTUNMRAAFT GSBOTSDOLVLEVSVTARVPMSCLARGGTVLLDTUNMRAAFT GSBOTSDOLVLEVSVTARVPMSCLARGGTVLLDTUNMRAAFT SGSBOTSDOLVLEVSVTARVPMSCLARGGTTLLDTUNMRAAFT SGSBOTSDOLVLEVSVTARVPMSCLARGGTTLLDTUNMRAAFT SGSBOTSDOLVLEVSVTARVPMSCLARGGTTLLDTUNMRAAFT SGSBOTSDOLVLEVSVTARVPHSCLARGGTTLLDTUNMRAAFT TORDLARGRVLLEVSTAGDLTUNGLOGGSTODDTOLAGAVTYX TRARSBAVEDTFTRITVTAHTLATTERTERGG SFPTTOLAGGOPWATALLEVOAGGGRT TDDVAFSDADSGRADAOLVLTRKDLLFGSIVAVDEPTPFITY TORDLARGRVLFVHSGADRGAVTALLGOGGATALLEVOAGS TTDVAFSDADSGRADAOLVLTRKDLLFGSIVAVDEPTPFITY TORDLARGRVLFVHTGADGRATATLE				HVKPULIDVULVRGSAFARAAPESPWISHIIRGIVRVVFFFFFF
HREGDGSTIDNTQEGAVQNHGTGTSISUSGTVRDLMHAPFEL GSKKANSIDKSTGTDTNQVSLDGKKTVKSGEGGIONEPQCE: IRPETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGYSI RRHVDRTSEGVLKNRKSHHYKKHYPNBDAPKSGTSCSSCSSI QDSSARPESETEDVLWEDLLACARCHSSCTSSTDVENNQIND VKKEVRDDPFRQSHLDWLHSSHPGLEKISAIVWEGNDCKKADM VLEISGMIMNRVNSHIPGIOQUIGENGUSLLGLIFDYRRISQ TOLEQLTAHSASELYVIAPGSNEDVIVLSWYIIFFVRUSQU TDLEQLTAHSASELYVIAPGSNEDVIVLSWYIIFFVRUSQU FFFLLCVAERTYKQVGIM*TSSGVLRNKKSHHYKKHYPNEDAP SGTSCSSCSSSSCSSSSSSSSSSSSSSSPESSSRPBEEDVLWEDLLHCARCHSSC SETDVENNQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISA VMEGNDCKKADMSVLEISGMINNTNSHIPGIGVQIFGRAVSL LGLTPFVFRLSQATDLEQUTAHSASELVVIAFGSNEDVIVLSM ILSFVURVSLWHIFFFLLCVAERTYKQVGIM 5450 8136 1242 GQQFASFFG*NHPBSVTVANAI/TDIDLQQFSMSQPBALLLAA PADHLLLQLYSGHLQVKLVULGGEELRLCTPAETLLSDSIPHV LTVVEKWARTLSVDGFINASSAVPGALPPAGTLLSDSIPHV LTVVEKWARTLSVDGFINASSAVPGALPVAGTTLSDSIPHV LTVVEKWARTLSVDGFINASSAVPGALPVAGTTLSDSIPHV ALGFSGPHSLAAFPAWGTQBEGTLEFTLTTOSKQAPLAPQAG RRODFIYVDIFFGHLRAVVEKSQGTVLLHNSVPVADQQPHEVS HIMARLEISUDQYPTHTSNRGVLSYLEPRGSLLLGGLDABAS HLGHHLGLTPBATNASLLCCHEBLYNGQNGRGLREALLTRIM AGCRLEEESYEDDAYGHYBAFGTLAPEAWPAMELPPECVPEG PPVFANFTQLLTISPLVARGGTANKHVHQYPJLDLMEAELR SQVLFSVTRGAHYGLLEIDLAQQARKMFTLLDVVNRKARFIH GSBDTSDQLVLEVSVTARVWPSCLRGGTVLLDHAGAEL SQULFSVTRGAHYGLLEIDLINGRHPDPBACEGLTFQVLG SSGLPVERDDGGFPATEFSCRLEAGSLVYVHCGGPAQDLTF VSCGLAASPPATLKVAURTPALOIHSSTGLLAQGSAMPILPP LSVETNAVGQDVSVLFRVTGALQFGLQKHSTGGVGAGEMWAT AFFIQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQELISS SPPVTIGRATVWMLEPELHTQNTQTTTTAHLBATLEBAGI PPTHYEVVQAPRKKNLQLQGTRLISGGGFTDDDIQAGRYTYT TARASSAVDDTEFFRYTAPPFFSCHTPFHIGGTDDAPVLTT TARASSAVDDTEFFRYTAPPFFSCHTPFHIGGTDDAPVLTT TARASSAVDTTEFFRYTAPPFFSCHTPFHIGGTDAPVLTT TODKTTMVTSFTNEDLLERGLVYQDDDSETTEDDIPFATDDIPFTTTY TODKTTMVTSFTNEDLLERGLVYQDDDSGFTTEDDIPFTTTATHLBATLEBAGI PPTHYEVVQAPRKNLQLQOTKLSGVAQDGATLBVQAGG TTDDVAFSDADGGPADAGLVLTKKDLLFGSIVAVDEFTRITY TQDELARREVLFVHAGAPARWILQTVLALENGLAUVGSGALADDA TARASSAVDDTEFFTYTY TQDELARREVLFVHAGAPARWILQTVLALENGLAUVGSGALADDA SVEAGFVHTDATLQVTLALEGFLAPKLVHKKITVYGGBAAI RRDQLEAAGGAVPDADIVFSKSPSAGTLAUKSGALADDE LDDVOGFSGEAUVTGALDVLY	•	-{		KWWDQVTSKVIFFWDDVDYDDQVAAIVDFCSTSSPASIPDIEVI
GSKKAKNSIDKSTETONGYUSLDGKKTVKSGEDGIONHEPQCE: IRPETAWNTGTLENGFSKDTORTIVSDEVSEESGEFTGYSI RRHVDRTSEGVLRWRSHHYKKHYPNEDAPKSGTSCSSRCSSISI QOSESARPESSTEDVLWEDLLHCARCHSSCTSSTDVENHQIND* VKEKYKDPFFGGSLUPMLHSSHPGLERISAIVWEGDCKKADM* VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTFPVFRLSG* TDLEQLTAHSASELYVLAPGSNEDVILLSWIJISFYVRYSLW* PFFLLCVAERTYKQVGIM*TSSGVLRWRKSHHYKKHYPNEDAP* SGTSCSSRCSSSRGDSESARPESETEDVLWEDLLHCARCHSSC* SETDVENHQINFOVKKSYNDDPFHGSHLPWLHSSHPGLEKKISA VWBGNDCKKADMSVLEISGMINNRVNSHIPGIGYQIFGNAVSL LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSM IISFVVRVSLWWIFFFLLCVAERTYKQVGIM* SGOFASPFG*NHPBVTVANALTDIDLQLGFSMSGDFELLLLAA VWBGNDCKKADMSVLEISGMINNRVNSHIPGIGYQIFGNAVSL LGLTPFVRLSUMVIFFFLLCVAERTYKQVGIM* PACHLLGLYSGHLQVARLVGGGGGTVLLHASPEDAPLLSDSIPHTV LTVVEGWATLSVDGFINASSAVPGAPLEVPYGLFVGGTGTLGL YLRGTSRPLRGCLHAATLNGRSLRRPLTPDVHEGCAEEFSASD VALGFSGFHSLAAPFAMSTDDSGTEFFTLTTQSRQAPLAPQAG RRGDFIYVDIFEGHLRAVVEKGGGTVLLHNSVVVADQCPREESASD VALGFSGFHSLAAPFAMSTDDSGTEFFTLTTQSRQAPLAPQAG RRGDFIYVDIFEGHLRAVVEKGGGTVLLHNSVVVADQCPREESASD HANAHLEISVDOYPTTSTNSRGVLSERGSLTLGGLDDARS HLQEHRLGLTPEATNASLLGCMSDLSVNGQRGLRRALLTRNM AGCRLEEESYSDDAYGHYVEAFSTLAPEAMPAMELPEPCVPEPG PPVFANFTQLTISPLVVABGGTAMLEWRHQPTLDLMGABLR SQVLFSVTRGAHYGELBIDLIGAQARKWFTLLDVNNKARFIF GSBDTSDDAVLSVSTARVMPBSCLRRGGTTLLDVNNKARFIF GSBDTSDDAVLSVSTARVEMPSCLRRGGTVLLBIQVNPVNDG HIIFPGSLMVILEHTQKPIGPEVPQAYDPBSACEGLTFQULC SSGLPVERDDGGGPRATEFSCELEAGSLVVYCGGPAQDLTF VSCLQASSPATLKVALVATRPAIQHENGTLABLAVQVGGBLSA AFHQRDVEGGRVRXISTDPGHHAYDTVENLALEVQVGGELSA PPTTHEVVQARRKONLQLGGTRLSSGGSFTDDIQAGRATLEVA TQRDKTMVTSPTNEDLLEGRLVYQHDDSETTEDDIPFAVTRQ SSGMAMEEVRGVFRVAIQFVNDHAPVQTISRIFHUGGBPADPVLTT TARRSERVDDTFFRAAPAGADRGHIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDLRSGDFFTDDITAPVATRG SGGMAMEEVRGVFRVAIQQFVNDLAFSKUSLSFEDDINGSESPEDVHAAGGGRIGHTAPVALHLDTNLDLRSGDFFTDDITAPVATRG TGDDKTTMVTSPTNEDLLEGRLVYQHDDSETTEDDITPVATRG SSGGMAWEEVRGVFRAAFSQORLHGLVANGHABLEVQASI YLRVANGSSLVVPQGGQGTIDTAVLHLBUTNLDLRSGDFFTDDITAPVATRG SVEAGFWHTDATLQVTIALBEPLAPKKVPHKKKIYVFQGEABA RRDQLEAAGEAVPADAIVFSKSSLSPSAGTLUNGSGLSFEDIM			1	GPIWEMEDEGTVHCQIVSTRTPRPPESTGGRRRRRRRRRAAHDEV
I IRRETAMNTGTLRINGPSLDTQRTITAVSDEVSSERGPETGYSI RRHVDRTSEGVLRNRKSHHYKKHYPREDAPKGTSCSSRCSSI QNSSSARPESETEDVLWEDLHCARCHSCTSETDVENHQIND VKKEYRDDPFRQSHLDWLHSSHPGLEXISATUWGRDCCKADM VLEISGMANNRVNSHPLGIGYQIFGNAVSLILGLTPPYRILSQ TDLEQLTAHSASELYVIAPGSNEDVIVLSWYI19FVRVSQU FPFLLCVAERTYKQVGIM*TSSGVLRNRKSHHYKKHYPNEDAP SGTSCSSCSSSSSOSSSRSDESSARPSETEDVLWEDLHCAECHSSC SETDVENHQINDFCVKKEYRDDPFHGSHLDWLHSSHPGLEKISA VWEGNDCKKADMSVLBISGMINNRVNIBIPGIGVQIFGNAVSL LGITPFVRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSM IISFVRVSLWWIFFFLLCVAERTYKQVGIM SAMPHANDA SERVENDEVINLAM IISFVRVSLWWIFFFLLCVAERTYKQVGIM PADHLLQLYSGHLQVELVLGGBELRLGTPAETILLSDSIPHYV LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGL YLKGTSFLRGCLHAATLANGSLLARPITDOHBCCAERESASD VALGFSGPHSLAAFPANGTODEGTLEFTLTTDSRQAPLAFQAG RRGDFIYVDIFFGHLRAVVEKGGGTVLLHNSVPVADGOPHEVS HINAHRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEAS HLQHRLGLITPANNASLACCHEDLSVRGGRERGALITENA AGCRLEESYEDDAYGHYBAFSTLAFRAWMELPPECVPERG PPVFAMFTQLLTISPLVVARGGTAMLEWRHVQPTLDLMFAELR SQVLFSVTRGAHYGELEDILGAQARKMFTLLDVNKRAFFH GSBDTSDQLVLEVSVTRAVPMPSCLRRRGGTTLLPIQVNPVNDE HIIFPRGSLMVILGHTOKPDFVCAVDPDSACEGLTFCVULG SSGLPWERDQOGEPATEFSCRELEGSLVVYHCGGPAQDLTT VSDGLQASPPATLKVVARPAIQTHENSLACEGVEGAEWMAI AFIQRDPVEGGRVTLSTDPGHHAYDTVENLALEVQVAGGETLSS SFPVTIORATVWMLRLEPLHTONTQQETTTTAHLBATLEBAG PPFTHYEVVQAPRKGNLQLQGTRLSLAGGSAMPILPW SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TDDVAFSBABAGFADAQLVTRKDLLAGGIVAGGRATYK TARASSAVEDTFFRVTAPPYFSPLTTPFHIGGDPDAPVLTT LLVVPRGGBGVLSANHLFVKSLMSASYLYEWRRPRLGRLAWM TOKKTMVTSFTIBEDLLAGRLVVQHODESTTEDDIPTYATRQ SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSBABAGFADAQLVTRKDLLAGSIVAVDEPTRPIY TQELLRRRRVLFVHSADARGMCIQLQGTTTDDIDTRYATRQ SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSBABAGFADAGLUCNSOGHQATALLEVQASI YLRVANGSSLVVPQGQGGTTDTAVHLDIRTBLDRSDEVHYHH AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNOSLSLEPEDTM SVEAGFVHTDATIQVTIALBGPLAPLKLVRHKKIYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGTLVMSGRGLADED LDDYOGSFOGEAUTGRVLYLHISTPERMSTRANSGRAFLDE LDDYOGSFOGEAUTGRVLYLHISTPERMSTRANSGRAFLDE LDDYOGSFOGEAUTGRVLYLHISTPERMSTRANSGRAFLDE			1	HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFKDDWHAAFFES
RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSTISCSSRCSSIS QDSSARPSSTEDVLWEDLLHCARSCTSETDVENIQINM VKEYRDDPFRQSHLEWLHSSHPGLEKISAIVWEGNDCKKADM VKEYRDDPFRQSHLEWLHSSHPGLEKISAIVWEGNDCKKADM VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGIFFPVERLSQ. TDLEQLTHARSASELVVLAFGNEDVLVLSMVIISFYVERVSLWW PPPLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAP SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSC SETDVENNGINPCVKKEYRDDPFHQSHLPWHHSSHFGLEKISA VWEGNDCKKADMSVLEISGMINNRVNSHIPGIGTQIFGNAVSL LGITPPVFRLSQATDLEGUTAHASSELVVIAFGSNEDVIVLSM LISFVVRVSLVWIFFPLLCVAERTYKQVGIM 1ISFVVRVSLVWIFPFLLCVAERTYKQVGIM 1ISFVRVSLVWIFFPLLCVAERTYKQVGIM 1ISFVRVSLVWIFFPLLCVAERTYKQVGIM 1ISFVRVSLVWIFFPLLCVAERTYKQVGIM PACHLLDLYSGHLQVELVLGGGEELRLQTPAETLLSDSIPHTV LTVVEGWATLSVDGFINASSAVPGAPLEVPVGLFVGGTGTULGL YLRGTSRPLRGCLHAANTINGSLLLAFLTPDVHECCAEFSASD VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTOSRQAPLAPOAG RRGDFIYVDIFEGHLRAVVEKGGGTVLLHNSVVVAOCQPHEVS HINAHLEISVDQYPTTSTRSRGVLEPRGSLLLGGLDAEAS HLQHRLGLTPPATNASLLGCMBDLSVRGGREGREALLTRINM AGCRLEEESYEDDAYGHYEAFSTLAPERSSLLLGGLDAEAS HLQHRLGLTPPATNASLLGCMBDLSVRGGREGREALLTRINM AGCRLEEESYEDDAYGHYEAFSTLAPERWPMELPEPCVPEG PPVFANFTQLLTISPLVVABGGTAWLEWRHVQPTLDLMEAELR SQVLFSVTRGHHYGELEIDLIGAQARKHFTLIDVVNKRAFFIH GSBDTSDDOLVLEVSTARVMPSGLERGGTVLLDLUVNFNND HIIFPIGSLMVILBETKKPLGPEVFQAVDPBACEGLTFQVUL SSGLPVERRDQPGEPATEFSCRELEAGSLVVYHCGGAQDLTF VSCGLQASPPATLKVVATRPATGIHRSTGLRLAQGSAMPILPA LSVETMAVGQDVSVLFRVTGALQFGERGGTTLLDVNKRAFFIH LSVETMAVGQDVSVLFRVTGALQFGERGGTTCDULGAGRWTYC TARRSBRAVDDTFFRYTAPPYFSPLTTPHHIGGDPDAPVLTT LLVVPEGGEGVLSANHLFVKSLNSASYLVEWREPRIGRLAW TODKTTMVTSFTINEDLLAGRLVVQHDDSETTEDDI PFVATROC SSGMAWEEVRGVFRVAIQPVNDHAPVQTISRIPHVARGGRI TTDDVAFSDADSGPADAGLVITRKDLLFGSTVADDETTRIT PFVATROG SSGMAWEEVRGVFRVAIQPVNDHAPVQTISRIPHVARGGRI TTDDVAFSDADSGPADAGLVITRKDLLFGSTVADDETTRIT TQEBLERRRVLFVHSAGARGRIGLOVSDGGHQATALLEVQASI YLRVANGSSLVVPQGGGGTTDTAVLHLDTNLDIRSGDEVHYH AGPRWGLVRAGQPATAFSQQDLLDGAVLYSHNGSLESEPDTM SVEAGFVHTDATLQVTLALBEPLAPLKVVRNKKLYVFQGEAAI RRDQLEAAQEAVPADIVFSVKSPSAGTVAWSRGALLAGEPL LDDVOSFSGEAUVDGRVLYLHSRASELSEDFTM			·	GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCEI
QUSESARPESTEDVLWELGLEISATWEGNDCKKADN VKEYRDDPFHQSHLPWHSSHPGLEKISATWEGNDCKKADN VLEISGMIMNRVNSHIPGIGYGFGRAVSLILGLTPFVFRLSQ TOLEQLTHHSASELYVLAFGSNEDVIVLSWIJSFVFVRSUW PFPLLCVARFTYKQGIM*TSEGVIRNISFVFVRSUW PFPLLCVARFTYKQGIM*TSEGVIRNISFVFVRSUW PFPLLCVARFTYKQGIM*TSEGGVIRNISFVFVRSUW SGTSCSSRCSSSRQDSESARPESETEDVLWEDLHCAECHSSC SETDVENNGINFCYKEREYRDPFHQEHLPWLHSSHPGLEKISA VMEGNDCKKADNSVLEISGMIMNRVNSHIPGIGYQIFGNAVSL LGIJTPFVFFLSQATOLEGLTHARSBELYVLAFGSNEDVIVLSM IISFVVVRVSLVWIFFPLLCVARRTYKQVGIM 5450 8136 1242 GQQFASFFG*NBFEVTVAMAITDDLQLQFSMSQPEALLLLAA PADHLLIOLYSGHLQVRIVLGQEELRQJFPAETLLSDSIPHTV LTVVEGWATLSVDGFINASSAVPGAPLEVPYGIFYGGTTILGL YLRGTSRPLRGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASD VALGFSGPHSLAAFPAMGTODEGTLETTLTTGRQAPLAFOAG RGCDFIYVDIFFEGHLRAVVEEGGVTULHMSVEVADGQPHEVS HINAHLBISVDQYPTHYSNRGVLSVLEPRGSILLGGLDAEAS HLQEHRIGLIPFEATNASLLGCMEDLSVNGQRRGLREALTJRRM AGCRLEEESYEDDAYGHRAFSTLAFBAMPAMELPEPCVPEPG PPVFANFTGLLTISPLVVABGGTAHLEWRHVQPTLDLMERELR SQULFSVTRGAHPGLELDILGARMFTILLDVUNKARFIH GSEDTSDQLVLEVSVTARVPMPSCLRRGOTTLLPIQVNRWAFFIH HIFPHGSLMVILEHTQKFLGFEVFQAYDPDSACEGLTFQVLG SGGLPVERRDQCGPATFESCELEAGSLVYVHCGGPAQDLTT VSDGLQASPPATLKVVATRPATQHRSTGLRLAQGSAMPTLP LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEAWAH AFHGRDVEGGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSS SPPVTIQRATVWHLRLEPHTONTQCETLTTAHLEATLEBAG PPTTFMEVVQAPRKGMLOLQGGTTDDOLQARVTYT LLVVPEGGEGVLSADHLFVKSLNSASVLYSVMERPRIGRLAW TORETTTMVTSFTREDLLRGRLVYQGDDSETTEDDIPVATRQC SSGDMAWEBURGVFRVALQFVNDHDAPVQTISRIFHVARGGRR TDDVAFSDABGGPADAQLVLTRKOLFGSVAVDEPTTPIY CSSGMAWEBURGVFRVALQFVNDHDHAPVQTISRIFHVARGGRR TTDDVAFSDABGGPADAQLVLTRKOLFGSVAVDEPTTPIY TGEBLRRRVLFFHSADRGNTQLCVSNGGQRTATLEVQASS YLRVANGSSLVVPGGGGGTTDTAVLHLDTNLDIRSGDEVHYH AGPRWGQLVRRGQDFATAFSGOLDAGVLYSLSPEDTMS SVEAGFVHTDATLQVTIALEGPLAPLKLVRKKLYVFQGEAA RRDQLERAQRAVPPADIVSVKSPSPSAGVLIWMSGRALADEP, LDPVOSSSGEMVAGRAVALDGFVINDSGRALADEP.)		IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGISL
VKKEYNDDFFIGSHLPMLHSSHPQLERISAIVWEGNDCKKADM VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQ TDLEQLTAHSASELYVLAFGSNEDVIVLSMVIISFVVRVSLW FFPLLCVARFTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAP SGTSCSSRCDSSSRQDSSARPESETEDVLWEDLHCAECHSSC SETDVENNIGINPCVKKEYRDDPFIQSHLPWLHSSHPGLEKISA VMEGNDCKKADMSVLEISGMIMNRVSHHIPGIGYQIFGNAVSL LGLTPFVFRLSQATDLEQLTHARSBELYVLAFGSNEDVIVLSM IISFVVRVSLVWIFFPLLCVARRTYKQVGIM 5450 8136 1242 GQOFASFFC*NIPEVTVWANAITDDLQLGPSMQCPEALLLLAA PADHLLIOLYSGHLQVGRUNGQEERRLQTFMETLLSDSIPHTV LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGL YLKGTSRPLRGCLHAATLINGRSLLRPLTPDVHEGCAEEFSASD VALGFSGPHSLAAFPAWGTOGEGTLEFTLTTOSRQAPLAFOAG RRGDF1YVDIFEGHLRAVVEKGQGTUVLHNSVEVADGQPHEVS HINARRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEAS AGCRLEEESYEDDAYGHVEAFSTLAPERAPMMELPEPCVPERG PPVFANFTQLLTISPLVVABGGTAWLERRHVQPTDLDMRAELR; SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIE GSEDTSDQU/LEVSVTARVPMPSCLRRGQTYLLPIQUNVNNDE HIIFPGSLMV LIEHTOKPLLGPVAYDPDSACEGLTFQVLG SSGLPVERRDQPGEPATEFSCRELEAGSLVVVHGGRAQDLTF VSDCLQASPPATLKVVALRPAIQHRRSTGLRAGGSAMPILPA LSVETTNAVGDGVSUFPVTGALQFGELQKHSTGGVEGABRWAT AFHQRDVEQGRVXJSTDPQHHAYDTVENLALEVQVGGBILSS SFPVTIQRATVWALRLEPLHTQNTQGETLTTAHLEATLEEAGI PPTTHYEVVQAPRKGNLOLQGTRLSDGGGFTQDDIQAGRVTY TARASEAVEDTFFRFVTAPPYFSPLYTPPHIGGDPDAPVLTT LLVVPEGGEGVLSADHLFVKSLINASYLYEWMERPRIGRILAW TODKITMVTSFTINEDLLRGRLVYQHDDETPRIYT TQDKTTMVTSFTTEDLLRGRLVYQHDDFTRIYT TQDKTTMVTSFTTEDLLRGRLVYQHDDFTRIYT TQDLRRRVLFVHSGADRGWQLVLTKULLFGSLVAUDFFTRIYT TQDLRRRVLFVHSGADRGWQLVLTKULLFGSLVAUDFFTRIYT TQDLRRRRVLFVHSGADRGWQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPGGGGGTIDTAVLHLDTNLDIRSGGEWHYH AGPRGGLVRAGGAVAFSQADAALVLTKULLFGSLVAUDFETRIYT TQEDLARRRVLFVHSGADRGWQLGGGTLDTAVLHLDTNLDIRSGGEWHYH AGPRGGLVRAGGAVAFSQADAALVLTKULLFGSLVAUDFFTRIYT TQEDLARRRVLFVHSGADRGWQLGGGTLDTAVLHLDTNLDIRSGGEWHYH AGPRGGLVRAGGAVAFSQADAACLVLTKULLFGSLVAUDFFTRIYT TQEDLARRRVLFVHSGADRGWQLGGGTLDTAVLHLDTNLDIRSGGEWHYH AGPRGGLVRAGGATAFSGQULGAVLYBLGEADLEVAGGAAA RRDQLEAAGEAVPPADIVFSVKSPSBAGVLJWMSGRAGLADEPI LDPVOSSGERUNDGRVLVLHSRESPENMSDASLDVASGLADEP				RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR
VLEISCMINNRVNSHIPGIGYQIFCNAVSLILGLIPFVFRISQUED TO TDLEQLITAHSASELYVIAFGSNEDVIVLSMVIIS FVVRVSLVY FFFLLCVARETYKQVGIM* TSEGVLRNKKSHYKKHYPNEDAP! SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCARCHSSC* SETDVENHQIND PCVKKEYRDDPHQSHLPWLHSSHPGLEKISA* VWEGNDCKKADMSVLEISCMIMNRVNSHIPGIGYQIFGNAVSL* LGITFFVFRLSQATDLEQLITAHSASELYVIAFGSNEDVIVLSM* LGITFFVFRLSQATDLEQLITAHSASELYVIAFGSNEDVIVLSM* LGITFFVFRLSQATDLEQLITAHSASELYVIAFGSNEDVIVLSM* LGITFFVFRLSQATDLEQLITAHSASELYVIAFGSNEDVIVLSM* LGITFFVFRLSQATDLEQLITAHSASELYVIAFGSNEDVIVLSM* SQQFASFFG*NHPEVTVAMALTDIDLQLOFSMGQPBALLLLAA* PADHLLLQLYSGHLQVRLVLGQEELRLQTPAETLLSDSIPHTV* LTVVEGWATLSVDGFINASSAVPGAPLEVPYGLFVGGTGTLGL* YLKGTSRPLRGCHAATLNGSLLAPLTDVHEGCAEFSASD* VALGFSGPHSLAAFPAMGTQBEGTLEFFTLTTOSGADALAPQAG* RRGDFIYVDIFEGHLRAVVEKGGGTVLLHNSVPVADGQPHEVS* HINAHRLEISVDQYPFHTSNRGVLSYLEPRGSLLLIGDDAEAS* HLQEHRLGILTPEATNASLLGCMBDLSVNGQRSGLREALITRNM* AGCRLEEESYEDDAYGHYBAFSTLAPRAWPAMELPPECVPEFG* PPVFAMFTQLLTISPLVVARGGTAMLERHVQHYTLDLMEAELK* SQVLPSTRGAHYGELEDIJGAQARKMTTLLDVVMRKARFIH* GSEDTSDQLVLEVSVTARVPMPSCLRRGGTYLLPIQNVENDP* HIIFPHGSLMVILEHTQKPLGPBVQAYDPDSACEGLTFQVLG* SSGLPVERRDQPGEPATEFSCRELEAGSLVYHCGGPAQDLTF* VSDGLQASPPATLKVVAIRPAIQHHSTGLRLAQGSAMPILD* LSVETNAVGQDVSVLPRVTGALQFGELQKHSTGGVBEABWAT* AFHQRIVQCGRVSVLSATDLQFGELQKHSTGGVBCABWAT* AFHGRIVQCGRVSVLSATDLQFTLTTAILLBATLEEAGI* PPTTHYEVVQAPRKGNLQGTRLISDGGGTODDIQARVTY* TARASEAVEDTFRFRVTAPPYFSSLTYPPHIGGDPAPVLTT* LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAW* TODDKTTMTTSFTNEDLLERGLVYQHDDSETTEDDIPVATRQC* SGCMMMEEVRGVPRVAIQPVNDHAPVQTTSRIFHVARGGRRITTDDVAFSDADGSGPADALVLTRKDLLFGSIVAVDEPERFRITTQELLGRENIVTQEGGGTUDTAVLHLHDTHLDTRSGGEVHYTH* TQEDLRRRVLFVHSGADRGMIQLLQVSDGGHQATALLEVQASI* YLRVANGSSLVVPGGGGGTTDTAVLHLHDTHLDTRSGGEVHYTH* AGPRIGQLVPRAGQATAFSQGDLLDGAVLYSHGSLSPETIM* AGPRIGGQLVRAGQATAFSGAYDATGVLLYLHSTREAMSALAPSILVPAGGLAABLADPADFSLDVASGLAABPITH* AGPRIGGDLVRAGQATATSCGGATDATALLEVGRALABGEABPITH* AGPRIGGDLVRAGQATATALEGAPATALLEVQASI* LLDPVOSFSGEARDTOTAVLYLHSTREAMSALFSLDVASGLAABPITH* AGPRIGGDLVRAGQATATALLEGAPATALLEVQASI* AGPRIGGLVARAGGATATALEGAPATALEVGALABPITHTATATATATATATATAT				QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC
TDLEQLTAHSASELYVIAFGSNEDVIVLSMYIISFVWRVSLVW FFFLLCVAERTYKQVGIM*TSEGVLRNKKSHHYKKHYPNEDAP SGTSCSSCRSSSRQDSESARPSEFTEDVLWEDLLHCAECHSC SETDVENHQINPCVKKEYRDDFFHGSHLFWLHSSHPGLEKISA VWEGNDCKKADMSVLEISGMIMNRVMSHIPGIGYQIFGNAVS LGHTPFVFHLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSM IISFVVRVSLVWIFFFLLCVAERTYKQVGIM GQQFASFFG*NHPEVTVAMAITDIDLQLQFSMGQPEALLLLAA PAPHLLLQLYSGHLQVRLVLGQEELRLQTPAETLLSDSIPHTV LTVVEGWATLSVDGFINASSAVPGAPLEVPYSLFVGGTGTIGL YLRGTSFPLREGCHAATLNGRSLLAPLTPOVHEGCAEFFSASD VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAPQAG RRGDFIYVDIFFECHLRAVVEKGGGTVLLHIMSVFVADAGOPHEVS HINAHRLEISVDGYPHTENRGVLSVLEPRGSILLGGLDAEAS HLQEHRLGLTPEATNASLLGCMEDLSVNGQRGRGLREALLTRIM AGCRLEEEEYEDDAYGHYRAFSTLAPRAWPAMELPEPCVPEPG PVVFANFTQLLTISPLVVARSGGTANLENRRVQPTLDLMRAELR SQVLFSTTRGAHYGELELDILGAQARKMFTLLDVVNRKAFFIH GSBTTSDQUVLEVVSVTARVPMPSCLRRGQTYLLPIQVNPVNDH HIIFPHGSLMVILEHTQKPLGFEVFQAYDPDSACRGLTRQVLG SGLPVERRDQDGPAPATSSCRELEAGSLVVVHCGGPAQDLTT VSDGLQASPPATLKVVALRPAIQLHRSTGLRLAQGSAMPILP LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVBGAEWAT AFHQRDVEQGRVRYLSTDFQHHAYDTVENLALEVQVGQETLES SPPVTIQRATVWMLRLEPLHTQNTQCETLTTAHLBATLERAGE PPTTHYEVVQAPRKGNLQLGGTELSDGGFTQDDIQAGRVTYC TARASEAVEDTFRRRVTAPPYFFSLTYPPHIGGDDAPVLTT LLVVPEGGEGVLSADHLFVKSLNSASYLYEWRERPRIGRLAW TODKTTMYTSFTREDLLRGRLVYQHDDSETTEDDIPFVATRQ SGGMAMEEVRGVPRVALQCVNDHABYOTTSRITHVARGGRRI TDDVAFSDABOGPADAQLUTRDLLFTGSIVANDEFTRPIYT TQEDLRRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGGGTIDTAVLHLIDTHLDTRSGEWHYTH AGPPRRGOLVRAGQPATAFSQQULLDGAVLYSHMGSLSPEDTM SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKTYVPGGRAAH RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSGGALADEPI LDVVQSFSGGRADDTGVLVLYHSRPEARSDAFSLDVASGLAADE LDVPQGSGGRADTGTALVLHISTREAMSALADEDI		}	Į.	VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
PPPLLCVARRTYKQVGIM*TSSGVLRNKKSHHYKKHYNEDAP; SGTSCSSRCSSRQDSSSARPESETEDVLWEDLLHCAECHSSC SETDVENHQINPCVKEYENDDFHOSHLPWLHSSHPGLEKISA VWEGNDCKKADMSVLEISGMINNRVNSH PGIGYQI FENAVSL LGITPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSM IISFVURVSLVWIFFFLLCVARRTYKQVGIM 5450 8136 1242 GQQFASFFG*NHBEVTVANALITDIDLQCFSMSQPSALLLLA PADHLLLQLYSGHLQVRLVLGQEELRLQTPAETLLSDSIPHTV LTVVEGWATLSVDGFLNASSAVGAPLEVPYGLFVGGTGTLGL YLRGTSRPLRGCHAATLNGRSLLRPLTPDVHEGCAEFFSASD VALGFSGPHSLAAFPAMGTQDEGTLEFTLTTQSRQAPLAPQAG RGGPIYVDIFECHLRAVVEKGGGTVLLHINSVPVADGQPHEVS HINAHRLEISVDQYPHTENRGVLSYLEPRGSILLIGLDAEAS HLQEHRLGITPFATNASLLGCMEDLSVNGQRRGLREALLTRNM AGCRLEEEEVEDDAYGHYBAFSTLAFBAMPAMELPBPCVPERG PPVFANFTQLLTI9PLVARSGGTAWLBWRRVQPTLDLMEAELR SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIL GSEDTSDQLVLEVSVTRAVPMPSCLERGGTYLLPIQVNPVNDB HIIFPHGSLMVILEHTQKPLGPBVFQAYDPDSACEGLTGVULG SSGLPVERROQPGEPATEFSCRELEAGSLVVVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILEP LSVETNAVGQDVSVLFRVTGALQGGELGKHSTGVERGEBWANA AFHGRDVEQGRVRYLSTDQCHAYDTVELALEVQVGGBLSS SFPVTIQRATVMMRLBPLHTQNTQQETLTTAHLBATLEEAGF PPTFHYEVVQAPRKGNLQLGGTRLSDGGGFTODDIQAGRVTYC TARRSBEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPULTN LLVVPEGGEGGVLSADHLFVKSLNSASYLIVEVMERPRLIGRLAMF TQDKTTMVTSFTNEDLLRGRLVYQHDDSFTTEDDIFPVATRQC SSGMAMEEVRGVPRVAIQPVNDHAPVQTISRIFHVARGGRIL TQDKTTMVTSFTNEDLLRGRLVYQHDDSFTTEDDIFPVATRQC SSGMAMEEVRGVPRVAIQPVNDHAPVQTISRIFHVARGGRIL TQDKTTMVTSFTNEDLLRGRLVYQHDDSFTTEDDIFPVATRQC SSGMAMEEVRGVPRVAIQPVNDHAPVQTISRIFHVARGGRPT TQDDLRKRRVLFVHSGADRGWQCAYALLEVQASI YLRVANGSSLVVPGGGGGTIDTAVLHLDTRLDIRSGDEVHYM AGPERRGQLVTRAGQAPATFSQQDLLDGAVLYSHMGSLSPEDTM AGPRRGQLVTRAGQAPATFSQQDLLDGAVLYSHMGSLSPEDTM SVEAGPVHTDATLQVTIALEGPLAPLKLVRKKIYVPGGRAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGTVLMVSGGALADEPI LDPVOSFSGGEADTOTGVLLYHLSRFEAMSDAFSLDVASGLGAPI LDPVOSFSGEADATGTVLLYHLSRFEAMSDAFSLDVASGLGADELDLDPVOSFSGEADATGTLLVLHLDTRADGRYDAFSLDVASGLGADELDLDPVOSFSGEADATGTLLVLHLDTRADGRYDAFSLDVASGLGADELDLDPVOSFSGEADATGTLLVLHLDTRADGRYDAFSLDVASGLGADELDLDPVOSFSGEADATGTLLVLHLDTRADGRAALADEPI			}	VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
SGTSCSSRCDSESAPPESETEVLWEDLLHCARCHSSC SETDVENHQINPCVKKEYRDDFHQSHLPWLHSSHPGLEKISA VWEGNDCKKADMSVLEISGMIMNEVNSHI PGIGYQI FGNAVSL LGITPFVFRLSQATDLEQLTHASASBLYVIAFGSNEDVIVLSM IISFVVRVSLVWIFFFLLCVAERTYKQVGIM 5450 8136 1242 GQQFASFFG*NHPSVTVAMAITDIDLQQFSMSQPEALLLLAA PADHLLLQLYSGHLQVRLVLQGEBLRLQTPAETTLLSDSIPHTV LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGL YLRGTSRPLRGCHAATLNGKSLLRPLTPDVHEGCAEFFSASD VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAFQAG RRGDFIYVDIFEGHLRAVVEKGQGTVLLHNSVPVALQGPHEVS HINAHALEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEAS HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNM AGCRLEEEEYEDDAYGHYAFSTLAPEAMPAMELPEPCVPERG PPVFANFTQLLTISPLVVAEGGTAWLEWHVQPTLDLMEAELR SQVLFSVTRGAHYGELELDILGAQARKWFTLLDVVNRKARFTH GSEDTSDQLVLEVSVTRAYPTSCLARLAGGSAMPILPR HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLG SSGLPVERRDQFGPFATTFSCRELEAGSLVYVHCGGPAQDLTT VSDGLQASPPATLKVVATRATQHTHSTLRLAQGSAMPILPR LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVGSLEWMAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGGEILES SPPYIORATMVMRLEPLHTONTQCETLTTHLEATLEEAG PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYC TARASEAVEDTFRFRVTAPPYFSPLYTPFHIGGDEDAPVLTY LLVVPEGGGEVLSADHLFVKSLNSASYLYEVMERPRLGRLAW TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQ SSGDMAMEEVRGVFRVATQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSBADSGFADAGLVLTRKDLLFGSIVAVDBPTRPIY TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGQGTIDTAVHLDITNIDIRSGDEPHTPIY TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGQGTIDTAVHLDITNIDIRSGDEPHTPIY TQEDLRKRRVLFVHSGADRGWIQLVYSNGSISSPEDTMI SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVPGGEAAI RRDQLEAAQEAVPPADIVFSVESPPSGYLVMYRGALADEPI LDPVOSFSOEAADTGRVLYLHLERPEAWSDAFSLDVASGLGAPI				TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
SGTSCSSRCDSESAPPESETEVLWEDLLHCARCHSSC SETDVENHQINPCVKKEYRDDFHQSHLPWLHSSHPGLEKISA VWEGNDCKKADMSVLEISGMIMNEVNSHI PGIGYQI FGNAVSL LGITPFVFRLSQATDLEQLTHASASBLYVIAFGSNEDVIVLSM IISFVVRVSLVWIFFFLLCVAERTYKQVGIM 5450 8136 1242 GQQFASFFG*NHPSVTVAMAITDIDLQQFSMSQPEALLLLAA PADHLLLQLYSGHLQVRLVLQGEBLRLQTPAETTLLSDSIPHTV LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGL YLRGTSRPLRGCHAATLNGKSLLRPLTPDVHEGCAEFFSASD VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAFQAG RRGDFIYVDIFEGHLRAVVEKGQGTVLLHNSVPVALQGPHEVS HINAHALEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEAS HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNM AGCRLEEEEYEDDAYGHYAFSTLAPEAMPAMELPEPCVPERG PPVFANFTQLLTISPLVVAEGGTAWLEWHVQPTLDLMEAELR SQVLFSVTRGAHYGELELDILGAQARKWFTLLDVVNRKARFTH GSEDTSDQLVLEVSVTRAYPTSCLARLAGGSAMPILPR HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLG SSGLPVERRDQFGPFATTFSCRELEAGSLVYVHCGGPAQDLTT VSDGLQASPPATLKVVATRATQHTHSTLRLAQGSAMPILPR LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVGSLEWMAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGGEILES SPPYIORATMVMRLEPLHTONTQCETLTTHLEATLEEAG PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYC TARASEAVEDTFRFRVTAPPYFSPLYTPFHIGGDEDAPVLTY LLVVPEGGGEVLSADHLFVKSLNSASYLYEVMERPRLGRLAW TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQ SSGDMAMEEVRGVFRVATQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSBADSGFADAGLVLTRKDLLFGSIVAVDBPTRPIY TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGQGTIDTAVHLDITNIDIRSGDEPHTPIY TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGQGTIDTAVHLDITNIDIRSGDEPHTPIY TQEDLRKRRVLFVHSGADRGWIQLVYSNGSISSPEDTMI SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVPGGEAAI RRDQLEAAQEAVPPADIVFSVESPPSGYLVMYRGALADEPI LDPVOSFSOEAADTGRVLYLHLERPEAWSDAFSLDVASGLGAPI		1	1	FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAPK
SETDVENHQINPCVKKEYRDDPFHQSILPWIHSSHPGLEKISA VWEGNDCKKADMSVLEISGMIMRRVNSHIPGIGYQIFGNAVSL LGITPFVFRISQATDLEQLTHASASELYVIAFGSNEDVIVUSM IISFVVRVSLVWIFFFLLCVAERTYKQVGIM GQOFASFFG*NHPEVTVAMALTDIDLQLQFSMSQPEALLLAA PAPHLLQIVASGHLQVKIVUTQGEEIRLQTPAETLLSDSIPHTV LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGL YLRGTSRPLRGCLHAATLNGRSLLERPLTPDVHEGCAEFSASD VALGFSGPHSLAAFPANGTODEGTLEFTLTTQSRQAPLAFQAG RRGDFIYVDIFEGHLRAVVEKGQGTVLLHNSVPVADGQPHEVS HINAHRLEISVDQYPTHTSNRGVUSYLEPRGSLLLGGLDAEAS HLQERLIGLTPEATNASLLGCMEDLSVNGQRGLREALLTRNM AGCRLEEEEYEDDAYGHYEAFSTLAPEAWPAMELPEPCVPEPG PPVFANFTQLLTISPLVVARGGTANLEWRHVQPTIDLEMEALER SQVLFSVTRGAHYGELEUIGADARMSFTLDVVNKRAFFH GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDF HIIFPHGSLMVILEBTCKPLGPEVPQAVDPDSACEGLIFPQVIC SSGLPVERDQDGFBPATFSCRELEAGSLVYVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSVLFRVTGALQFELQKHSTGGVEGAEWMAT AFFQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVQGEILSS SFPYTIQRATVWMERLEPLHTQNTQQETLTTAHLEATLEEAGF PPTFHYEVVQAPRKGNLQLQGTRLSDGGFTQDDIQAGRVTYX TARASEAVEDTFFFRVTAPPFYSPLYTPPHIGGDPAPVLTT LLVVPEGGEGGVLSADHLFVKSLNSASYLYEVWERPRLGRLAWF TQDKTTMYTSFTNEDLLRGRLVYQHDDSETTEDDIFVATRQC SSGMAWEEVRGVFRVALQPVNDHAPVQTISRIFHVARGGRRI TDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIY TQEDLRRRVLFVHSGADRGVJQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPGGGGGTIDTAVLLDTNLDIRSGDEVYHY AGPRWGOLVRAGQDATAFSQQDLLDGAVLYSHNGSLSPEDTM SVEAGPVHTDATLQVTLALEEGPLAPLKLVRHKKIVVFGGEAAH RRDQLEAAQEAVPPADIVFSVKSPPSASYLVWNSGLAEDFI LDVVGSFSOEAADTGRVLYLHSRPEAWSDAFSLDVASGLGAPI LDPVGSFSOEAADTGRVLYLHSRPEAWSDAFSLDVASGLGAPI			}	SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
VWEGNDCKKADMSVLEISGMINNRVNSHIFGIGYQIFGNAVSL LGITPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSM IISFVVRVSLVWIFFFLCVARRTYRQVGIM 5450 8136 1242 GQQFASFFG*NHPEVTVAMALTDIDLQLQFSMSQFEALLLLAA PADHILLQLYSGHLQVRLVILGGEELRLQTFAETLLSDSIPHTV LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGGTGTLGL YLRGTSRPLRGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASD VALGFSGFHSLAAFPAMGTQDEGTLEFTLTTQSRQAPLAFQAG RRGDFIYVDIFEGHLRAVVEKGQGTVLLHNSVPVADGQPHEVS HINAHRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEAS HLQEHRLGLTPEATNASLLGCMBDLSVNGQRRGLREALLTRIM AGCRLEEEEYEDDAYGHYEAFSTLAPEAWPAMELPEPCVPEPG PPVFANFTQLLTISPLVVAEGGTAMLEWRRVQPTLDLMGAELRS SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIH GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDF HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLFFQVLG SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQHRSTGLRAGCSAMPILEP LSVETNAVGQDVSVLFRVTOALQFELCKHSTGGCGAEWWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGGELSN SFPVTIQRATVMNLRLEPLHTQNTQCETLTTAHLEATLEEAGF PPTFHYEVVQAPRKGNLQLQGTRLSDGGGFTQDDIQAGRVTYC TARASEAVEDTFFRYTVAPFYFSFLYTPFHIGGDPDAPVLTT LLVVPEGGEGVLSADHLFVKSLNSASYLYEWMERPRLGRLAWF TORKTHMVTSFTNEDLLRGRLVYQHDDSETTEDDIFFVATRQC SSGDMAWEEVRGVFRVAIQLVVQHDDSETTEDDIFFVATRQC SSGDMAWEEVRGVFRVAIQLVVQHDDSETTEDDIFFVATRQC SSGDMAWEEVRGVFRVAIQLVVQHDDSETTEDDIFFVATRQC SSGDMAWEEVRGVFRVAIQLVVQHDDSETTEDDIFFVATRQC TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFYHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGQGTTDTAVLHLDTNLDIRSGDEVHYH AGPRRGQLVRAGGPATAFSQQDLLDGAVLYSHNGSLSPEDTM SVEAGFVHTDATLQVTTALEGPLAPLKLVRHKKIYVFQGBAAF RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI SVEAGFVHTDATLQVTTALEGPLAPLKLVRHKKIYVFQGBAAF RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSGGAVDTGRYLVYHSRPEAWSDAFSLDVASGLAADEPI LDPVOSFSGGAVDTGRYLVYHSRPEAWSDAFSLDVASGLAADEPI				SETDVENHOINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
LGITPFVFRLSQATDLEQUTAHSASELYVIAFGSNEDVIVLSM IISFVVRVSLVWIFFFLLCVAERTYKQVGIM GQGFASFFG*NHPEVTVAMALTDIDLQLQFSMSQPEALLLIAA PADHLLLQLYSGHLQVRLVLGQEELRLQTPAETLLSDSIPHTV LTVVEGWATLSVDGFLNASSAVPGAFLEVYPGLFVGGTGTLGL YLRGTSRPLGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASD VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAPQAG RRGGFIYVDIFEGHLRAVVEKGGGTVLLHNSVPVADGQPHEVS HINAHRLEISVDQYPHTSNRGVLSYLEPRGSLLLIGGLDAEAS HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNM AGCRLBEEEYEDDAYGHYBAFSTLAFRAWPAMBLPEPCVPEFG PPVFANFTQLLTISPLVVABGGTAWLBWRHVQPTLDLMEAELR SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIE GSEDTSDQLVLESVYTARVPMPSCLRRGQTYLLPIQVMFVNDP HIIFPHGSLMVILEHTQKPLGPEVFQAYDDPSACEGLTFOVLG SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPP LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGGBILSS SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGF PPTFHYEVVQAPRKGNLQLQGTRLSDGGFTQDDIQAGRVTYG TARASEAVEDTFFRFVTAPPYFSSLYTPPHHIGGDPDAPVLTT TARASEAVEDTFFRFVTAPPYFSSLYTPPHHIGGDPDAPVLTG TARASEAVEDTFFRFVTAPPYFSSLYTPPHHIGGDPDAPVLTG TODVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFYHSGADRGWIQLQVSBGQHQATALLEVQASI YLRVANGSSLVVPQGGGGTIDTAVLHLDTNLDIRSGDEVHYH TQEDLRKRRVLFYHSGADRGWIQLQVSBGQHQATALLEVQASI YLRVANGSSLVVPQGGGGTIDTAVLHLDTNLDIRSGDEVHYH AGPRIGGLYRAGGPATAFSQQDLLDGAVLYSHNGSLSPBDTM SVEAGPVHTDATLQVTIALEGPLAPLKLVHKKIYVFQGBAA RRDQLEAAQEAVPADIVFSVKSPSAGYLLWVSRGALADEPI SVEAGPVHTDATLQVTIALEGPLAPLKLVHKKIYVFQGBAA RRDQLEAAQEAVPADIVFSVKSPSAGYLLWVSRGALADEPI		i	1	VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI
11SFVVRVSLWMIFFFLLCVAERTYKQVGIM 5450 8136 1242 GQQFASFFG*NHPEVTVANALTDIDLQLQFSMSQPEALLLAA PADHLLQLYSGHLQVRLVUGQEELRLQTPAETILISDSIPHTV LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGL YLRGTSRPLRGCLHAATLINGRSLLRPLTPDVHEGCAEFFSASD VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAPQAG RRGDFIYVDIFFERHRAVVEKGQGTVLLHNSVEVADGQPHEVS HINAHRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEAS HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNM AGGCRLEEEFYEDDAVGHYEAFSTLAPEAMPAMELPEPCVPERG PPVPANFTQLLTISPLVVABGGTAWLEWRHVQPTLDLMEABLR SQVLFSYTRGAHYGELELDILGAQARKMFTLLDVYNRGAFFH HIIFPHGSLMVILEHTQKPLGPEVRQAYDPDSACEGLTFQVLG SSGLPVERRQDQEPATEFSCRELEAGSLVYVHCGGPAQDLTF VSDGLQASPPATLKVVALIRPAIQHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEMWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSS SFPVTIQRATVWMLREPLHTQNTQQETLTTHAHLEATLEEAGI PPTFHYEVVQAPRKGNLQLQGTRLSGGGFTQDDIQAGRVTYC TARASEAVEDTFFRVTAPPYFSPLYTFPIHIGGDPDAPVLTT TARASEAVEDTFFRVTAPPYFSPLYTFPIHIGGDPDAPVLTT LLVVPEGGESVLSADHLFVKSLNSASYLVEVMERPRLGRLAWG TQDKTTMVTSFTNEDLLRGRLVVQHDDSETTEDDIPFVATRQC SSGDMAWEEVRGVPRVA1QPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGRIQLQVSDGGHQATALLEVQASI YLRVANGSSLVVPQGGGGTIDTAVLHLDTNLDIRSGDEVHYH AGPRMGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMI SVEAGPVHTDATLQVTIALEGPLAPLKLVVRKKIVVFQGEAAA RRDQLEAAQEAVPADIVFSVKSPPSAGYLVMVSRGALADEPI SVEAGPVHTDATLQVTIALEGPLAPLKLVVRKKIVTYGGEAAA RRDQLEAAQEAVPADIVFSVKSPPSAGYLVMVSRGALADEPI				LGLTPEVERLSOATDLEOLTAHSASELYVIAFGSNEDVIVLSMV
\$450 \$136 \$136 \$136 \$1242				TISEVVEVSLVWIFFFLLCVAERTYKOVGIM
PADHLLLQLYSGHLQVRIVIGQEELRLQTPAETLLSDSIPHTV LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGL YLRGTSRPLRGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASD VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAPQAG RRGDFIYVDIFEGHLRAVVEKGGGTVLLHNSVPVADGQPHEVS HINAHRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEAS HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNM AGCRLEEEYEDDAYGHYEAFSTLAPEAWPAMELPEPCVPEFG PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEAELR SQVLFSVTRGAHYGELELDILGAQARKNFTLLDVVNKKARFIH GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDF HIIFPHGSLMVILEHTQKFLGPEVFQAYDPDSACEGLTFQVLG SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQTHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSS SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGF PPTFHYEVVQAPRKGNLQLQGTRLSDGGGFTQDDIQAGRVTYG TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTT LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWH TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIFFVATRQC SSGDMAWEEVRGVFRVAIQPVNDHAPVGTISRIFHVARGGRRI TDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIY TQEDLRKRRVLFVHSGADARGWIQLQVSDQQHQATALLEVQASI YLRVANGSSLVPQGGGGTIDTAVLHLDTNLDIRSGDEVHYHH AGPRWGQLVRRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMM SVEAGPVHTDATLQVTIALEGPLAPLKLVWHKKTYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVWSSGLAADEPI LDPVQSFSOEAVDTGRVLVLHSRPEAWSDAFSLDVASGLGAPI			1222	COORDERCAMUREUTVAMALTRIDIOLOFSMSOPEALLLLAAG
LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGL YLRGTSRPLRGCLHAATLINGRSLLRPLTPDVHEGCAEFSASD VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTGSRQAPLAFQAG RRGDFIYVDIFECHLRAVVEKGGTVLLHNSVPVADGQPHEVS HINAHRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEAS HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNM AGGRLBEEEYEDDAYGHYEAFSTLAPEAWPAMELPEPCVPEPG PPVFANFTQLLTISPLVVAEGTAWLEWRHVQPTLDLMEAELR SQVLFSVTRGAHYGELELDILGAQARMFTLLDVVNRKARFIH GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLP IQVNPVNDP HIIFPHGSLMVILETUGKPLGPEVFQAVDPDSACEGLTFQVLG SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSN SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGE PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYC TARASEAVEDTFFRFVTAPPYFSPLYTPFIHIGGDDAPVTY TARASEAVEDTFFRFVTAPPYFSPLYTPFIHIGGDDAPVTY TARASEAVEDTFFRFVTAPPYFSPLYTPFIHIGGDDAPVTY TOKKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQC SSGDMAWEEVRGVPRVAIQPVNDHAPVQTISRIFHVARGGRRI TDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTM SVEAGFWHDDATLQVTIALEGPLAPLKLVRHKKTYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVQSFSQEAVDTGRVLVLHSRPEAWSDAFSLDVASGLGAPI	5450	8136	1242	DADULT OF ASCHLORE AND COEFFER OF PARTILISTS I PHTVV
YLRGTSRPLRGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASD VALGFSGPHSLAAFFAWGTQDEGTLEFTLTTQSRQAPLAFQAG RRGDFIYVDIFEGHLRAVVEKGQGTVLLHNSVPVADGQPHEVS HINAHRLEISUQYPTHTSRRGVLSYLEPRGSLLLGGLDAEAS HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNM AGCRLEEEEYEDDAYGHYEAFSTLAFEAWPAMELPEPCVPEFG PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEABLR SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIH GSEDTSDQLVLEVSYTARVMPSCLRRGQTYLLPIQVNPVNDF HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLG SSGLPVERRDQPGEPATEFSCRELEAGSLVVVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSN SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGF PPTFHYEVVQAPRKGNLQLQCTRLSDGGFTQDDIQAGRVTYG TARASEAVEDTFFFRVTAPPYFSPLYTFPIHIGGDPDAPVLTT LLVVPEGGEGGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWF TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQC SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASG YLKVANGSSLVVPQGGGGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTM SVEAGPVHTDATLQVTTALEGPLAPLKLVRHKKIYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEP LDPVOSFSOEANDTGRVLYLHSBRPEAMSDAFSLDVASGLAADEP LDPVOSFSOEANDTGRVLYLHSBRPEAMSDAFSLDVASGLAADEP				I THE PROPERTY OF THE PROPERTY
VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAFQAG RRGDFIYVDIFEGHLRAVVEKGQGTVLLHHNSVPVADGQPHEVS HINAHRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEAS HLQEHRLGITPEATMASLLGCMEDLSVNGQRRGLEBALLTRNM AGCRLEEEYEDDAYGHYEAFSTLAPEAWPAMELPEPCVPEPG PPVFANFTQLLTISPLVVABGGTAMLEWRHVQPTLDLMEAELR SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIH GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDP HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLG SSGLPVERRDQPGEPATEFSCRELEAGSLVVVHCGGPAQDLTF VSDGLQASPPATLKVVALRPAIQIHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSN SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGF PPTFHYEVVQAFRKGNLQLQGTRLSDGQFTQDDIQAGRVTYG TARASEAVEDTFFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTM LLVVPEGGEGGULSADHLFVKSLNSASYLYEVMERPRLGRLAWR TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQC SSGDMAWEEVRGVFRVAIQPVMDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGGGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTM SVEAGPVHTDATLQVTTALEGPLAPLKLVRHKKIYVFGGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEP) LDPVOSFSOEADDTGRVLYLHSRPEAMSDAFSLDVASGLABAP	1	·		DIVVEGWAI DO VOOT DIVASSAVEGAT DEVE TODE VOOTOTEEEESASDD
RRGDFIYVDIFEGHLRAVVEKGQGTVLLHNSVPVADGQPHEVS HINAHRLEISUDQYPHTISNRGVLSYLEPRGSLLLGGLDAEAS HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRIM AGCRLEEEEYEDDAYGHYEAFSTLAPEAWPAMELPEPCVPEFG PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEAELR SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVMRKARFIH GSEDTSDQLVUEVSVTARVPMPSCLRRGGTYLLPIQVNPVNDH HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLG SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDFQHHAYDTVENLALEVQVGGEILS SFPVTIQRATVWMLRLEPLHTQNTQCETLTTAHLEATLEEAG PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTODDIQAGRVTYC TARASEAVEDTFFFRVTAPFYFSFLYTFPIHIGGDPDAPVLTT LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWF TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIFVATRQC SSGDMAWEEVRGVFRVAIQFVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRRRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMI SVEAGPVHTDATLQVTIALEGPLAPLKKLVRHKKIYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSOEAVDTGRVLVHISRPEAWSDAFSLDVASGLGAPI	1		1	YERGISKPERGCERMATEROADERFEIT BYTHOGENAPLA FOACG
HINAHRLEISVDQYPTHTSNRGVLSYLEPRGSILLGGLDARAS HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRM AGCRLEEEYEDDAYGHYEAFSTLAPEAWPAMELPEPCVPEPG PPVFANFTQLTTISPLVVARGGTAWLEWRHVQPTLDLMEAELR SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIH GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDP HIIFPHGSLMVILLEHTQKPLGPEVFGAYDDDSACEGLTFQVLY SSGLPVERRDQPGEPATEFSCRELEAGSLVVVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSN SFPVTIQRATVWMRRLEPLHTQNTQQETLTTAHLEATLEEAGE PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYG TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTT LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWF TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQG SSGDMAMEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGPADAQLVLTKKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGRIQLQVSDGQHQATALLEVQASI YLKVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMI SVEAGPVHTDATLQVTIALEGFLAPLKLVRHKKIYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSOEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPI	\	1	1	VALGESGPHSLAAF PAWG TODEGT DEFT THI TOSKQAFDAF QAGO
HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNM AGCRLEEEYEDDAYGHYEAFSTLAPEAWPAMELPEPCVEEG PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEAELR SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIH GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDP HIIFPEGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLG SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSUFRVTGALQFGELQKHSTGGVEGABWWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSN SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGE PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYG TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTN LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERRRLGRLAWE TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRGC SSGDMAWEEVRGVPRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYI TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYH AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTM SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAM RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPYOSFSGEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAP	Î			
AGCRLEEEYEDDAYGHYEAFSTLAPEAWPAMELPEPCVPEPG PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEABLR SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIH GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDP HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLG SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSN SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGE PPTFHYEVVQAPKGRLQLQGTRLSDGQGFTQDDIQAGRYTYG TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTM LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWG TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQC SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASE YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTM SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSOEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAP	1			
PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEAELR SQVLFSVTRGAHYGELELDILGAQARKMFTILDVVNRKARFIH GSEDTSDQLVLEVSVTARVPMPSCLRRGGTYLLPIQVNPVNDH HI IFPHGSLMVLLEHTQKPLGPEVFQAYDPDSACEGLTFQVLG SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSN SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGI PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYC TARASEAVEDTFRFRVTAPPYFSPLYTFPHIGGDPDAPVLTM LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWH TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQC SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYH AGPRWGQLVRAGQPATAFSQDDLLDGAVLYSHNGSLSPEDTMM SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMYSRGALADEPI LDPYOSFSOEAVDTGRVVYLHSRPEAWSDAFSLDVASGLGAPI				HLQEHRLGLTPEATNASDLGCMEDLSVNGQKKGLKEADLTRNMA
SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIH GSEDTSQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDP HIIFPHGSLMVILEHTQKPLGPEVPQAYDPDSACEGLTFQVLG SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPP LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSN SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGE PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYG TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTN LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWF TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQG SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVASH YLRVANGSSLVVPQGGGTIDTAVLHLDTNLDIRSGDEVHYH AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTM SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAF RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPI		1		AGCRLEEEYEDDAYGHYEAFSTLAPKAWPAMELPEPCVPEPGL
GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDPHIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLG SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWANT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSM SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGH PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYG TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTT LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWH TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQG SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASH YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYH AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTM SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAH RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPH LDPVOSFSOEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAP	1	,		PPVFANFTQLLTISPLVVAEGGTAWLKWRHVQPTLDLMEAELRK
HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLG SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDFQHHAYDTVENLALEVQVGQEILSM SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGI PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYG TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTM LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWI TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQG SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRIV TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYI TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGGTIDTAVLHLDTNLDIRSGDEVHYHI AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMI SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPI]			SQVLFSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIHD
SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTF VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDFQHHAYDTVENLALEVQVGQEILSN SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGI PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYG TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTN LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWI TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQC SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGGTIDTAVLHLDTNLDIRSGDEVHYHI AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMI SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSQEAVDTGRVLYHSRPEAWSDAFSLDVASGLGAPI	1			GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDPP
VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPA LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSN SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGI PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYG TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTN LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWI TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQG SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMI SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSQEAVDTGRVLYHSRPEAWSDAFSLDVASGLGAPI	1		1	HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLGT
LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSN SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGH PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYG TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTN LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWH TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQG SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASH YLRVANGSSLVVPQGGGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMM SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAH RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSQEAVDTGRVLYHSRPEAWSDAFSLDVASGLGAPI			1	SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTFR
LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWAT AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSN SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGH PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYG TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTN LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWH TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQG SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASH YLRVANGSSLVVPQGGGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMM SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAH RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSQEAVDTGRVLYHSRPEAWSDAFSLDVASGLGAPI	1	1		VSDGLOASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPAN
AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSN SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGH PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYC TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTN LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWH TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQC SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASH YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMM SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAM RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSOEAVDTGRVLYHLSRPEAWSDAFSLDVASGLGAP	1	1		LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWATQ
SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGH PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYC TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTA LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWH TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQC SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASH YLRVANGSSLVVPQGGGGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMI SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSOEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPI		1	ł	AFHORDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSNL
PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYC TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTA LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWF TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQC SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASF YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMF SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAF RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAP			1	SFPVTIORATVWMLRLEPLHTONTOQETLTTAHLEATLEEAGPS
TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTM LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWF TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQC SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASF YLRVANGSSLVVPQGGGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMM SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAF RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAP	1	1		PPTFHYEVVOAPRKGNLOLOGTRLSDGOGFTODDIQAGRVTYGA
LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWF TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQC SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASF YLRVANGSSLVVPQGGGGTDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTM SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAF RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSOEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPI	}	1	i	TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTNV
TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQC SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMV SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSOEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPI	1	1	1	LLWVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWRG
SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRI TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASF YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTM SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAF RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAP	1	1		TODETTMUTSETNEDIARGRIAVYOHDDSETTEDDIPFVATROGE
TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYE TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASE YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTME SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAE RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPE LDPVOSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPE	1	1		CCCDMAWEEVPGVEDVATOPVNDHAPVOTISRIFHVARGGRRLL
TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASI YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMI SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPI				MEDDIA PODA DOCERADA OLATA PER VALLE VALLE VALLE DE LA VALLE
YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHV AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMI SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPI				TTDDVAFSDADBGFADAQDVDTKADDDFGSIVAVDDFIREIIRE
AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTM/ SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAA/ RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEP/ LDPVOSFSOEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAP/	· ·	1		TOWDLRKKKVLFVHSGADKGWIQLQVSDGQRQAIALDEVQASEF
SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPI	1	1		YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIKSGDEVHIHVI
RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPI LDPVOSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPI				AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF
LDPVOSFSOEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPI				SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI
LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAP:	1		1	RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS
A STATE OF THE DATE OF CALCULATION OF THE PROPERTY OF THE PROP				LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE
GATARTRADEWOULDALEADURAGETT	}			GVLVELEVLPAAIPLEAQNFSVPEGGSLTLAPPLLRVSGPYFPT

C 656			
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	sequence	\=possible nucleotide insertion)
	- Sequence	<u> </u>	LLGLSLQVLEPPQHGPLQKEDGPQARTLSAFSWRMVEEQLIRYV
1	1		HDGSETLTDSFVLMANASEMDRQSHPVAFTVTVLPVNDQPPILT
ĺ			TNTGLOMWEGATAPIPAEALRSTDGDSGSEDLYYTIEOPSNGRV
İ			VLRGAPGTEVRSFTQAQLDGGLVLFSHRGTLDGGFPFRLSDGEH
1			TSPGHFFRVTAQKQVLLSLKGSQTLTVCPGSVQPLSSQTLRASS
			SAGTDPQLLLYRVVRGPQLGRLFHAQQDSTGEALVNFTQAEVYA
1		•	GNILYEHEMPPEPFWEAHDTLELQLSSPPARDVAATLAVAVSFE
]		•	AACPORPSHLWKNKGLWVPEGORARITVAALDASNLLASVPSPO
			RSEHDVLFQVTQFPSRGQLLVSEEPLHAGQPHFLQSQLAAGOLV
1			YAHGGGGTQQDGFHFRAHLQGPAGASVAGPQTSEAFAITVRDVN
			ERPPOPOASVPLRLTRGSRAPISRAQLSVVDPDSAPGEIEYEVO
	1		RAPHNGFLSLVGGGLGPVTRFTQADVDSGRLAFVANGSSVAGIF
1	1		QLSMSDGASPPLPMSLAVDILPSAIEVQLRAPLEVPQALGRSSL
1			SQQQLRVVSDREEPEAAYRLIQGPQYGHLLVGGRPTSAFSQFQI
			DQGEVVFAFTNFSSSHDHFRVLALARGVNASAVVNVTVRALLHV
			WAGGPWPQGATLRLDPTVLDAGELANRTGSVPRFRLLEGPRHGR
	ļ	•	VVRVPRARTEPGGSQLVEQFTQQDLEDGRLGLEVGRPEGRAPGP
]			AGDSLTLELWAQGVPPAVASLDFATEPYNAARPYSVALLSVPEA
1	1		ARTEAGKPESSTPTGEPGPMASSPEPAVAKGGFLSFLEANMFSV
			IIPMCLVLLLLALILPLLFYLRKRNKTGKHDVQVLTAKPRNGLA
			GDTETFRKVEPGQAIPLTAVPGQGPPPGGQPDPELLQFCRTPNP
ļ	ļ		ALKNGQYWV
5451	1	2274	RDSSEQGRTGDTLGRPSACMDALKPPCLWRNHERGKKDRDSCGR
į	Į į		KNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFNFLFSPLP
•)		TPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARK
į	·		GVSQKNNDLTSCCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQ
1	1		PYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQFVGIFAQNRPEW
.			IISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQ
	'		KALVLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIEILSL
ł			YDAENLGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMITHQN
			IVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYS
	,		CGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNE
;			AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFWDKLIFAKIQDSL
}		•	GGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTECTGGCT
			FTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG
1			TNVFKGYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRK
	· .		KNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVHGESLRSSLVGV
	:		VVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKIGKE
1			SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQ
F450	·		IDSLYEHIQD
5452	1833	1138	SRVPSLCLSLSLSSPSREPVAGAPGCGTAGPPAMATLWGGLLR
]	ļ		LGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG
			HIYNKNISQKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSS
	l		VTIKVTIIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS
			DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ
5453		3.500	RKSVFDRHVVLS
3433	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV
	Ì		AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE
			PQEERSQQQDDIRELETKAVGMSNDGRFLKFDIEIGRGSFKTVY
			KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI
	}		VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL
			RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
		ı	LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
			LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII
[EGCIRONKDERYSIKDLLNHAFFQEETGVRVELABEDDGEKIAI
	j	;	KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG
5454		1500	YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
3434	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV
	ļ		AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE POFFPSOOODDIFFLETKAVGMSNDGPFLKEDIFIGEGSFKTVV
			PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAMGELODDVLTKGEROODBYFFAEMLKGLOUDNI
1	<i>.</i>		KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
<u> </u>	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 2 4	\=possible nucleotide insertion)
	sequence	 	VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL
j	} .		RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
[1	Ì	IGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
J	1	ļ	
		İ	LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII
J	j	ļ	EGCIRONKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI
		1	KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG
}		1.	YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5455	1359	377	LTMVSPATRKSLPKVKAMDFITSTAILPLLFGCLGVFGLFRLLQ
1 3.33	1		WVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNG
			GALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEIL
ł	1	į.	OCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALT
1		1	
l		1	KALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFF
1		1	DCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTT
l		1	TAQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPG
1			LFFSLMASRARKERKSKNS
5456	2	2332	CGAGLVAAGAVLVLYPASRAGERTRVPGSPAPSSLPLHSPGACG
1			TEVDMDPQRSPLLEVKGNIELKRPLIKAPSQLPLSGSRLKRRPD
1	1	1	QMEDGLEPEKKRTRGLGATTKITTSHPRVPSLTTVPQTQGQTTA
Į.		1	QKVSKKTGPRCSTAIATGLKNQKPVPAVPVQKSGTSGVPPMAGG
1.	(ĺ	KKPSKRPAWDLKGOLCDLNAELKRCRERTQTLDQENQQLQDQLR
1	1	1	DAQQQVKALGTERTTLEGHLAKVQAQAEQGQQELKNLRACVLEL
i .	1		EERLSTQEGLVQELQKKQVELQEERRGLMSQLEEKERRLQTSEA
1	ì	}	
1	Í		ALSSSQAEVASLRQETVAQAALLTEREERLHGLEMERRRLHNQL
1			QELKGNIRVFCRVRPVLPGEPTPPPGLLLFPSGPGGPSDPPTRL
f			SLSRSDERRGTLSGAPAPPTRHDFSFDRVFPPGSGQDEVFEEIA
}	1		MLVQSALDGYPVCIFAYGQTGSGKTFTMEGGPGGDPQLEGLIPR
	1		ALRHLFSVAQELSGQGWTYSFVASYVEIYNETVRDLLATGTRKG
ì	-	*	QGGECEIRRAGPGSEELTVTNARYVPVSCEKEVDALLHLARQNR
	l .	1	AVARTAQNERSSRSHSVFQLQISGEHSSRGLQCGAPLSLVDLAG
1		1	SERLDPGLALGPGERERLRETQAINSSLSTLGLVIMALSNKESH
1	1		VPYRNSKLTYLLQNSLGGSAKMLMFVNISPLEENVSESLNSLRF
1	•	· .	ASKVEPSVLFGTAQSNRKWKTDPDLCVCVCVCVCVCVCVCVCVP
1	•		MSMYRVRGGRVAGGCFIGWRAPCPRAIK
	 	1540	DDFVERRRWTRTTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA
5457	2	1540	LLRSAERLMRKVKKLRLDKENTGSWRSFSLNSEGAERMATTGTP
1	1 .		TADRGDAAATDDPAARFQVQKHSWDGLRSIIHGSRKYSGLIVNK
1	1	j	TADRGDAAATDDPAARFQVQKHSWDGDKSIIHGSKKISGDIVKK
1	,		APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV
		1	RKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGI
1	1	1	TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK
1		1	PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER
1			RLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW
1			EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT
1		1	GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI
1	1	1	ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA
1	1	1	ASLCQSCPQECPAVCGVRGGHQRLDQCS
			ASLCQSCPQECPAVCGVRGGRQRUQCS
5458	6642	4022	FVPGLREPQWEPAQPSATMSAPSEEEEYARLVMEAQPEWLRAEV
1			KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA
1			IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY
1		1	VRKVLELQTELKQLRNVLTNTQSENERLASVAQELKEINQNVEI
1		j	QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ
1	1	1	VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET
,	,	1	LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA
1		[EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS
	1	1	DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG
	{		DIPPETINT SET TOTAL MANAGEMENT OF CARDONAL DATE AND DESIGNATION OF THE PROPERTY OF THE PROPERTY OF
		1	SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG
			DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ
	1		HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS
			DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML
		}	DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA
1	1	1	DGGTGDSSPSPGSSLPSPLSDPRREPMNIYNLIAIIRDQIKHLQ
1			AAVDRTTELSRQRIASQELGPAVDKDKEALMEEILKLKSLLSTK
1	1	. 1	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
 	 	 	REQITTLRTVLKANKQTAEVALANLKSKYENEKAMVTETMMKLR
	[NELKALKEDAATFSSLRAMFATRCDEYITQLDEMQRQLAAAEDE
İ			KKTLNSLLRMAIQQKLALTQRLELLELDHEQTRRGRAKAAPKTK
	ļ		PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD
5459	316	1262	RGGHRLSGMASNFNDIVKQGYVRIRSRRLGIYQRCWLVFKKASS
			KGPKRLEKFSDERAAYFRCYHKVTELNNVKNVARLPKSTKKHAI
			GIYFNDDTSKTFACESDLEADEWCKVLQMECVGTRINDISLGEP
i		İ	DLLATGVEREQSERFNYYLMPSPNLGCYMGECALQITYEYICLW
1			DVQNPRVKLISWPLSALRRYGRDTTWFTFEAGRMCETGEGLFIF
1		[QTRDGEAIYQKVHSAALAIAEQHERLLQSVKNSMLQMKMSERAA
į.			SLSTMVPLPRSAYWQHITRQHSTGQLYRLQDVSSPLKLHRTETF
İ			PAYRSEH
5460	45	2097	RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPBVLRGRSP
1			GLGLAEMPSCGACTCGAAAVRLITSSLASAORGISGGRIHMSVL
	ł		GRLGTFETQILQRAPLRSFTETPAYFASKDGISKDGSGDGNKKS
			ASEGSSKKSGSGNSGKGGNQLRCPKCGDLCTHVETFVSSTRFVK
			CEKCHHFFVVLSEADSKKSIIKEPESAARAVKLAFOOKPPPPPK
J	ļ		KIYNYLDKYVVGQSFAKKVLSVAVYNHYKRIYNNIPANLROOAB
{			VEKQTSLTPRELEIRRREDEYRFTKLLQIAGISPHGNALGASMQ
]	j		QQVNQQIPQEKRGGEVLDSSHDDIKLEKSNILLLGPTGSGKTLL
	'		AQTLAKCLDVPFAICDCTTLTQAGYVGEDIESVIAKLLQDANYN
}	1		VEKAQQGIVFLDEVDKIGSVPGIHQLRDVGGEGVQQGLLKLLEG
			TIVNVPEKNSRKLRGETVQVDTTNILFVASGAFNGLDRIISRRK
1			NEKYLGFGTPSNLGKGRRAAAAADLANRSGESNTHODIEEKDRL
			LRHVEARDLIEFGMIPEFVGRLPVVVPLHSLDEKTLVOILTEPR
i i		,	NAVIPQYQALFSMDKCELNVTEDALKAIARLALERKTGARGLRS
1			IMEKLLLEPMFEVPNSDIVCVEVDKEVVEGKKEPGYIRAPTKES
			SEEEYDSGVEEEGWPROADAANS
5461	1481	160	INPPPPPKSPCGRARKWRRRRRPGAPEAAVMELPSGPGPERLFD
			SHRLPGDCFLLLVLLLYAPVGFCLLVLRLFLGIHVFLVSCALPD
		1	SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDH
-	* .		NIVNLLTTCSTPLLNSPPSFVCWSRGFMEMNGRGELVESLKRFC
1	· ·		ASTRLPPTPLLLFPEEEATNGREGLLRFSSWPFSIQDVVQPLTL
	:	•	QVQRPLVSVTVSDASWVSELLWSLFVPFTVYQVRWLRPVHROLG
	,		EANEEFALRVQQLVAKELGQTGTRLTPADKAEHMKRQRHPRLRP
			QSAQSSFPPSPGPSPDVQLATLAQRVKEVLPHVPLGVIQRDLAK
			TGCVDLTITNLLEGAVAFMPEDITKGTOSLPTASASKFPSSGPV
1 : 1			TPQPTALTFAKSSWARQESLQERKQALYEYARRRFTERRAQEAD
5462	663	3353	KIKEROMSANNSPPSAOKSVLPTAIPAVLPAASPCSSPKTGLSA
	1		RLSNGSFSAPSLTNSRGSVHTVSFLLQIGLTRESVTIEAQELSL
			SAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSENILOLIT
			SADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDY
)			CGEMLWGLVRQGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSN
			VSLPGPGLSVPRPLQPEYVALPSEESHVHQEPSKRIPSWSGRPI
1	Į		WMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGMQC
	1		KDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDN
			NDINSDSSRGLDDTEEPSPPEDKMFFLDPSDLDVERDEEAVKTI
	ĺ		SPSTSNNIPLMRVVQSIKHTKRKSSTMVKEGWMVHYTSRDNLRK
1 1			l ~
			RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS
			QGSNPHCFEIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS
			WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE
(ſ		NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM
j l			RFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEK
	ſ		LHGDMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC
	ļ		DLKPENVLLASAEPFPQVKLCDFGFARIIGEKSFRRSVVGTPAY
1 !			LAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTFPFNEDEDINDQI
, ,	1		QNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSVDKSLSHP
	F		
			WLQDYQTWLDLREFETRIGERYITHESDDARWEIHAYTHNLVYP
F4.53	0.2.5		KHFIMAPNPDDMEEDP
5463	237	1012	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
{	sequence	2542255	\=possible nucleotide insertion)
<u> </u>	Bedgerice	 	LSPCECTGTLGTIHRSCLEHWLSSSNTSYCELCHFRFAVERKPR
Į			PLVEWLRNPGPOHEKRTLFGDMVCFLFITPLATISGWLCLRGAV
}	1	i	1
١,	,		DHLHFSSRLEAVGLIALTVALFTIYLFWTLVSFRYHCRLYNEWR
1	[RTNQRVILLIPKSVNVPSNQPSLLGLHSVKRNSKETVV
5464	195	677	SPSMNPRKKVDLKLIIVGAIGVGKTSLLHQYVHKTFYEEYQTTL
1			GASILSKIIILGDTTLKLQIWDTGGQERVRSMVSTFYKGSDGCI
1	1	1	LAFDVTDLESFEALDIWRGDVLAKIVPMEQSYPMVLLGNKIDLA
	İ	į.	DRKYQSILENHLTESIKLSPDQSRSRCC
5465	5278	3348	KGDPREFIRVHREALECDYVSAHLHEWIDLIFGYKQQGPAAVEA
5405	3270	3340	VNVFHHLFYEGOVDIYNINDPLKETATIGFINNFGQIPKQLFKK
1	1	1	PHPPKRVRSRLNGDNAGISVLPGSTSDK1FFHHLDNLRPSLTPV
ı			
1	1	1	KELKEPVGQIVCTDKGILAVEQNKVLIPPTWNKTFAWGYADLSC
1			RLGTYESDKAMTVYECLSEWGQILCAICPNPKLVITGGTSTVVC
1			VWEMGTSKEKAKTVTLKQALLGHTDTVTCATASLAYHIIVSGSR
1			DRTCIIWDLNKLSFLTQLRGHRAPVSALCINELTGDIVSCAGTY
1		1	IHVWSINGNPIVSVNTFTGRSQQIICCCMSEMNEWDTQNVIVTG
l			HSDGVVRFWRMEFLQVPETPAPEPAEVLEMQEDCPEAQIGQEAQ
i		ļ	DEDSSDSRADEQSISQDPKDTPSQPSSTSHRPRAASCRATAAWC
1			TDSGSDDSRRWSDQLSLDEKDGFIFVNYSEGQTRAHLQGPLSHP
1	1	ı	HPNPIEVRNYSRLKPGYRWERQLVFRSKLTMHTAFDRKDNAHPA
1			EVTALGISKDHSRILVGDSRGRVFSWSVSDQPGRSAADHWVKDE
1		i	GGDSCSGCSVRFSLTERRHHCRNCGQLFCQKCSRFQSEIKRLKI
]		1	SSPVRVCQNCYYNLQHERGSEDGPRNC
L			
5466	3	992	HACAHASAHASGRLVRWWRKRRSVMGIQTSPVLLASLGVGLVTL
1	j	1	LGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTKRF
1		1	RFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQG
1	ł	į	YVDLVIKVYLKGVHPKFPEGGKMSQYLDSLKVGDVVEFRGPSGL
1	1		LTYTGKGHFNIQPNKKSPPEPRVAKKLGMIAGGTGITPMLQLIR
1		[AILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLW
}	1	1	FTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMV
į		}	OLACHPNLDKLGYSQKMRFTY
5467	2103	1 4	GEALRYGTRGCRRDLPDPQARIFIQKKDLEEDESVTAAHLKSRG
3407	2103	1	RSPRKIDOFCNSSNMVHGSVTFRDVAIDFSQEEWECLQPDQRTL
į	i i		YRDVMLENYSHLISLAGSSISKPDVITLLEQEKEPWMVVRKETS
ì	ł		RRYPDLELKYGPEKVSPENDTSEVNLPKQVIKQISTTLGIEAFY
	į	1	
1		1	FRNDSEYROFEGLOGYQEGNINOKMISYEKLPTHTPHASLICNT
1	1.	1	HKPYECKECGKYFSCGSNLIQHQSIHTGEKPYKCKECGKAFQLH
	: *		IQLTRHQKFHTGEKTFECKECGKAFNLPTQLNRHKNIHTVKKLF
			ECKECGKSFNRSSNLTQHQSIHAGVKPYQCKECGKAFNRGSNLI
1	1.		QHQKIHSNEKPFVCKECGMAFRYHYQLIEHCQIHTGEKPFECKE
1			CGKAFTLLTKLVRHQKIHTGEKPFECRECGKAFSLLNQLNRHKN
1	1	1	IHTGEKPFECKECGKSFNRSSNLVQHQSIHAGIKPYECKECGKG
i			FNRGAHLIQHQKIHSNEKPFVCRECEMAFRYHCQLIEHSRIHTG
1	1		DKPFECQDCGKAFNRGSSLVQHQSIHTGEKPYECKECGKAFRLY
i	1	1	LQLSQHQKTHTGEKPFECKECGKFFRRGSNLNQHRSIHTGKKPF
1	İ]	
1			ECKECGKAFRLHMHLIRHQKLHTGEKPFECKECGKAFRLHMQLI
L	1	1	RHQKLHTGEKPFECKECGKVFSLPTQLNRHKNIHTGEKAS
5468	225	2976	SFLTDLFQSLAQLENLCKQLYETTDTTTRLQAEKALVEFTNSPD
I	1		CLSKCQLLLERGSSSYSQLLAATCLTKLVSRTNNPLPLEQRIDI
1]	RNYVLNYLATRPKLATFVTQALIQLYARITKLGWFDCQKDDYVF
1	1.		RNAITDVTRFLQDSVEYCIIGVTILSQLTNEINQVSATAFLIEA
1	ľ	1	DTTHPLTKHRKIASSFRDSSLFDIFTLSCNLLKQASGKNLNLND
1		1	ESQHGLLMQLLKLTHNCLNFDFIGTSTDESSDDLCTVQIPTSWR
1	1	1	
1			SAFLDSSTLQLSTIGRCEYEKTCALLVQLFDQSAQSYQELLQSA
1	1		SASPMDIAVQEGRLTWLVYIIGAVIGGRVSFASTDEQDAMDGEL
j	1		VCRVLQLMNLTDSRLAQAGNEKLELAMLSFFEQFRKIYIGDQVQ
ł	[KSSKLYRRLSEVLGLNDETMVLSVFIGKIITNLKYWGRCEPITS
Į.		1	KTLQLLNDLSIGYSSVRKLVKLSAVQFMLNNHTSEHFSFLGINN
1	1	1	QSNLTDMRCRTTFYTALGRLLMVDLGEDEDQYEQFMLPLTAAFE
1			AVAQMFSTNSFNEQEAKRTLVGLVRDLRGIAFAFNAKTSFMMLF
1			EWIYPSYMPILQRAIELWYHDPACTTPVLKLMAELVHNRSQRLQ
L	<u> </u>	_l	The second secon

C130	1 Dec 23 11 1	T	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
1	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	}	\=possible nucleotide insertion)
		 	FDVSSPNGILLFRETSKMITMYGNRILTLGEVPKDQVYALKLKG
i	İ		ISICFSMLKAALSGSYVNFGVFRLYGDDALDNALQTFIKLLLSI
-	}		PHSDLLDYPKLSQSYYSLLEVLTQDHMNFIASLEPHVIMYILSS
	1		ISEGLTALDTMVCTGCCSCLDHIVTYLFKQLSRSTKKRTTPLNO
			ESDRFLHIMQQHPEMIQOMLSTVLNIIIFEDCRNOWSMSRPLLG
1	ł	•	
			LILLNEKYFSDLRNSIVNSQPPEKQQAMHLCFENLMEGIERNLL
5469	 		TKNRDRFTQNLSAFRREVNDSMKNSTYGVNSNDMMS
5469	134	2653	DQEFETSLVPWHLPMGWLCSGLLFPVSCLVLLQVASSGNMKVLQ
			EPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLSEAHTC
i	[ĺ	VPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPS
1		1	EHVKPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVN
			IWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQ
[1		CYNTTWSEWSPSTKWHNSYREPFEQHLLLGVSVSCIVILAVCLL
1	}	}	CYVSITKIKKEWWDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQ
J .			EPAKCPHWKNCLTKLLPCFLEHNMKRDEDPHKAAKEMPFQGSGK
		•	SAWCPVEISKTVLWPESISVVRCVELFEAPVECEEEEEVEEEKG
 	ľ		SFCASPESSRDDFQEGREGIVARLTESLFLDLLGEENGGFCOOD
			MGESCLLPPSGSTSAHMPWDEFPSAGPKEAPPWGKEQPLHLEPS
			PPASPTQSPDNLTCTETPLVIAGNPAYRSPSNSLSQSPCPRELG
}			PDPLLARHLEEVEPEMPCVPOLSEPTTVPQPEPETWEOILRRNV
j			LOHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGEAG
[]			
1 1			YKAFSSLLASSAVSPEKCGFGASSGEEGYKPFQDLIPGCPGDPA
1			PVPVPLFTFGLDREPPRSPQSSHLPSSSPEHLGLEPGEKVEDMP
			KPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCHGQEDGG
1	-		QTPVMASPCCGCCCGDRASPPTTPLRAPDPSPGGVPLEASLCPA
			SLAPSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYM
			RVS
5470	17	1418 .	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF
			KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI
{			INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY
1 1		-	SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA
		•	LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA
• [**	•	LILATORISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP
1 -1			YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA
	-		LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF
[1 4 4 4	ug	PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL
1	:		
[· [GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT
5471	1868	<u> </u>	EGEDSAMTDMPPTEEVTDIVEMREENE
] -*/-	1000	658	RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGGEPRRTEGV
			GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR
1			KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR
j j	1		ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR
]			GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD
1 1	·		HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
1			NRPIFPGKHYLDQLNHILGILGSPSQBDLNCIINMKARNYLQSL
} I			PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP
] [•	YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFO
1		1	PGVLEAP
5472	1469	753	LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR
1 1			DPOALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWOGDTFHR
1 !	ŀ		GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA
[
į l			VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEA
; !	1		IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA
 		·	VGTMLPCFCPTEQALALV
5473	3	2119	FMNVKLLIQDLEDIEQRVPVMDAQYKIITKTAHLITKESPQEEG
	ļ		KEMFATMSKLKEQLTKVKECYSPLLYESQQLLIPLBELEKQMTS
į l	†		FYDSLGKINEIITVLEREAQSSALFKQKHQELLACQENCKKTLT
[1		LIEKGSQSVQKFVTLSNVLKHFDQTRLQRQIADIHVAFQSMVKK
		1	TGDWKKHVETNSRLMKKFEESRAELEKVLRIAQEGLEEKGDPEE
		İ	LLRRHTEFFSQLDQRVLNAFLKACDELTDILPEQEQQGLQEAVR
! !	j		KLHKQWKDLQGEAPYHLLHLKIDVEKNRFLASAEECRTELDRET

Predicted Pred				
Mociation Corresponding to first maino acid residue of samino acid residue of samino acid residue of samino acid sequence P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, Q-Glutamie, R-Arginie, P-Proline, P-Prol	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence Proline, Q-Glutamine, R-Arginine, Corresponding amino acid sequence Proline, Q-Glutamine, R-Arginine, Codon, Y-Stophan, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosin	ID	beginning	nucleotide	
to first amino acid residue of amino acid sequence sequ	NO:	nucleotide	location	
to first amino acid residue of amino acid sequence sequ		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first amino acid residue of amino acid residue of amino acid sequence ##Typtophan, %=7yrosine, %=1dhine, %=5cop Codon, %=possible nucleotide deletion, %=possible nucleotide insertion) ##Typtophan, %=7yrosine, %=1dhine, %=5cop Residue of ##Typtophan, %=7yrosine, %=1dhine, %=5cop Residue of ##Typtophan, %=7yrosine, %=1dhine, %=5cop Residue of ##Typtophan, %=7yrosine, %=1dhine, %=5cop Residue of ##Typtophan, %=7yrosine, %=1dhine, %=5cop Residue of ##Typtophan, %=7yrosine, %=1dhine, ##Typtophan, %=1dhine, %=1dhine, %=1dhine, %=1dhine, ##Typtophan, %=1dhine, %				
amino acid residue of amino acid sequence divergine of amino acid sequence divergine of amino acid sequence divergine of codon, /-possible nucleotide deletion, /-possible nucleotide disection) KLMPQESSEKITERIPYPSOKOPHILCERIQUIERICVILPY RDVPRUPPOTCHTIKERIAANIDSTYRKINEEDEPOKNOVITSERS ETSMISHERIVATIVESSERRARGOGENELAKISSERRALIVER RDVPRUPPOTCHTIKERIAANISTSKRANGUNGANGAGGEGOGENE RETSMISHERIVATIVESSERRARGOGENELAKISSERRALIVER ETSMISHERIVATIVESSERRARGOGENELAKISSERRALIVER RUPERUPPOTCHTIKERIAANISTSKRANGUNGANGAGGEGOGENELAKIDTE NIFERQUILHHRONTKISTAKKRUNUOQIAAQGGEGOGENEKILDTE NIFERQUILHHRONTKISTAKKRUNUOQIAAQGGEGOGENEKILDTE NIFERQUILHHRONTKISTAKKRUNUOQIAAQGGEGOGENEKILDTE NIFERGUILHHRONTKISTAKKRUNUOQIAAQGGEGOGENEKILDTE NIFERGUILHHRONTKISTAKKRUNUOQIAAQGGEGOGENEKILDTE NIFERGUILHHRONTKISTAKKRUNUOQIAAQGGEGOGENEKILDTE NIFERGUILHHRONTKISTAKTOR VAROMENULANGATATARGEMARVIKSOMLIKGOSTI LOQATOROPPOKKSICAGIAVASKOSPRUFAGEMARVIKSOMLIKGOSTI LOQATOROPPOKKSICAGIAVASKOSPRUFAGEMARVIKSOMLIKGOSTI LOQATOROPPOKRISTAVIKSOMLIKGOSTI SICARSTUDICLARKEPI LOQATOROPPOKRISTAVIKSOMLIKGOSTI SICARSTUDICLARKEPI LOQATOROPPOKRISTAVIKSOMLIKGOSTI SICARSTUDICLARKEPI LOQATOROPPOKRISTAVIKSOMLIKGOSTI VITARARGANITAKI LOQATOROPPOKRISTAVIKSOMLIKGOSTI VITARARGANITAKI TERRITYTOROPROKREBELIANDUGGANITAKAANITAKI STRATTYTOROPROKREBELIANDUGGANITAVIKAANITAKI STRATTYTOROPROKREBELIANDUGGANITAVIKAANITATI STRATTYTOROPROKREBELIANDUGGANITAVIKAANITATI STRATTYTOROPROKREBELIANDUGGANITAVIKANDITATI STRATTYTOROPROKREBELIANDUGGANITAVIKANDITATI STRATTYTOROPROKREBELIANDUGGANITAVIKANDITATI STRATTYTOROPROKREBELIANDUGGANITAVIKANDITATI STRATTYTOROPROKREBELIANDUGGANITAVIKANDITATI STRATTYTOROPROKREBELIANDUGGANITAVIKANDITATI STRATTYTOROPROKREBELIANDUGGANITAVIKANDITATIATIATIATIATIATIA STRATTYTOROPROKREBELIANDUGGANITAVIKANDITATIATIATIATIATIATIATIATIATIATIATIATIAT) · · · · ·	
remidue of amino acid sequence (Codon, 'poposible nuclectide deletion, 'poposible nuclectide deletion, 'poposible nuclectide deletion,' poposible nuclectide nuclectide deletion,' poposible nuclectide deletion,' poposible nuclectide deletion,' poposible nuclectide n				Paproline, Quolucalizate, Kanightine,
amino acid sequence Codom, /-possible nucleotide desletion,		amino acid		S=Serine, T=Threonine, V=Valine,
Aspossable mucleotide insertion		residue of	amino acid	
Sequence \		amino acid	sequence	Codon, /=possible nucleotide deletion,
RIMPOESSERITKERHEVFFSBSPHILCERRIGULIERICVKLIPV RDPVEDTOTICHVILLERARIDDETVIKKIMEDDPOKMYDTSFE'S EFSSHISTMETOLKGI KGEALDTAMIGEVRAVEBIRKGYTKER ETISMIKSRIKAULTEUSBERAGNGGOBLAKLSSSFRAVITLS EVERMISSREVOLGISESSERORGOBARILDTE HUFFRAGOLLHHONGYKR ISAKKRUVOGLIAGNGGSGOLPER HEIRKIKESTLIGGEBSERORGRIGVTHERKERFETNKETVUR LVERASETPLGGOLHHONGYKER ISAKKRUVOGLIAGNGGSGOLPER HEIRKIKESTLIGGESSERORGRIGVTLERKERFETNKETVUR LVERASETPLGGONGLIQOGAKSIKEGVKKLEDTLEEFYVIDK S 5474 2 7860 TPDVRQLQASREGIAVASKCSPRØFAGERRAFVKSGMLIGGSTI LUXERASETPLGFONKOLLQOGAKSIKEGVKKLEDTLEEFYVIDK GECROTOPPDEKSIKOMLQIVCROCKTISLCASSTDOCLANKFT LOGANOVEPYGGAYPROTOVVYANNGOAYAPYOYPYARJIYOO PANOVITIEREYNDIDISLALAGHAGAATAPPALGSLEWY LOQANOVEPYGGAYPROTOVVYANNGOAYAPYOYPYARJIYOO PANOVITIEREYNDIDISLALAGHAGAATAPPALGSLEWY VORKOMEDYLAMIALISLATRALLILEPKSKIEGGORMATVETI STERNYTVOPDVOVEERBDLESVOLEKCOTITVMEERILUCVYK GEWANNENSHILLEEDIALAGHAGAATAPPALGSLEWYF VORKOMEDYLAMIALISLATRALLILEPKSKIEGGORMATVETI STERNYTVOPDVOVEERBDLESVOLEKCOTITVMEERILUCVYK GEWANNENSHILLEENIALISLATRALLILEPKSKIEGGORMATVETI VORKOMENSHILLEEDIALAGHAGAATAPPALGSLEWYF VORKOMENSHILLEEDIALAGHAGAATAPPALGSLEWYF VORKOMENSHILLEEDIALAGHAGAATAPPALGSLEWYF VORKOMENSHILLEENIALISLATRALLILAGAATAPALAGLIKATVATYPTYT STERNYTVOPTOVEERBOLESVOLEKCOTITVMEERILUCVYK GEWANNISPERANGAAGAATARAKATAPPATATAPPATATAPPATA PSTRASEVLCSTNVSHYSERJOHAGAATARAKATAPPATATAPPATATAPPATA STRASEVLCSTNVSHYSERJOHAGAATARAKATAPPATATAPPATATAPPATATAPPATATAPPATATAPPATATAPPATATAPPATATAPPATATAPPAT				
RDPVRDTPGTCHVILKELRAALDSTYRKIMBED PKORNTTSRES ETSSHLKSELKVILEVSSEREADKOODELAKLSSSFRAUVTLLS EVERHLASPIDCUTYSELEVINSLESSLEIGSKEVOODAOGEGELPERG ETISHLKSELKVILEVSSEREADKOODELAKLSSSFRAUVTLLS EVERHLASPIDCUTYSELEVINSLESSLEIGSKEVOODAOGEGELPERG HEIGHAGUTLAHKOOKTREISAKKEDVOODAOGEGELPERG HEIGHAGUTLAHKOOKTREISAKKEDVOODAOGEGELPERG HEIGHAGUTLAHKOOKTREISAKKEDVOODAOGEGELPERG LVKEASETILEGPONKOLLOOQAKSIKEOVKILBOVTLERVEYPETTINKETVV YLOVOOSSHERFILSPSSLESISSILGOKEPSKRTESIAVOARN LVKEASETILEGPONKOLLOOQAKSIKEOVKILBOVTLERVEYVIDK STOPVROLOASREOTAVASROSSPRIPAGEMAFVKSCHLLOOSTI LKRWKKNWPDLWSDGRILTYTDOOTROUTEDWINDPROCHILKTV OCCHTUTPEPPERSECHLISTELAASSTODOLAKPET LOOSSTITTAVVGSANVATOROTROUTEDWINDPROCHILKTV OCCHTUTPEPPERSECHLISTELAASSTODOLAKPET LOOSSTITTAVVGSANVATOROTROUTEDWINDPROCHILKTV SCHAMMEDITAANITOTETSVUSSPPYTATAADAPSVGRTLS LOOSTITTAVVGSANVATOROTROUTEDWINDPROCHILKTV STRAYTVOODOLAVAROOONTAVPYOYTYTAALOONTAVPYOYTAALOONTAVPYOYTYTAALOONTAVPYOYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTYTYTY STRAYTVOODOHAVANOOONTAVPYOYTYTAALOONTAVPYOYTYTAALOONTAVPYOYTYTYTYTYTY STRAYTVOODOHAVANOOONTAVPYOYTYTYTYTYTYTY STRAYTVOODOHAVANOOONTAVPYOYTYTYTYTYTYTY STRAYTVOODOHAVANOOONTAVPYOYTYTYTYTYTYTYTY STRAYTVOODOHAVANOOONTAVPYOYTYTYTYTYTYTYTYTYTY STRAYTVOODOHAVANOOONTAVPYOYTYTYTYTYTYTYTYTYTY STRAYTVOODOHAVANOOONTAVPYOYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTYTY		sequence		
EPSSWISTINTQLKGIKGRATUTAMHGEVERAVETINGVITKS ETISMIKSRIKVITEVSSENDRAKGDELAKUSS SFRALVITLIS EVERMLSRIPGOCQYKEIVRISLELI SGSKEVQEOARKILITUT NLERAQOLLHHIQOKTRI ISAKRAYDQOLIAQAQGGGLPDRA HEBLARLESTLDGLERSRERGERRIQVILKWERFETNIETVVR YLEYGTSSHERTLESSLISISSEBLEGOVERSFEKKILVAQARN LVXEASETPLGPONKOLLQQAKS IKEQVKKLEDTLEEETYIDK S 5474 2 780 PPDVRQLABARRATUASSKSPRW FAGEMAYVXSGPLLIVYDDT LVXEASETPLGPONKOLLQQAKS IKEQVKKLEDTLEEETYIDK S 5475 CECROTOPPGGKSKOCHLQIUVCROKTISLACASTDDCLAWKFY LQDATYNYDYGAMYDTSVYSKEPPVTYAAARDVRITKY QECROTOPPGGKSKOCHLQIUVCROKTISLACASTDDCLAWKFY LQDATYNYDYGAMYDTSVYSKEPPVTYAAARDVRITLS LQDATYNYDYGAMYDTSVYSKEPPVTYAAARDVRITKY QECROTOPPGGKSKOCHLQIUVCROKTISLACASTDDCLAWKFY LQDATYNYDYGORAPPOTOVYAANOOAYAVPYOYFYAGLIVOO PANOVI IRERYRDNISDLALKAKAGAATGMAGSLFVWF SAGNISLISIJTCCTTYPPSSSPCLLHSPETFITMPFHLTGYYTL GERNITYOPPVOVEFFEBLISVUGKKCOTIVTWEERHIVUTQK GEVPNRORKRINLAGANTISLAWKILLLIKEDREITHFMFHLTGYTL STERNITYOPPVOVEFFEBLISVUGKKCOTIVTWEERHIVUTQK GEVPNRORKRINLAGEMALVISLATDRACKAGVATUTHEERHIVOTO VITKITNIBENCHSEELKALQAAVILLSHIPFRIPNITTYTYTYTYC VITKITNIBENCHSEELKALQAAVILLSHIPFRIPNITTYTYTYTYV SHAMIYASY FRATGSASQULARYTPREMBENTTYKYTYTYTYTY VITKITNIBENCHSEELKALQAAVILSHIPFRIPNITTYTYTYTYTY SHAMIYASY FRATGSASQULARYTPREMBENTTYKYTYTYTY VITKITNIBENCHSEELKALQAAVILSHIPFRIPNITTYTYTYTYTY SHAMIYASY FRATGSASQULARYTPREMBENTYSKERHIPSKATTACABRA AVTOPPOTSTSVOPHLE BLAQDLAVTNISGLEHLASPARGAN YLGYBOCHERA SAGNISAGULARYTPROKETTYSKERHITYSKTATACEL ASGCYPTOPMETRYGHILQAKUTLSHIPTSKATTYSKERHIPSKATTACABRA AVTOPPOTSTSVOPHLE BLAQDLAVTNISGLETYSSKERHIPSKATACAG SQVBISGIGESVLINSSCHITYNSKARHITYSSKTEPSKATACAG SQVBISGIGESVLINSSCHITYNSKARHITYSSKTEPSKATACAG SQVBISGIGESVLINSSCHITYNSKARHITYSSKTEPSKATACAG SQVBISGIGESVLINSSCHITYNSKARHITYSSKATHYSSKATACAGAA VORKYPKCHILQARVICHAGHATUASHATAAAAAVAATAAAAAAAAAAAAAAAAAAAAAAAAAA		1	(
ETISNIKSRIKVILTEVISSINBAQKQODELAKIJSSIFKALIVILTE RVEKNISNINGOVYKEVINSISELEL ISGISKUVGOQAKSILDTE NLPEAQOLLUHHQOKTKE ISAKKRUVQOJIAQAQQEGOLIPON HEIKAKLESTILOLERSERPEGERI OYVILKWERPETENKETVUV YLPOTOSSHERFIJSSILSSILSOINSFERNTSILAVQARN LVKRASEIPIGPONKQLLQQQAKSI KEQVKKLEDTILEEVIVIDX S 5474 2 780 FPDVRGLQASRRITAVASKCSERPFAGESHAPVKSGMLLRGSTI LKURKKANNPDLASDCHLIYVDOTRONIEDKVHMMMDCINIENG QCCDTQPPDGASKCHCULQIVVEGOKTISILCASETDCLAMKEP LQDSRTNTAVVGSAMMDETSIVVSS PPYTAVAAPADEVGREIL LQQATYOTOPYGGAYPPOTOVVANAMOANAVPYVAGILYQQ PARQVI IRENTADNISDLALCMLAGAATGAAGSLEPWP 5475 2 506 ARGMLESISJITCQTTFFFSSCLLHSFETT IRTMFFNLITGYTYFF VOKNMEDIVAJANISLAVRICALLIKFFDETEIRTMFFNLITGYTYFF VOKNMEDIVAJALNISLAVRICALLIKFFDETEIRTMFFNLITGYTYFF VOKNMEDIVAJALNISLAVRICALLIKFFDETEIRTMFFNLITGYTYFF VOKNMEDIVAJALNISLAVRICALLIKFFDETEIRTMFFNLITGYTYFF VOKNMEDIVAJALNISLAVRICALLIKFFDETEIRTMFFNLITGYTYFF VOKNMEDIVAJALNISLAVRICALLIKFFDETEIRTMFFNLITGYTYFF VOKNMEDIVAJALNISLAVRICALLIKFFDETEIRTMFFNLITGYTYFF VOKNMEDIVAJALNISLAVRICALLIKFFDETEIRTMFFNLITGYTYFF VOKNMEDIVAJALNISLAVRICALLIKFFDETEIRTMFFNLITGYTYFF VOKNMEDIVAJALNISLAVRICALLIKFFDETEIRTMFFNLITGYTYFT VITKITNIBERCHEERILARJGRAVLISHFFRHENITTTWTWTYFTV VITKITNIBERCHEERILARJGRAVLISHFFRHENITTTWTWTYFTV VITKITNIBERCHEERILARJGRAVLISHFFRHENITTTWTWTYFTV VITKITNIBERCHEERILARJGRAVLISHFFRHENITTTWTWTYFTV SHAMVISSPFAAVSSASALLISHVFRKGMKEBSQDSILSILLPRAYNKESI SAUDSGIGESVUVSSGTHVANSDHEINTSKRITESPSFIVALUCL LQOPPEKPBRASSLLISHVFRKGMKEBSQDSILSILLPPAYNKESI SLPPULPFTERECEPPPEROSTWEF LRYMMISSENTHANSSMYPSPSPLISTSTRUFTALVILU PAFGGALITMKQVBFSKULDHITTSSKRITESPSFIVALU LQOPPEKPBRASSLLISHVFRKGMKEBSQDSILSILLPPAYNKESI SLPPULPFTERECEPPPELOSTWEF LRYMMISSENTHANSSMYPSPSPLITFSSKRITSSTRUKKLILL PAFGGALITMKQVBFSKULDHITTSSKRITSSTRUKKLILL REGEREREBERSTINSSRAPSPSVRPTILTHRANDARSORANDARVICAL VVRVAHTHOKHOLISTANDARSORANDARSORANDARVICALUS BUDGATVK VKWAHTHOKHOLISTANDARSORANDARSORANDARVICALUS BUDGATVA VKWAHTHOKHOLISTANDARSORANDARSORANDARVICALUS BUDGATVANDARVI DICHENTALISTANDARSORANDARSORANDARVICALEBORLIKU DICHENTAVARVHORISTAVA		}	1	
BVERMLSNYGDCVQYREIVRISLEELISGSKEVQGOARKILDYR ##ELRALESTLOGLERSBERGERRIQVTLEKWERFETNETVVW YLEQTOSSHERTLESSLESISGELEGOVETSFEKRIZVAVAEN LVKEASEIPLIGPQNKQLLQQAKSIKEQVKKLEDTLEEETVIDK S \$474 2 780 **TPDVRQLQASRGIAVASWCSPRFAGEENAFVKSGMLLRQSTI LKRWKKNWFDLASGGHLIYDDQTRQMIEDKVHNPMDCINITYD GECROTQPPDGKSCKOMLQIVUGDGRTISLAKESTDCLARKET LQORTNTAVUSANMTDETSVSSIPPTATAARABEWGRTLS LQQATVATAVUSANMTDETSVSSIPPTATAARABEWGRTLS LQQATVATAVUSANMTDETSVVSSIPPTATAARABEWGRTLS LQQATVATAVUSANMTDETSVVSSIPPTATAARABEWGRTLS LQQATVATAVUSANMTDETSVVSSIPPTATAARABEWGRTLS LQQATVATAVUSANMTDETSVVSSIPPTATAARABEWGRTLS LQQATVATAVUSANMTDETSVVSSIPPTATAARABEWGRTLS LQQATVATAVUSANMTDETSVVSSIPPTATAARABEWGRTLS LQQATVATAVUSANMTDETSVVSSIPPTATAARABEWGRTLS LQQATVATAVUSANMTDETSVVSSIPPTATAARABEWGRTLS STERRYTVOPDUWEFPEDLASVUSANGSTERVYPTAGLUGQ PARQVITRENYRUNDSDLALGMAGAATGWALGSLEFWVF VSQKMMEDYLQALINISLAVRKIALLLEPDEKEHLOVQK GEVPNNGKRINLEGGMLYLLELTARDAVCEQUFFKVR STRAYTVOPDUWEFFEDLASVUSANGCOTTVUMEREHLUVQK GEVPNNGKRINLEGGMLYLLELTARDAVCEQUFFKVR \$476 192 1457 \$5476 192 1457 \$588LLDCPCTSTRQVSLAFBEGGFTS HIGYLVDEPTLASSS PSTRASEVLCSTNAVSHYELQVEIGRGFDINLTSVHLARHTPTTVTV VTKIKTNILEGAVRGSLAFTYGVESLAFBEGGFTS HIGYLVDEPTLASSS PSTRASEVLCSTNAVSHYELQVEIGRGFDINLTSVHLARHTPTTVTV VTKIKTNILEGAVRGSLAFTYGVESLAFBEGGFTS HIGYLVDEPTLASSS PSTRASEVLCSTNAVSHYELQVEIGRGFDINLTSVHARHTPTVTV ### AVVERPOPPENTSTQVSLAFBEGGFTS HIGHLYDDEPTLASSS PSTRASEVLCSTNAVSHYELQVEIGRGFDINLTSVHARHTPTVTV ### AVVERPOPPENTSTQVSLAFBEGGFTS HIGHLYDDEPTLASSS PSTRASEVLCSTNAVSHYELQVEIGRGFDINLTSVHARHTPTVTVTV ### AVVERPOPPENTSTQVSLAFBEGGFT HIGHLYDDETSVHARHTPTVTVTVTV ### AVVERPOPPENTSTQVSLAFBEGGFT HIGHLYDDETSVHARHTPTVTVTVTV ### AVVERPOPPENTSTQVSLAFBEGGFT HIGHLYDDETSVHARHTPTVTTVTVTVTV ### AVVERPOPPENTSTGVARASSCALLSHAPPTANASSCARPSTGVARASGCARPTATATURSVHY ### AVVERPOPPENTSTGVARASSCALLSHAPPTANASSCARPTATATURSVHYCEDDGGFTVASDDKTVK ### AVVERPOPPENTSTGVARASGCARPTATATURSSBTTKALDLU ### AVVERPOPPENTSTGVARASGCARPTATATURSSBTTKALDLU ### AVVERPOPPENTSTGVARASGCARPTATATURSSBTTKALDD ### AVVERPOPPENTSTGVARASGCARPTATATURSSBTTKALDD ### AVVERPO		:		EFSSWISTNETQLKGIKGEAIDTANHGEVKRAVEEIRNGVTKRG
NLFEAQQLILHHIQOKTREISAKKRDVQQJIAQAQGEGGLDPDE HREIKRESTIDGLERSBERGERGT (VVILKWERFERNETIVO YLEQTOSSHERFISFSSLSSISSERLEGTKEF FERTESIAVQARN LVKEASEIPLIGPONKQLQQAKSIKEQVKKLEDTLEEBYVIDK S				ETLSWLKSRLKVLTEVSSENEAQKQGDELAKLSSSFKALVTLLS
NLFEAQQLILHHIQOKTREISAKKRDVQQJIAQAQGEGGLDPDE HREIKRESTIDGLERSBERGERGT (VVILKWERFERNETIVO YLEQTOSSHERFISFSSLSSISSERLEGTKEF FERTESIAVQARN LVKEASEIPLIGPONKQLQQAKSIKEQVKKLEDTLEEBYVIDK S		j	j	EVERMI.SNEGDCVOYKEIVKNSLEELISGSKEVOEOAEKILDTE
HREIARLESTLDGLERSBERGERRQVTLKWERFETNIKETVUR VLEYGESHERTLESSLSSLSESLESGLENGTESFEKRIAVQARN LVXEASETPLGPONKOLLQQQAKS I KEQVKKLEDTLEEETYIDK S 5474 2 780 TPDVRGLGASRRGTAVASNGSPRFFAGEENAFVKSGWILKGGSTI LKRWKKNAMPDLASGCHLIYYDDGTONLENGVENGTURTETG GECRDTQPPDGKSLOCHLQLVCROKTISLCAESTDDCLAMKEPT CHOCKANGEN PLANSCOCHLIYYDDGTONLENGVENGTURTETG GECRDTQPPDGKSLOCHLIYYDDGTONLENGVENGTURTETG GECRDTQPPDGKSLOCHLIYYDDGTONLENGVENGVENGVENGVENGVENGVENGVENGVENGVENGV			1	
THEOTOSSHERPLISTSSLESLESSELECTKEPSKETSSLAVANNE LVKRASEIPLGPQNKOLLQQAKSIKEQVKKLEDTLEETYVIDK S TOTOVROLGASRGIAVASMCSPRWBAGEEMAPVKSGWLLEGSTI LKRWKRNNFDLWSDGHLIYYDDCTRQNIEDKVHMPMDCINIRIG QECROTQPPDGKSKDCHLQIVCROGKTISLCARSTIDCLARKFI LQQAYOFOYGGAYPPGTQVVXANGQAYAPPGYPYAGAFREG SA75 2 506 ARGMLESIGLTCOTTPPSSPCLLHSPETFIHTMPENLTGYRF VSQKNMEDYLQALNISLAVKRALALLKPPKEEHQGNHMTVRIL STRNYTVQFDVOVEFEEDLRSVDGRKCOTIVTWEEHLVCVQK GEVPNGRRHRWLGEMLYLLELTARDAVCSQVPREKN SQRNMEDYLQALNISLAVKRALLLLEPKEEHQGNHMTVRIL STRNYTVQFDVOVEFEEDLRSVDGRKCOTIVTWEEHLVCVQK GEVPNGRRHRWLGEMLYLLELTARDAVCSQVPREKN SQRNMEDYLQALNISLAVKRALLLLEPKEEHQGNHMTVRIL STRNYTVQFDVOVEFEEDLRSVDGRKCOTIVTWEEHLVCVQK GEVPNGRRHRWLGEMLYLLELTARDAVCSQVPREKN SQRNMEDYLQALNISLAVKRALLLEPKEEHQGNHMTVRIL STRNYTVQFDVOVEFEEDLRSVDGRKCOTIVTWEEHLVCVQK GEVPNGRRHRWLGEMLYLLELTARDAVCSQVPREKN SQRNMEDYLGEGPDNLTSHAPANTYPTVG WILKINGENSHALGKAVILSHFPHHDTTTYWTYVG SWLMVISPMAYGSAQLLETYPEGWSBILLTWILLGAVRGUN YLKINGCHRSIKASHLIJSGDJLVTLSGLSHLHSLVKHGQRHR AVTDFPGRSTSVOPHLSFELLKQLLKGLFRVTWSDLYSHTPSTKGLIKG ASGGVPFGOMBRITQMLLGUKKREGGPDYLTKRILLFGAVRGNUN LQOPEKRESSSLISHTPKYRKMESGONLISLSLPPANNKPSI SGRUSGIGESVLNSSGTHTVNSDRLHTPSSKTFSPAFFSLVQL LQOPEKRESSSLISHTSVRKMESGONLISLSLPPANNKPSI LLQOPEKRESSSLISHTSVRYKMESGONLISLSLPPANNKPSI SLPPULPMTRBCOFPOBKOSYWEF SLPPTULPMTRBCOFPOBKOSYWEF SLPPTULPMTRBCOFPOBKOSYWEF UPKTMINSAENFTANSSNAYPSLVAMASGRQAKIQHYKGKRELE HRISAMKSAVSGADDERVRYVLLHLGRWINGTHSADKTYLL PAFGGALTMKVQNPSRKLDHLARABEHPANNAGRQAKIQHYKGKELE HRISAMKSAVSGADDERVRYVLLHLGRWINGTSLEFESTOQ UPSLPTMTVSSVYPSRKDLEFTANSGRQSDEVVYPFILTIRNMAQAKVFGA QYPSLPTMTVSSVYPSRKDLISLEFESTOR STRNYLIVPNVKGESTVFRAHTATVRSVYFCSDGGSFVTASDDKTV KWAATHRIKGRISTSJGGHINWYCAKRSPDGRLIVVSASDDKTVK LMPESSRECVISYCEHGGFVTYDFHPBGTCTAAAGMDRTVKVM DVTTHLLICHTQLHSAANNGLSFHPSGNVLITASSDSTIKLIDL MEGGLLYTHHGHGGPATTVARSRTGEYFASGSDEQNWWKSNF DIGHGGEVTKVPRPPATLASSMGNLTVSILEPCKKACC LENQOLIMGAATP VKWAATHRIKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT KALVAMENTEVENDERFTGETFASGEDDGOVWWKSNF DIGHGGLVTKVPRPPATLASSMGNLTVSILEPCKLKCC LENQOLIMGAATP LENGOLIMGAATP LENGOLIMGAATP STRNTTHON TOTOR REGERBARESSIEDTYAN			1	
LUXEASEIPLGPQNKQLLQQAKSIKEQVKKLEDTLEEEYVIDK S S TPDVRQLQASRGIAVASHCSPRFAGEEKAPVKSGHLRGSTI LKRNKKNNFDLASGCHLIYYDDQTRQNIEDKUHMPMDCTNIRTG QECROTQPPDGKSKDCHQIVCRQGKTISLCAGSTDCLARKFT LQDSRRNTAVVGSAVMTDETSVUSSPPTAYAAPAPEWGRISLS LQQAYGYGPYGQAYPOTQVVAANGQAYAWPYQYPYAGIIGQQ PANQVI IRERYRDNDSDLALGHLAGAATGMLGSLEWWY VQQKNEDYLGAINTSLAVRKTALLLEPKEIEHGOCHHTVRTL STRANTVQFOVOVEREBURGYGRCGTUTGPEHTVPPRLAGSIFVC GEVPNGGREHWLIGGHMIYIELTARDAVCEQVERKYR STRANTVQFOVOVEREBURGHGANGAATGMLGGHEWYRT STRANTVQFOVOVEREBURGHGANGAATGMLGGHEWYRT STRANTVQFOVOVEREBURGHGANGAATGMLGGHEWYRTT STRANTVQFOVOVEREBURGHGANGAATGMLGGHEWYRTT STRANTVQFOVOVEREBURGHGANGAATGMLGGHEWYRTT STRANTVQFOVOVEREBURGHGANGAATGMLGGHEWYRTT STRANTVQFOVOVEREBURGHGANGAATGMLGGHEWYLVDEPTLSWSR PSTRASEVLCSTRVSHYELQVEIGRGPDNLTSVHLARHTPTOTL VTIKITNLENCNEBELRALQKAVILSHFRINIEGAVRGLM AVVDFFQFSTSVOVOMESELLARQLHGAVWKSDLTSVGTACCH ASGQVPFQDMHRTQMLLQKLKGPYSPLDISIFFOGSSERMINSQ GSUDSIGESVLVSSGTHTVMSDLHTPSSKTFSPAFFSLVQLC LQQDPKRPSASSLLSHVFKQMKBSGDSILSLLPPAYMRSI SLPPVLPWTEBECPPDEKDVSDLHTPSKTFSPAFFSLVQLC LQQDPKRPSASSLLSHVFKQMKBSGDSILSLLPPAYMRSI SLPPVLPWTEBECPPDEKDUBLDHFSRTSPAFFSLVQLC LQQDPKRPSASSLLSHVFKQMKBSGDSILSLLPPAYMRSI SLPPVLPWTEBECPPDEKDVFFCHTATURGLHCHVAAFFE LPKTMINSAENHTANSSATPSLVAMASQRQAKQQAYCQAYCKRELB HRISAMKSAVESQQADDERWEYTYLLHLGRWIDISLEETESIDQ BIKILERDSSRRATSNSSRQSRPVKPFILTRINAQAKVGA GYPSLPTMVYBOWYSGHKKYGALPPQGLAXAAPBEFFKAAQQQE BQEEKBEEDDEOTLHRAREWDDWKOTHFRGYGNRQUNG DIGHGHTVKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQL LWRSSRCVISYCCHGGFFVYDFBGGGFTAAAGMDTVVKW DVPTHALLQHVQLHSAANAGLSPHSGNYLITASSDSTLKLIDL MEGRILYTHHGQCPATYVARSPTGVEFTASGDSFVTASDDKTV LWRSSRGVISYCCHGGFFVYDFBGGGFTAAAGMDTVVKW DVFTHALLQHVQLHSAANAGLSPHSGNYLITASSDSTLKLIDL MEGRILYTHHGQCPATYVARSPTGVEFTASGDSFVTASDDKTV LWRSSRGVISYCCHGGFFYVYDFHSGGTCAAAGMDTVVKW DVFTHALLQHVQLHSAANAGLSPHSGNYLITASSDSTLKLIDL MEGRILYTHHGHQCPATYVARSPTGVEFTASGDSFVTASDDKTV LWRSSRGVISYCCHGGFFYTYDFHSGTCTAAAGMDTVCKW DVFTHALLQHVQLHSAANAGLSPHSGNYLITASSDSTLKLDL MEGRILYTHHGHQGAPTVAFRSTCTEFTASGDSTLKKLIDL MEGRILYTHHGHQGAPTVAFRSTCTEFTASGDSTLKKLIDL MEGRILYTHHGHQGAPTVAFRSTCTEFTASGDTLKVDLGG L		1		1
5474 2 780 TEDVRQLQASERGIAVASWCSPRWFAGEEMAPVKSGWLLRGSTI LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCTNIRTS QECRDTQPPDGKSRDCMQI VCROGKTI SLCARSTIDCLARKET LQDAYGYOFYGGAYPDGTQVYAANGQAYMAPABPEWGRTIS LQQAYGYOFYGGAYPDGTQVYAANGQAYMAPABPEWGRTIS LQQAYGYOFYGGAYPDGTQVYAANGAAAAMVEYGYPYAAGIGQQ PANQVI IREKYRNDSDLALGHAGAAATMALGSLWWP 5475 2 506 ARGWLESISJTCOTTPPSSPCLLHSPETFIHTMPPHLIGTYRF VGKNMENDYLQAAINSLANKALALLKPPKEEBIGGNHMTVRTI. STERNTYOFDVGWEEBBLRSVORKCOTIVTWEEBHLVCVQK GEVPNRGMRHWLEGEMLYLBLARDAVCSGWPYEKYR STERNTYOFDVGWEEBBLRSVORKCOTIVTWEEBHLVCVQK GEVPNRGMRHWLEGEMLYLBLARDAVCSGWPYEKYR VTHKINLENDRENKALQKAUTLSHFFFRHENTTYWTVFTVG SWLMVISPPKAYGSASQLLRTYPEGGBTDLITSVHLARHIPTGTI. VTIKINLENDRENKALQKAUTLSHFFFRHENTTYWTVFTVG SWLMVISPPKAYGSASQLLRTYPEGGBTDLITSVHLARHIPTGTI. VTIKINLENDRENKALQKAUTLSHFFRHENTTYWTVFTVG SWLMVISPPKAYGSASQLLRTYPEGGBTDLITSVHLARHIPTGTI. VTIKINLENDRENKALQKAUTLSHFFRHENTTYWTVFTVG SWLMVISPPKAYGSASQLLRTYPEGGBTLITRHILFGAVGGLM AVTOFFORTSVOPMISPELLRQLHGTWKSDIYSGGTHAA AVTOFFORTSVOPMISPELLRQLHGTWKSBIYSGGRM AVTOFFORTSVOPMISPELLRQLHGTWKSBIYSGGRMS SGVDSGIGBSVUNSGGTHTVASDRILTFSSKTF9DAFSRMXNS SGVDSGIGBSVUNSGGTHTVASDRILTFSSKTF9DAFSRMXNS SGVDSGIGBSVUNSGGTHTVASDRILTFSSKTFSPAFSLVQLC LQQPEKRPGASSLLSHVPFKQMKESQQDSILSLLPPAYMKPSI SLPPULPMTBPECDPPDEKDSTWEE S477 3 1044 RGMSRLRXSHHDELQLFRLPEIFGRGLDEVEVATEPAGSRI VQEKVFKGLDLEKRABALLSGLDESNENDLEETASTDLKYLLV PAFGGALTMKQVNPSKRLDHLGRARBHFINVLTQCHCYHVAFF LPKTMMSSAFRUNSNANTSVLAMSGORGERPVVPP LHANDAVKFS RESPRANTANSNANTSVLAMSGORGERPVVP DICHCYHVAFF LPKTMSANSAVSSGQADDERVEVYLLHLGRWTDISLEETESIDQ EIKLLERENSSRRGSTSSKRSPPVPP FILMAQAKVFGKKKEE RESPRANTANSVANTSSVLAMSGORGFTVASDDKTVK LWDRSSRCUNSVCHGGSFTVYTVDEHSGGTCAAAGMDRTVKVW DVRTHKLLQHVQLHSAANVGLSFHPSGNYLITASSDSTLKLDL MEGGLLYTHLHGGGAPTTVAFSTSTCEYFASGSDFOWWWKSNF DIGHGEVTKVPRP PATLASSMONLTVS LLEGRLTLEEDKLKQ LENQOLLMGRATP 5479 2 635 KTVRIWYPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKTV VKWATHRKKVEPSTVGERGGFVTYDDFHSGTCTAAAGMDRTVKV DVRTHRLLGHVQLHSAANVGLSFHPSGTCTAAAGMDRTVKVM DVRTHRLLGHVQLHSAANVGLSFHPSGTCTAAAGMDRTVKVM DVRTHRLLGHVQLHSAANVGLSFHPSGTCTAAGGSDEVMWKSNF DIGHGEVTKVPRP PAT		1	1	YLFQTGSSHERFLSFSSLESLSSELEQTKEFSKRTESIAVQAEN
5474 2 780]	1	LVKEASEIPLGPONKOLLOQOAKSIKEQVKKLEDTLEEEYVIDK
5474 2 780			1	
LKRMKNMPDLWSDGLLTYPDOTTRONIEDKVIMPMDCTINITRO ORCHDTOPDEKSKDCMLJUCKDROKT ISLESTDDCLARKET LQDSRTNTATYGSAWATDETSVUSS PPYTAYAAPAPBUGETLS LQDSRTNTATYGSAWATDETSVUSS PPYTAYAAPAPBUGETLS LQDSRTNTATYGSAWATDETSVUSS PPYTAYAAPAPBUGETLS LQDSRTNTATYGSAWATDETSVUSS PPYTAYAAPAPBUGETLS LQDSRTNTATYGSAWATDETSVUSS PPYTAYAAPAPBUGETLS LQDARGYPTOGAVPYDANGOAPAPOSLEWY SARGHEDSLALCOMARGAATGPALOSLEWY SARGHEDYLOANISLAWARGAATGPALOSLEWY SORNEDYLOANISLAWARGAATGPALOSLEWY VORNEDYLOANISLAWARGLATICHSTETHTMPENITGYTRY STRANTYOPDVGVEEBBLASVLOGKCOTTVWEEBEHLOCVOK GEVPNROGWHENLBEBELINJELTARDAVCOQVFRUN STRANTYOPDVGVEEBBLASVLOGKCOTTVWEEBEHLOCVOK GEVPNROGWHENLBEBELINGLETARDAVCOQVFRUN STRANTYOPDVGVEEBBLASVLOGKCOTTVWINDTATYCOK GEVPNROGWHENLBEIGHTVATHARTHYOTTL VITKITNIENCHERIKAALQKAVILSHFFRHENITTYWIVFTVG SMAWYISPFMAYGSASQLLRTYFPEGMSETLIRULTGAVAGUN YLHONGCHERIKAALQKAVILSHFFRHENITTYWIVFTVG SMAWYISPFMAYGSASQLLBURTYPFEGMSETLIRULTGAVAGUN YLHONGCHERIKAALQKAVILSHFFRHENITTYWIVFTVG SMAWYISPFMAYGSASQLLBURTYPFEGMSETLIRULTGAVAGUN YLHONGCHERIKAALQKAVILSHFFRHENITTYWIVFTVG SMAWYISPFMAYGSASQLLBURTYPFEGMSETLIRULTGAVAGUN YLHONGCHERISIAASSULKROPPYS PLDI SIFPOSSSRMINSQ SQUDSGIGESVLVSSGTHTVANSDELHTPSSKTIFSPAFFSLVQLC LQOPEKREBESASSLLSHVYFKOMERSGSLSHHINSVGTHAKAS SQUDSGIGESVLVSSGTHTVANSDELHTPSSKTIFSPAFFSLVQLC LQOPEKREBESASSLLSHVYFKOMERSGSASQLAVCKYVKKELE ARGOVEFOMBRITANSSMAYPSIVAMASGCAKLQRYKCKKELE HRLSAMKSAVESGQADDERVERYYLHHLQRVIDISETESIDO EIKHLERERSSRRSSRSSRROEPPVERYPTLHTENMAQAKVFGA GYBELPTMYUSDWYEGHRKVGALDOGIAKAAPBEFTRAAQOQE SQEKKBEBEDBOTHHARRAKDOGIAKAAPBEFTRAAQOQE SQEKKBEBEDBOTHHARRAKDOMOTHOPFILTVANGAKVFGA GYBELPTMYNDWYEGESTVFRAFTATVRSVHFCSDGGSFYTASDDKT VKWAATHROKFTLIFGGQPATVASSRGSEPPVWKSNSTALKILDI MEGGLLYTHICHGQPATTVASSRGSSDEWYMWKSNF DIGHGEVTKVPRPPATLASSRGSHTVSTLIEDEKLKQC LENQGLIMQRATP VKWATHROKPTLIFGGPATTATVASSRGSSDEWYMWKSNF DIGHGEVTKVPRPPATLASSRGSLTVSTLIFLEDKLKQC LENGGLIMQRATP LENGGLIMGRATP SARSON TORTHANDAGAKRONDOHOLOGICONISCHI KALYMBISTATURDOLRAFICHTSISVERSGGSDEWYMVKSNF DIGHGEVTKVPRPPATLASSRGSDEDOMWKSNF DIGHGEVTKVPRPPATLASSRGSDEDOMWKSNF DIGHGEVTKVPRPPATLASSRGSDEDOMWKSNF DIGH		 		
QECRDTOPPOCKS ENCHALOUVED, CARREST DELCARKET LQDSPRITATY VGSANATDET SAVS PP PYTAAPAPEVERTLS LQQAYGYGPYGGAYPPGTOVVYANGQAYAPPOYCYPAGLYGQQ PANQVITERERYRNDSDLALGMLAGAANGGANLGENWOY AGRONGAY TO THE PROPERTY OF TH	5474	j 2	780	
LODSERTNTAVYGSAWTDETSVUSSPPPYTAYAAPPGYPEVGRIS LQQAYGYGYPGAYDPGYQYDYANGQAYPGYYPYAJIGQQ PANGYLIRERYENDEDIALGMLAGAATGMALGSLEWWP SAFS 2 506 ARGWLESISLTCQTTPFFSSPCLLHSPETFIHTMPNLTGYYFF VSQKNMEDYLQALNISLSAVRILALLKLPSETFIHTMPNLTGYYFF VSQKNMEDYLQALNISLSAVRILALLKLPSETFIHTMPNLTGYYFF VSQKNMEDYLQALNISLSAVRILALLKLPSETFIHTMPNLTGYYFF STERNTTVQFDVGYGEFEDLGSVUGRKCQTTVTWEEBELHAVCVQ GEVPNRGWRHKLGEMENLYLELTARDAVCGQVFKXVR 5476 192 1457 SDBMSILDCFCTSRTGVESLPFEKGGFTSHQTVLVDEPTLSWR SDBMSILDCFCTSRTGVESLPFEKGGFTSHQTVLYDPTLSWR VTIKITNLENCMEERIKALQKAVLISHFFRIENITTYTVTVTVC SWLWYISPFMAYGSASQLLRTYFFEGMSETILIRNILFGAVRGIN YLHQNGCHRSISKASHILISGDCLVTLSGISHHISLVKHGQRHR AVTDFPGTSTSVOPWLSPELLRQDLHGYNVKSDITSVGTACEL LQQDPKKRPSASSLLSSVYFXQMKESSQISHHISLVKHGQRHR AVTDFPGTSTSVOPWLSPELLRQDLHGYNVKSDITSVGTACEL LQQDPKKRPSASSLLSSVYFXQMKESSQISHLSLSLPPANTKPSI SGUDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFELVQLC LQQDPKKRPSASSLLSSVYFXQMKESGSGARGAKIQKYKGKLS SGUDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFELVQLC LQQDPKKRPSASSLLSSVYFXQMKESGARGAKIQKYKGKLE ARGGREFFSHASSLSLSSVYFXQMKESGARGAKIQKYKGKELE LPKTMNNSABNETANSSNATYSSLVMASGCRAKIQKYKGKELE HRLSAMKSAVESGGADDERVERYYLLHLQRNIDISLEDEFTGHCHVAEFE LPKTMNNSABNETANSSNATYSSIVMASGCRAKIQKYKGKEGLE HRLSAMKSAVESGGADDERVERYYLLHLQRNIDISLEETESIDO EKIKLEERDSSRRASTISNSRQEPPVENPFILTRINAQAKVFGA GYBSLPTMTVSGWYEGHRYVGALBOQGIAKAPBEFFRAQOQE GYBSLPTMTVSGWYEGHRYVGALBOQGIAKAPBEFFRAQOQE GYBSLPTMTVSGWYEGHRYVGALBOQGIAKAPBEFFRAQOQE GYBSLPTMTVSGWYEGHRYVGALBOGGIAVYGAWFG UNDKSSRECVHSYCEHGFVTYDFHESGTCIARAGMDNTVKW LWDKSSRECVHSYCEHGFVTYDFHESGTCIARAGMDNTVKW DVRTHRLLCHYQLGHAAVANGLSFHPSGNTLITASSDTKLILDI MEGGLLYTLHCHGQPATTVAFSRTGSTFAGGSGEDWMWKSNF DIGHGEVTKVPRPPATLASSMGALTVSILEGRKLKQC LENQGLIMGRATP VKWMATHRQKFLFSLSOHIMWRCAKFSDGGSFTVASDDKTV LWDKSSRECVHSYCEHGFVTYDFHPSGTCIARAGMDNTVKWD DVRTHRLLCHYQLGHATTAVFSRTGSTFAGGGSDEWMWKSNF DIGHGEVTKVPRPPATLASSMGALTVSILEGRKLKGC LENQGLIMGRATP VKWMATHRQKFLFSLSGHIMGNACHGHTSSGGSDEWMWKSNF DIGHGEVTKVPRPPATLASSMGALTVSILEGEKLEDKLKQC CERNOGLIMGRATP SAFTENDAM THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TO	}	1		LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINIRTG
LODSERTNTAVYGSAWTDETSVUSSPPPYTAYAAPPGYPEVGRIS LQQAYGYGYPGAYDPGYQYDYANGQAYPGYYPYAJIGQQ PANGYLIRERYENDEDIALGMLAGAATGMALGSLEWWP SAFS 2 506 ARGWLESISLTCQTTPFFSSPCLLHSPETFIHTMPNLTGYYFF VSQKNMEDYLQALNISLSAVRILALLKLPSETFIHTMPNLTGYYFF VSQKNMEDYLQALNISLSAVRILALLKLPSETFIHTMPNLTGYYFF VSQKNMEDYLQALNISLSAVRILALLKLPSETFIHTMPNLTGYYFF STERNTTVQFDVGYGEFEDLGSVUGRKCQTTVTWEEBELHAVCVQ GEVPNRGWRHKLGEMENLYLELTARDAVCGQVFKXVR 5476 192 1457 SDBMSILDCFCTSRTGVESLPFEKGGFTSHQTVLVDEPTLSWR SDBMSILDCFCTSRTGVESLPFEKGGFTSHQTVLYDPTLSWR VTIKITNLENCMEERIKALQKAVLISHFFRIENITTYTVTVTVC SWLWYISPFMAYGSASQLLRTYFFEGMSETILIRNILFGAVRGIN YLHQNGCHRSISKASHILISGDCLVTLSGISHHISLVKHGQRHR AVTDFPGTSTSVOPWLSPELLRQDLHGYNVKSDITSVGTACEL LQQDPKKRPSASSLLSSVYFXQMKESSQISHHISLVKHGQRHR AVTDFPGTSTSVOPWLSPELLRQDLHGYNVKSDITSVGTACEL LQQDPKKRPSASSLLSSVYFXQMKESSQISHLSLSLPPANTKPSI SGUDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFELVQLC LQQDPKKRPSASSLLSSVYFXQMKESGSGARGAKIQKYKGKLS SGUDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFELVQLC LQQDPKKRPSASSLLSSVYFXQMKESGARGAKIQKYKGKLE ARGGREFFSHASSLSLSSVYFXQMKESGARGAKIQKYKGKELE LPKTMNNSABNETANSSNATYSSLVMASGCRAKIQKYKGKELE HRLSAMKSAVESGGADDERVERYYLLHLQRNIDISLEDEFTGHCHVAEFE LPKTMNNSABNETANSSNATYSSIVMASGCRAKIQKYKGKEGLE HRLSAMKSAVESGGADDERVERYYLLHLQRNIDISLEETESIDO EKIKLEERDSSRRASTISNSRQEPPVENPFILTRINAQAKVFGA GYBSLPTMTVSGWYEGHRYVGALBOQGIAKAPBEFFRAQOQE GYBSLPTMTVSGWYEGHRYVGALBOQGIAKAPBEFFRAQOQE GYBSLPTMTVSGWYEGHRYVGALBOQGIAKAPBEFFRAQOQE GYBSLPTMTVSGWYEGHRYVGALBOGGIAVYGAWFG UNDKSSRECVHSYCEHGFVTYDFHESGTCIARAGMDNTVKW LWDKSSRECVHSYCEHGFVTYDFHESGTCIARAGMDNTVKW DVRTHRLLCHYQLGHAAVANGLSFHPSGNTLITASSDTKLILDI MEGGLLYTLHCHGQPATTVAFSRTGSTFAGGSGEDWMWKSNF DIGHGEVTKVPRPPATLASSMGALTVSILEGRKLKQC LENQGLIMGRATP VKWMATHRQKFLFSLSOHIMWRCAKFSDGGSFTVASDDKTV LWDKSSRECVHSYCEHGFVTYDFHPSGTCIARAGMDNTVKWD DVRTHRLLCHYQLGHATTAVFSRTGSTFAGGGSDEWMWKSNF DIGHGEVTKVPRPPATLASSMGALTVSILEGRKLKGC LENQGLIMGRATP VKWMATHRQKFLFSLSGHIMGNACHGHTSSGGSDEWMWKSNF DIGHGEVTKVPRPPATLASSMGALTVSILEGEKLEDKLKQC CERNOGLIMGRATP SAFTENDAM THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TO		1	}	
LQQAYGYGPYGGAYPGTQVVYAANGQAYAPYCYPYAGLYGQQ PANQVIIRERYRONDSDLALGMAGAATOPYCYPYAGLYGQY \$475 2 506 ARGHLESLSLTCQTTPPPSSPCLLHSPETFIHTMPPNLTGYYRF VSQKNMEDYLQALNISLAVRKIALLLKPDKSIBGGGSMITVRTL STFRNTYOPFOVGWEEEBLDENSUGRKCQTTVTWEEBHLVCVQK GEVPNRGWRHNLBGRMLYIBLTARDAVCGQVFRKYN \$5476 192 1457 SDSMSLLDCFCTSRTQVSLESPERIGGETFIHTMYPDVTLG SWLWISPPMAYGSAGLLRTYPPEGNSETLIRNILFGAVRGLN VTIKITNLENCHERIKALQKAVILHFPRIPNITTYWTVTVG SWLWISPPMAYGSAGLLRTYPPEGNSETLIRNILFGAVRGLN YLHQNGCHRSIKASHLIISGDGLVTLSGLSHLHSLVKGQRHK AVOFPQFSTSVOPWLSSELLRQDLIGNTSDIYSGTACEL ASGQVFQDMIRTGMLLQKLKGPPYSPLDISIFPGSSRMKNSG SGVDSGIGSSVLVSSGTHTVNSDRLHTPSSTTFSPAFFSLVQLC LQQDPBKRDSASSLLSHVPFKQMKEBSQDSILSLLPPAYNKPSI SLPPVLPWTEPBCDPPDERDSYWEF \$477 3 1044 RGNSRLRTSHEDBLQLEFLFSTGRQLLDEVEVATEPAGSRI VQEKVFKGLDLLEKAABMLSQLDLFSRNBDLEETAFDLKYLLV PARGGALTHKOVNPSKRLDHLQARRHFINLTJCCCCHVHVAEFF LPKTMINSAENHTANSMAYPSLVAMASGQAKIGKYKÇKKELE HRLSAMKSAVESGQADDEVREYLYLLHLQKWIDISLBETESIDQ EIKLLRERDSSRRASTSNSSRQERPPVKPPFILTENNAQAKVFGA GYPSLPTMIVSDMYEQHRYVGALPGVGINGMIG 5478 2 835 KTVRIWPPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKTV LWDKSSRECVHSYCEHGGVTTVDFHESGTCLAAAGMDTVKVW DVFTHRLLQHYQLHSAAWGLSPHPSGNLTLTASSDSTLKLIDL MEGRILYTHGGQPATTVAFSRTGEYFASGGSDBQWWWKSNF DIGHHEVTKVPRP PATLASSMGRLVSILEGRLIEDRLKQD LEMQGLIMGRATP 5479 2 835 KTVRIWPPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKTV LWDKSSRECVHSYCEHGGVTYVDFHESGTCLAAAGMDTVKVW DVFTHRLLQHYQLHSAAWGLSPHPSGNLTITASSDSTLKLIDL MEGRILYTHGGQPATTVAFSRTGEYFASGGSDBQWWWKSNF DIGHHEVTKVPRP PATLASSMGRLTVSILEGRLIEDRLKQC LENQGLIMGRATP 5479 2 835 KTVRIWPPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKTV LWANSTRIKGKFLFSISGNLTHWRCAKFSPDGRLTVSASDDKTVK LWDKSSRECVHSYCEHGGVTYVDFHPSGTCLAAAGMDTVKVW DVFTHRLIGHYQLHSAAWGLSPHPSGNLTTASSDSTLKLIDL MEGRILYTHHGGGPATTVAFSRTGEYFASGGSDBQWWWKSNF DIGHHEVTKVPRP PATLASSMGRLTVSILEGRLTEEDKLKQC LENQGLIMGRATP 5480 444 1952 LSLTSRMERABLIVKRGLGAITDKKKQEHSGSCBCERKKRONQODGHOLOVLEGSI LRLKERIDDLEKRRULDGISSKROEMKKNONQODGHOLOVLEGSI LRLKERIDDLEKRRULDGISSKROEMKKNONQODGHOLOVLEGSI LRLKERIDDLEKRRULDGISSKROEMKKNONQODGHOLOVLEGSI LRLKERIDDLEKRRULDGISSKSTRESHINSKS				
PANQVIIRRYRDNOSLALGALGATGMALGSLFWPF \$475 2 506 ARGHLESLSUTCOTTPPPSS PCILLAR PETFITHMPPNLTGYYRF VSCKNNEDYLOALNISLAVRKIALLLKPDKEIEHQGNHMTVRTL STFRNTTVOFDUGVEFEBOLRSVOGRKCOTIVTWEEHLUVCVCK GEVPNRKOMKHMLEGMANLVLELTRARDAVCEQUFFKVR \$476 192 1457 SDEMSILDCFCTSKTGVESLEPEKGSETSIHGYLVDEFTLSWSR PSTRASEVLCSTNVSHELDLVBIGGGFDNLTSVHARHTPTGTL VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVFTVG SWLMVISPFMAYGSASQLLETTFEGGMSETLIRILFGAVKGIN AVTDFPCFSTSVOPWLSPELLSQDLHGTNVKSDITSVGITACEL ASGQVPPOMHRTOMILGKKEPPSPSJDISIFPOSESRMINSQ SGVDSGIGSSVLVSSCTHTVNSDRLHTPSSKTFSPAFFSLVQLC LQQDPEKRPSASSLLSHVFFKQMKESSQDSILSLPPAYNKPSI SUPPVLPWTEPSCDFPDEKDSVWEF VORKVYRGDLLEKRARMLSQLDLESRNEDLEEIASTOLKYLLV PAPGGALTMKQWIPSKLDHLGRAREHFINYLTQCHCYHVAEFF LPKTMINSAENHTANSSMAYPSLVMARQAXIQRYKGKELE HRISAMKSAVESGQADDERVRFYYLLHLQRWIDISLEEISSTOLKYLLV PAPGGALTMKQWIPSKLDHLGRAREHFINYLTQCHCYHVAEFF LPKTMINSAENHTANSSMAYPSLVMARQAXIQRYKGKELE HRISAMKSAVESGQADDERVRFYYLLHLQRWIDISLEEISSTOLKYLLV PAPGGALTMKGWIPSKELDHLGRAREHFINYLTQCHCYHVAEFF LPKTMINSAENHTANSSMAYPSLVMARGAXIQRXKFELE HRISAMKSAVESGQADDERVRFYYLLHLQRWIDISLEEISSTOLKYLLV VERVERFRENSERSASTENSSRGGRFPVKFFLITRNAGAKVFGA GYBELDTWINSWYSGERFRKYGALPPOGIAKAAPBEFRKAAQOQ EQEBKEBEEDDEGTLHRAREHDDWITHFRGYGROMMG SCHEKEBEDDEGTLHRAREHDDWITHFRGYGROMMG VVWATHRUSHYNKGESTVFRAHTAVESVHFCSDGGSFVTASDDKTV LWDKSSRECVHSYCHGGFVTTVDFHSGTVLIAAGMINTVKVW DVRTHRLLGHYQLIABANNOLSFHPSGTVLITASSDSTLKILDL MEGRILJTHLGHQGPATTVAFSRTGEYFASGGSDEQVWWKSNF DIGHHGEVTKVPRPPATLASSMGHLTVSILEGRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPRVKGESTVFRAHTAVRSVHFCSDGGSFVTASDDKTV LWDKSSRECVHSYCHGGFVTTVDFHPSGTVLIAAAGMINTVKVW DVRTHRLGHOPALTASSMGHLTVSILEGRLTLEEDKLKQC LENQQLIMQRATP SHARD SHARDARAMANGLSFHPSGTVLTASSDCTIKLIDE MEGRILJTLHGHQGPATTVAFSRTGEYFASGGSDEQVWWKSNF DIGHHGEVTKVPRPPATLASSMGHLTVSILEGRLTLEEDKLKQC LENQQLIMQRATP SHARDARAMANGLSFHPSGTVLTASSDCTIKLIDE MEGRILJTLHGHGGPATTVAFSRTGETSFAGGSDEQWWKSNF DIGHHGEVTKVPRPPATLASSMGHLTVSILEGRLTLEEDKLKQC LENQQLIMQRATP SHARDARAMANGLSFHPSGTYLTASSDCTIKLIDEL MEGRILJTLHGHGGPATTVAFSTGGSGREGDEQWAWKSNF DIGHGEVTKVPRPPATLASSMGHLTVSILEGRLTLEEDKLKQC R	ì			
\$475 2 506 ARGHLESLGLTCOTTPPPSSPCLLHSPETPIHTMPPNLTGYYRE VSKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMYTWTL STERNTTVOFDUGUEFEEDLRSUGGRCOTIVTWEEBEHLVCVQK GEVPNRGMRHMLEGEMLYJELTARDAVCEQUPFKVR 5476 192 1457 SDAMSLLDCPCTSRTQVSJERPEKQSSTSTHQYLVDEPTLSWSR PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPTGTL VTIKITNLENCNEERLKALQKAVILSHFFRENITTYWTVTVG SWLMVISPPMAYGSASQLLETYFPEGMSETLIRNILFGAVRGUN YLHGNGCIHRSIKASHILISGDLYTLSGLSHLHSLVKHGGRIH AVYDFPOFSTSVOPWLSPBLLKQDLHGVKSDITSVGITACEL ASGQVPPOMHRTOMLLQKLKGPPVSPLDISIPSOGSSRMINSQ SGGVDSIGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAPFSLVQLC LQQDPEKRESASSLLSHVFFKQMKEBSQDSILSLLPPAYNRPSI SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF GNSRLMSHSHEDELQLDERJEFFETGRQLLDEVEVATEPAGSRI VQEXVPKGLDLLEKAARMLSQLDLFSRNEDLERIASTDLKYLLV PAPGGALTMKQVNPSKRLDHLQRAIDISISETESIDQ EIKKLERRISSRBASTNSSRGREPVEYPILTRINNAQAKVGA GYPSLPTMYSGWYSQTRKYGALPDCGIAKAAPBEFRKAQQQE EQEBKEEEDDEQTIHRAREMDDMKDTHPRGYGNRQMMG 5478 2 835 KTVRIWYPNYKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHROKFIFSLSGHIMWYRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCHGFFVTYDHPBGTCIAAAGMDNTVKVW DVPTHRLLOHYQLHSAANGLSFHPSGNYLITASSDSTLKILDL MEGGLLYTHGHQGPATTVAFSRTGEYFASGGSDEQWMVKSNF DIGHGEVTKVPRPPATLASSMGNLTVSILEQRILDEBKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWYPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHRQKFIFSLSGHIMWYRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCHGFFVTYDFHPSGTCIAAAGMDNTVKVW DVPTHRLLOHYQLHSAANNGLSFHPSGNYLITASSDSTLKILDL MEGGLLYTHLGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGHGEVTKVPRPPATLASSMGNLTVSILEQRILTEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHRQKFIFSLSGHIMWYRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCHGGFVTYVDFHPSGTVLTAAGMDNTVKW DVRTHRLICHYQCHGAANNOLSFHPSGNYLITASSDSTLKILDL MEGGLLYTHLGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGHGEVTKVPRPPATLASSMGNLTVSILEQRKLKEG LENQQLIMQRATP LENGQLIMQRATP SHANDANGLAREMILLOGISGKEGEEMKRQNQQQDHGIQVLEQSI LRLEKEIQOLEKAELQISTKERAILKKLKSISHTETBDITRSVKV EREERAESIEDIYANIPDLEKSTIPSIRRENTEDITRSVKV EREERAESIEDIYANIPDLEKSTIPSIRRENTEDITRSVKV EREPAESIEDIYANIPDLEKSTIPSIRRENTEDITRSVKV EREPAESIEDIYANIPDLEKSTIPSIRRENTEDITRSVKV ERE	1	1	1	
USQKIMEDYLOAUNISLÄVRIKIALLIKPDKEIEHQGNIMTVRTL STFRYYTVQFDVGVEFEEDLRSVDGRKCQTTVTWEEEHLLVCVQK GEVPNRGWRHHLEGEMLYLELTARDAVCEQUFRKVR 5476 192 1457 SDSMSILDCFCTSRTQVESLRPEKGSETSIHQYUDEFTLSWSR PSTRASEVLCSTNVSHELQVEIGGEPDNLTSVHLARHTPTGTL VTIKITNLENCHERLKALQKAVILSHFFRHENITTYMTVETVG SMLWVISPFMAYGSASQLLRTYFPEGMSETLIRINLFGAVRGIN YLHQNGCIHRSIKASHLLISGDGLVTLSGISHLHSLVKHGQRHR AVYDFPQFSTSVQPMLSPELLADDLHGYNVKSDITSVGITACEL ASGQVPPQMHRTGMLLQKLKGPPYSPLDISIFPGSESRMINSQ SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC LQQDPEKRPSASSLISHVPFKOMKESDELISLIPPAYNKPSI SLPPVLPWTEPECDFPDEKDSYWEF 5477 3 1044 RGNSRLRYSHEDELQLERABELSDLHESVRATEPAGSRI VQRKVYREDSLISLLEPPAYNKPSI SLPPVLPWTEPECDFPDEKDSYWEF LPKTWNINSAENTTANSAMSAYSLUKMAGKAKIGVEYKGKKELE HRLSAMKSAVESGQADDEVREYYLLHLQRWIDISLESIESIDG EIKLLERRDSSRSATSINSSRQERSPFVKPFLTRNNAQAKVFGA GYPSLPTWYSWYSQHRKYGALPDQGIAKAAPBEFRRAQQOE BQBEKBEEDDEGTLHRAREMDDWKDTHERGYGROMG GYPSLPTWYSWYSQHRKYGALPDQGIAKAAPBEFRRAQQOE BQBEKBEEDDEGTLHRAREMDDWKDTHERGYGROMG 5478 2 635 KTVRIWYPWYKGESTVYRAKTATAVRSVHFCSDGQSFVTASDDKT VKWATHRQKFLFSLSGHIMWYCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLGHYQLHSAAVNGLSFHPSGNYLITASSDSTLKLLDL MEGRILYTLHGHQGPATTVAFSRTGEYPASGGSDQVMWKSNF DIGHGBEVTKVPRPPATLASSMGNILTVSILEGRILVSASDDKTVK LWDKSSRECVHSYCHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLGHYQLHSAAVNGLSFHPSGNYLITASSDRTKKIDL MEGRILYTLHGHQGPATTVAFSRTGEYPASGGSDCVMWKSNF DIGHGEVTKVPRPPATLASSMGNILTVSILEGRILVSASDDKTVK LWDKSSRECYHSYCHGGFVTYVDFHPSGTCIAAAGMDNTVKW DVRTHRLGHYQLHSAAVNGLSFHPSGNYLITASSDRTKKIDL MEGRILYTLHGHQGPATTVAFSRTGEYPASGGSDEQVMWKSNF DIGHGEVTKVPRPPATLASSMGNILTVSILEGRILVSASDDKTVK LWDKSSRECYHSYCHGGFVTYVDFHPSGTLITASSDDKTVK LWDKSSRECYHSYCHGGFVTYVDFHPSGTLIAAACMDNTVKW DVRTHRLGHYQLGHSAAVNGLSFHPSGNYLITASSDDKTVK LWDKSSRECYHSYCHGGFVTYDFHPSGNYLITASSDDKTVK LWDKSSRECYHSYCHGGFVTYDFHPSGNYLITASSDDKTVK LWDKSSRECYHSYCHGGFVTYDFHPSGNYLITASSDDKTVK LWDKSSRECYHSYCHGGFVTYDFHPSGNYLITASSDDKTVK LWDKSSRECYHSYCHGGFVTYDFHPSGNYLITASSDDKTVK LWDKSSRECYHSYCHGGFVTYDFHPSGNYLITASSDDKTVK LWDKSSRECYHSYCHGGFVTYDFHPSGNYLITASSDDKTVK LWCHATAR	L	<u> </u>	<u> </u>	
STERNYTVOPDVGVEFEBDLRSVDGRKCQTIVTWEEBHLVCVQK GEVPNRWRHWLEGEMLVLBLTARDACSQVBRKW 5476 192 1457 SDSMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLSWSR PSTRASEVLCSTNVSHYBLQVEIGREPDKLTSVHLARRITETGTL VTIKITKLENCKEBELKALQKAVLSHFFRHENITTYMTVFTVG SMLWYISPFRAYGSASQLLRTYFBEGMSETLIRNILFGAVRGIN YLHQNGCIHRSIKASHILISGDGLVTLSGLSHHSLVKHGQRHR AVYDFPCFSTSVQPMLSPELLRQDLRGYNVKSDIYSVGITACEL ASGQVPFQDMHRTQMLLQKLKGPPYSPLDISIFPGSESRMKNSQ SGVDSGIGBSVLVSSTTHTVNSDRIPPSKYFFSPAFPSLVQLC LQQDPEKRPSASSLLSHVFFKQMKESSQDSILSLLPPAYNKPSI SLPPVLPWTEPBECDPPDEKDSYWEF 4 RGNSRLRYSHEDELQLPFLFBLFFTGQLLDEVEVATEPAGSRI VQEKVFKGLDLLBKAAEMLSQLDLFSRNBLLEBIASTDLKYLLV PAPGGALTMKQVNPSKRLDHLQRAFFINYLTQCHCYHVAEFE LPKTMINSAENHTANSSMAYPSLVAMASQRQAKIQRYYQKKELE HRLSAMKSAVESQADDERVEFYLLHLQRMET INVLTGCHCYHVAEFE LPKTMINSAENSTNSSRQEPSPVKPFILTRIMAQAKVFGA GYPSLPTMTVSDWYSCHRKYGALPDQCIARAPBEFRRAAQQQE EIKLLRRDDSSRBASTSNSSRQEPPVKPFILTRIMAQAKVFGA GYPSLPTMTVSDWYSCHRKYGALPDQCIARAPBEFRRAAQQQE EOBEKBEEDDEGTLHARABWDDMBCTHPRGYGNKGNMG 5478 2 835 KTVRIWPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWAATHRQKFLFSLSQHIMWRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTVYDFHPSGTCIAAAGMNTYKWW DVRTHRLLGHYQLHSAANWGLSFHPSGNYLITASSDSTLKILDL MEGRILYTLHGHQGPATTVAPSRTGEYFAGGGSBQVWWWKSNF DIGHHGSVTKVPRPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQLIMQRATP 5479 2 835 KTVRIWPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKJWANTHRQKFLFSLSQHIMWRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFPPSGTCIAAAGMDNTVKWW DVRTHRLLGHYQLHSAANWGLSFHPSGNYLITASSDSTLKILDL MEGRILYTLHGHQGPATTVAPSRTGEYFAGGGSBQVWWKNSNF DIGHHGSVTKVPRPPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSITSRMEEABLVKGRLQAITDKRKYQEEIGKGRKKNGQDQHVWKNSNF DIGHHGSVTKVPRPPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP SHAFRICHGRATTVAPSRTGEYFAGGGBDQVWWKNSNF DIGHHGSVTKVPRPPPATLASSMGNLTVSILEQRLKKIEEDKLKKQC CHLKKKALRREKMLLDGISGKEGGEMKKONQOQDHQIQVLSQSI LRLKERJQDLEKAELQISTKEBATLKKLKSIRFTTEDIIRSVKV EREBABESIEDIYAMI PDLKKYIPPSRTRKEDDDECNR KALVAMBIKVEKDLKYGESTVFRSHIKKINGLGJGVESSI	5475	2	506	
S476 192 1457 SDSMSLLDGFCTSRTQVESLRPEKQSETSINGYLDEPTLSWSR PSTRASEVLCSTNUSHYBLQVEIGRGFONLTSVHLARHTPTGTI	ŀ		j.	VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTL
SQNMSLLDCPCTSRTQVBSLAPEKQSETSIHQTLVDEPTLSWSR	i	1	{	STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVCVQK
SQNMSLLDCPCTSRTQVBSLAPEKQSETSIHQTLVDEPTLSWSR		}	1	
PSTRASEVICSTAVSHIVELQVEIGRGPDNLTSVALARHTPTGTL VTIKITNLENCNEERLKALQKAVILSPFRHENITTYMTVTVTV SWIMVISPFMAYGSASQLLRTYFPEGMSETLIRNILFGAVRGIN YLHQNGCIHRSIKASHILISGDGLVTLSGLSHLHSLVKHGQRHR AVYDFPQPSTSVQPWLSPELLAGLHGTNSKATISVSVGITACEL ASGQVPFQDMHRTQMLLQKLKGPPYSPLDISIFPQSESRMKNSQ SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC LQQDPERRPSASSLSHVFFKMERSQDSILSLLPPAYNKPSI SLPPVLPWTEPECDFPDEKDSVWEF SLPPVLPWTEPECDFPDEKDSVWEF 5477 3 1044 RGNSRLRYSHEDBLQLFRLPEIFFTGRQLLDEVEVATEPAGSRI VQERVFKGLDLLEKAAEMLSQLDLFSRREDLEETASTDLKYLLV PAFQGALTMKQVMPSKRLDHLQRAREHFINVLTQCHCYHVAEFF LPKTWINNSAENHTANISMAYPSLVAMASQQQAKIQRYKQKKELE HRLSAMKSAVESQADDERVRFYLLHLQRHIDISLEEIESIDQ EIKILRREDSSRRASTSNSRGERPFVRFFILTRINMAQAKVFGA GYPBLPTWTVSDWYEQHRKYGALPOGIAKAAPBEFRKAAQQQ EQEEKEEDDEQTLHRAREWDDWKOTHPRGYGNRQNWG STATELHTANISMAYBLVGAKFSPDGRLIVSASDDKTVK LWDKSSRBCVHSVCHHGGFVTYDPHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFPPSGNYLITASSDSTLKLDL MEGRILVTLHGQBPATTVAFSRTGEYFARGSDEQVMVWKSNF DIGHHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHRQKFLFSLSGHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRBCVHSVCHHGGFVTYDPHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFPPSGNYLITASSDSTLKILDL MEGRILVTLHGHQGPATTVAFSRTGEYFASGSDEQVMVWKSNF DIGHHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHRQKFLFSLSGHINWVRCAKFSDGRLIVSASDDKTVK LWDKSSRBCVHSVCHHGGFVTYDPHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFPPSGNYLITASSDSTLKILDL MEGRILYTLHGHQGPATTVAFSRTGEYFASGSDEQVMVWKSNF DIGHHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEABELVKGRLQAITDKRKTQERISQKRLKIEEDKLKK REERFABESIEDVJANIPJRJFTJFSLRKREINEBEKDDERN KALYAMEIKVEKDLLGISTKERAILKKLKSIBRTTEDJIRSVKV RERERABESISTYANDFYRFTYPGRFTVTYPGFPFOGRRIKEREMEDEDSON KALYAMPIKVEKDLKTGESTVLSSIPLPSDFRKRIKEKEDDESON KALYAMPIKVELTAGDFFROGRETLAGLERSENKENSTEYTH BEVYANPSYRFTTPGGRTTYTPGFRTYTYPGFPFOGRRIKKTNOLGIGVWESI		 	1457	
VTIKITNLENCNEERLKALQKAVILSHPFRIENITTYWTVTVG SWLWYISPFMAYGSASQLLRTYFPEGMSETLIRNILFGAVRGLIN YLHQNGCIHRSI KASHILISGEGUVTLSGLSHHASUVKHOGRIR AVYDFPQFSTSVQPWLSPBLLKQDLHGYNVKSDIYSVGITACEL ASGQVPFQDMRTQMLLQKLKGPPYSPLDISIFPQSESRKINSQ SGVDSGIGESVLVSSCTHTVNSDRLHTPSSKTFSPAFFSLVQLC LQQDPEKRPSASSLLSHVFFKQMKERSQDSILSLLPPAYNKPSI SLPPVLPWTEPECDFPDEKDSYWEF S477 3 1044 RGNSRLRYSHEDBLQLPRIPELFETGRQLLDEVEVATEPAGSRI VQEKVFKGLDLLEKAAEMLSQLDLESREDLEETASTDLKYLLV PAPQGALTMKQVMPSKRLDHLQRAREHFINVLTCHCYHVAEFF LPKTWINNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESQQADDERVRFYYLLHLQRNIDISLEEISIDQ EIKILRERDSSRERSTSNSSRGPPVKPFILITNMAQAKVFGA GYPSLPTWTVSDWYEQHRKYGALPDQGIAKAAPBEFRKAQQQE EQEKKBEEDDEQTI-HRARREWDDWKDTHRYGNNROMM STVRIWWPNVKBESTVFRAHTAVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSGHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKLIDL MEGRLLYTLHGHQGPATTVAFSRTGEYFAGGSDBQVWVWKSNF DIGHGEVTKVPRVPAFTASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP VKVWATHRQKFLFSLSGHINWCCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKLIDL MEGRLLYTLHGHQGPATTVAFSRTGEYFAGGSDBQVWVWKSNF DIGHGEVTKVPRVPAFTLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP LWDKSSRECHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKLIDL MEGRLLYTLHGDQPATTVAFSRTGEYFAGGSDBQVWVWKSNF DIGHGGVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP SGTTSFRMEABSLVKGRIQATTDKRKIQERISGKRLKIEEDKLKQC LENQQLIMQRATP LENGELGTVANTPPRIPTSTRTGETSTYRSERSDEDQVMVKSNF GREERFAEESIEDVANT PLOTENTERSTEGENDEDRONG KALYAMEIKVEKDLKTGESTVLSSIPLPSDDPKGTGIRKVYDDGQ KSVYAVSSNHSAAVNGSTVLSSIPLPSDDPKGTGIRKVYDDGQ KSVYAVSSNHSAAVNGFFORFFORFYRSIRSKSPTEYH BEFVYANPFYRFTTPGRTTVTPGFFTYTPG	5476	192	145/	
SWLWVISPFMAYGSASQLLRTYFPEGMSETLIRNILFGAVRGIN YHHONGCHRSIKASHILISGDGUVTLSGELHHSUKHGQRIR AVYDFPGFSTSVOPWISPELLAGDLHGYNVKSDIYSVGITACEL ASGQVPFQDMHRTQMLLQKLKGPPYSPLDISIFPGSESRKNSQ SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFPSLVQLC LQQDPERRPSASSLSHVFFKQMKRESGOSILSLLPPAYNKPSI SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLWTEPECDFPDEKDSYWEF FROM ROMSREYSHEDBLQLFRLFETGRQLLDEVEVATEPAGSRI VQEKVFKGLDLLEKAAEMLSQLDLFSRREDLEETASTDLKYLLV PAFQGALTMKQVNPSKRLDHLQRAREHFINVLTQCHCYHVAEFF LPKTWINSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESGQADDERVRFYYLHHQRRIDISLEEIESIDQ EIKLLRERDSSREASTSNSSRGERPPVKPLFTLIRNMAQAKVFGA GYPSLPTWTVSDWYEQHRKYGALPDQGIAKAAPBEFRKAAQQQE EQEKREEDDEQTLHRAREWDDWKOTHFRGYGONROMG 5478 2 835 KTVRIWPRVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKWAATHRQKFLFSLSQHINWYCAKFSPDGRLIVSASDDKTVK LNDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKW DVRTHRLLQHYQLHSAAVNGLSFHPSGRYLITASSDSTLKILDL MEGRILYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGHGEVTKVPRPPATLASSMONLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWPRVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWANTHRQKFLFSLSGHINWYCAKFSPDGRLIVSASDDKTVK LWDKSSRSCVHSYCEHGGFVTYDFPHSGTCIAAAGMDNTVKW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGHGEVTKVPRPPATLASSMONLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP SHOWN SERVER STORM SERVER STORM SERVER		1		
YLHQNGCIHRSIKASHILISGDGLVTLSGISHLHSLVKHOGORIR AVYDFPOFSTSVOPWLSPELLRQDLIGYNVKSDIYSVGITACEL ASGQVPFOMBET CMLLQKLKGPYSFDLDISIFPOSESRKKNSQ SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC LQQDPEKRPSASSLLSHVFFKQMKESQDSILSLLPPAYNKPSI SLPPVLWTBPECDFPDEKDSYWEF S477 3 1044 RGNSRLRYSHEDELQLPRLPFLFFTGQLLDEVEVATEPAGSRI VQEKVFKGLDLLBKAAEMLSQLDLFSRNEDLEEIASTDLKYLLV PAFGGALTMKQVNPSKRLDHLQRAREHFINYLTQCHCYHVAEFF LPKTMNNSARNHTANSSMAYPSLVAMASQRQAXIQRYKQKKELE HRLSAMKSAVESQADDERVERYVLIHLQRWIDISLEEIESIDQ EIKLLRENDSSREASTSNSSRQERPPVKPFILTRNNAQARVFGA GYPSLPTMTVSDWYEQHRKYGALPDQCIAKAAPBEFRKAAQQOE EQEEKBEEDDEPTLHRAREMOMENTPHRGYGNRQNNG S478 2 835 KTVRIWPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT LWDKSSRCVISYCHGGFVTYVDFHBSGTCIAAAGMDNTVKW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTHHCHQGPATTVARSRTGETAAGGSDEQVMVKSNBF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP S479 2 835 KTVRIWPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT LWDKSSRCVHSYCEHGFVTYVDFHPSGTCIAAAGMDNTVKW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTHHCHQGPATTVAFSRTGETFASGGSDEQVMVKSNBF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTUSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTHHCHQGGPATTVAFSRTGEYFASGGSDEQVMVKSNBF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTUSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTHHCHQGPATTVAFSRTGEYFASGGSDEQVMVKSNBF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTUSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKW DVRTHRLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTHHCHQGPATTVAFSRTGEYFASGGSDEQVMVKSNB DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTUSADDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKW DVRTHRLQHTGLGGATTVTSFREATLKKKASIERTETDIIRSVKV EREERAEBSI EIDITANIPDLFKSYIPSBLKKENEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPJESDDFKGTGIKVYDDGQ KSYVANSNHSAANYGTDGLAFVSVELLRQASERNSKSPTEYH EFVYANPFYRPTTPOFFFTYTFOFFFTYFFOFFTYHFOFFFTYHFOFFFTYHFOFFTYFFFTHFOFFT		(1	VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVFTVG
AVYDFPOFSTSVOPMLSPELLRQDLHGYNVKSDIYSVGITACEL ASGCVPFQDMHRTQMLLQKLKGPPYSPLDISIFPQSESRMKNSQ SGVDSGIGESVLVSSCHTTVNSDRLHTPSSKTFSPAFFSLVQLC LQQDPEKRPSASSLLSHVFFKQMKESSQDSILSLLPPAYNKPSI SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPTERSTULDEVATEPAGSRI VQEKVFKGLDLLEKAEMLSQLDLFSKNEDLEETASTDLKYLLV PAFGGALTMKQVNPSKRLDHLQRARFIFTNYLTQCHCYHVAEFE LPKTMINSAEMHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESQQADDERVREYYLLHLQRWIDISLEETESIDQ EIKLLERDSSREASTSNSSRQERPPVKFFILTRINMAQAKVFGA GYPSLPTMTVSDWWEGIRKYGALPDQCIAKAPBEFFKAAQQOE EQEEKEEDDEQTLHRAREWDDWKDTHPRGYGNRQIMG KTVRIWPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKTV LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTHLHGHQGPATTVAFSRTGEYFASGSDEQVMVKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT KVWATHRUGHTSLHSGHTLYSSFTEKILDL MEGSLLYTHHGHQGPATTVAFSRTGEYFASGGSDEQVMVKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEGRLITASSDETKLILDL MEGGRLLYTHHGHQGPATTVAFSRTGEYFASGGSDEQVMVKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEGRLITASSDETKLILDL MEGGRLLYTHHGHQGPATTVAFSRTGEYFASGGSDEQVMVKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEGRLITASSDETKLILDL MEGGRLLYTHHGHQGPATTVAFSRTGEYFASGGSDEQVMVKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEGRLITASSDETKLKLDL MEGGRLLYTHHGHQGPATTVAFSRTGEYFASGGSDEQVMVKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEGRLITASSDETKLKLDL LENQQLIMQRATP LSLTTSRMEERELIKKGRLQGSTGKGQEMKKONQODQHQTQVLEQSI LRLEKEIQDLEKAELQISTKERAILKKLKSIERTTEDIIRSVKV EREBRAEESIEDIYANIPDLKSYIPSRLKREINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPJESDFNGTIKVTDDGQ KSYYANSNHSAAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EFYYANPPYRPTTPORETYTFOFFTYTFOFFTYTHOFFFTYHEFFTHYH EFYYANPFTPORETYTTFOFFTYTHOFFTYNTFOFFTYHEFFTH	ŀ)	1	SWLWVISPFMAYGSASQLLRTYFPEGMSETLIRNILFGAVRGLN
AVYDFPOFSTSVOPMLSPELLRQDLHGYNVKSDIYSVGITACEL ASGCVPFQDMHRTQMLLQKLKGPPYSPLDISIFPQSESRMKNSQ SGVDSGIGESVLVSSCHTTVNSDRLHTPSSKTFSPAFFSLVQLC LQQDPEKRPSASSLLSHVFFKQMKEBSQDSILSLLPPAYNKPSI SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPDEKDSYWEF SLPPVLPWTEPECDFPTERSTULDEVATEPAGSRI VQEKVFKGLDLLEKAEMLSQLDLFSKNEDLEETASTDLKYLLV PAFGGALTMKQVNPSKRLDHLQRARFIFTNYLTQCHCYHVAEFE LPKTMINSAEMHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESQQADDERVREYYLLHLQRWIDISLEETESIDQ EIKLLERDSSREASTSNSSRQERPPVKFFILTRINMAQAKVFGA GYPSLPTMTVSDWWEGIRKYGALPDQCIAKAPBEFFKAAQQOE EQEEKEEDDEQTLHRAREWDDWKDTHPRGYGNRQIMG KTVRIWPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKTV LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTHLHGHQGPATTVAFSRTGEYFASGSDEQVMVKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT KVWATHRUGHTSLHSGHTLYSSFTEKILDL MEGSLLYTHHGHQGPATTVAFSRTGEYFASGGSDEQVMVKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEGRLITASSDETKLILDL MEGGRLLYTHHGHQGPATTVAFSRTGEYFASGGSDEQVMVKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEGRLITASSDETKLILDL MEGGRLLYTHHGHQGPATTVAFSRTGEYFASGGSDEQVMVKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEGRLITASSDETKLILDL MEGGRLLYTHHGHQGPATTVAFSRTGEYFASGGSDEQVMVKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEGRLITASSDETKLKLDL MEGGRLLYTHHGHQGPATTVAFSRTGEYFASGGSDEQVMVKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEGRLITASSDETKLKLDL LENQQLIMQRATP LELKEIQULEKAELQISTKERAILKKLKSIERTTEDIIRSVKV EREBRAEESIEDIYANIPDLKSYIPSRLKKENEEREDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPJESDFNGKTGIKVYDDGQ KSYVANSNHSAAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EBYYANPPYRPTTPORETYTFOFFTYTFOFFTYTFOFFTYTFOFFTYTHOFFTYT	1	1	1	VLHONGCIHRSIKASHILISGDGLVTLSGLSHLHSLVKHGORHR
ASGQUPFQDMRRTQMLLQKLKGPPYSPLDISIPPQSESRMKNSQ SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC LQQDPEKRPSASSLLSHVFFKQMKEBSQDSILSLLPPAYNKPSI SLPPVLPMTEPECDPDEKDSYMEF 5477 3 1044 RGNSRLRYSHEDELQLPRLPELFETGRQLLDEVEVATEPAGSRI VQEKVFKGLDLLEKAAEMLSQLDLFSRMEDLEEIASTDLKYLLV PAPQCALTMKQVNPSKRLDHLQRAREHFINYLTOCHCYHVABFE LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESGQADDERVRFYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSRRASTSNSSRQERPPVKPFILTRNNAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPBEFRKAAQQQE EQEEKEEEDDECTLHRAREWDDWKDTHPRGYGNRQMMG 5478 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LNDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYGLHSAAVNGLSFHPSGNTLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQWWWKSNF DIGDHGEVTKVPRPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSUHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSGHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYGLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKHEEDKLKH QHLKKALREKHLLDGISGSKRQEBMKKQNQODOHQIQVLEQSI LRLEKEIQDLEKABLQISTKEREAILKKLKSIERTTEDIIRSVKV BREERABESIEDIYANIPDLPKSYIPSRLKKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIFLPSDDFKSTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAFVEELLRQASERNSKSPTEYH EFVYANPFYFPTTPQRETTYPGFNFOERIKKTNGLGIGVMESI		1	1	
SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC LQQPEKRPSASSLSHVFFKQMKEESQDSILSLLPPAYNKPSI SLPPVLPWTEPECDPPDEKGSYWEF 5477 3 1044 RGNSRLRYSHEDELQLPRLPELFGRQLLDEVEVATEPAGSRI VQRXVFKGLDLLEKARAMLSQLDLESRNEDLEEIASTDLKYLLV PAFQGALTMKQVMPSKRLDHLQRAREHFINVLTOCHCYHVAEFE LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKLRERDSSREASTSNSSRQERPVKPFILTRNNAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPBEFRKAAQQQE EQEEKBEEDDEQTLHRAREWDDWKDTHPRGYGNRQMMG GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPBEFRKAAQQQE EQEEKBEEDDEQTLHRAREWDDWKDTHPRGYGNRQMMG VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTTVDFHPSGTCIAAAGMDNTVKW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGBHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRIIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTTVDFHPSGTCIAAAGMDNTVKW DVRTHRLLQHYDLWSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGBHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKQL LENQQLIMQRATP LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKQL LENQQLIMGRATP LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKQL LENQQLIMGRATP LSLTSRMEEAELVKGRLQAITKKRLKSIERTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLKKEINEEKEDDEQNR KALYAMEIKVEKDLKYGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH ERFYANPFYFPTTPQRETVTPQFNFORFIKIKTNGLGIGVNESI	1			
LQQDPEKRPSASSLLSHVFFKQMKEBSQDSILSLLPPAYNKPSI SLPPVLPWTEPBCDSYWEF 5477 3 1044 RGNSRLRYSHEDELQDPRLPELFBTGRQLLDEVEVATEPAGSRI VQEKVFKGLDLLEKAAEMLSQLDLFSRNEDLEEIASTDLKYLLV PAFQCALTMKQVNPSKRLDBILQRAREHFINYLTQCHCYHVABFE LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSRBASTSNSSRQEPPVKPFILTRNMAQAKVFGA GYPSLPTWTVSDWYEQHRKYGALPDQGIAKAAPBEFFKAAQQQB EQEBKEEEDDEQTLHRAREMDDMKDTHPRGYGNROMM 5478 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSCHIMWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSVCEHGGFVTYVDFHPSGTCIAAAGMDNTVKW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHGPAATVAFSRTGEYFASGGSDBQVMWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKTV VKVWATHRQKFLFSLSCHIMWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSVCEHGGFVTYVDFHPSGTCIAAAGMDNTVKW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHGGPATTVAFSRTGEYFASGGSDEQVMWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP LENQQLIMQRATP 5480 444 1952 LSLTSRMEAELVKGRLQAITDKRKIQEBISQKRLKIEEDKLKH QHLKKKALREKWILDGISSGKBQEMKKQNQQDQHGIQVLEQSI LRLEKEIQDLEKABLQISTKERAILKKLKSIBFTETDIIRSVKV EREERARESEIEDIYANTPDLFKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKOLKTGESTVLSSIPLPSDDFKGTIKVYDDGQ KSYYAVSSNISAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EFBYYANPFIRPTTPQRSTVTTGDPFFQERIKIKINGLGIGVNESI	1			
SLPPVLPWTEPECDFPDEKDSYWEF 5477 3 1044 RGNSRIRYSHEDELQUPRIDELFETGRQLLDEVEVATEPAGSRI VQEKVPKGLDLLEKAAEMLSQLDLFSRNEDLEEIASTDLKYLLV PAFGGALTMKQVNPSKRLDHLQRAREHFINYLTQCHCYHVABFE LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESGQADDERVEFYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVAFPILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPBEFRKAAQQQE EQEBKEEEDDEQTLHRAREHDDWKDTHFRGYGNRQNMG 5478 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPP PATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEERELVKGRLQAITOKKKIQEFISQKELKIEEDKLKH CHLQLIMQRATP LENQQLIMQRATP SARBERSELVKGRLQDGTGIKKVKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKOLKTGESTVLSSIPLPSDDPKGTGIKVYDDGG KSYYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH ERVYANSPHYRPTTPQRSTVTTGOPNFQERIKIKINGLGIGVNESI	Ì	1	1	
\$477 \$ 1044 RGNSRLRYSHEDELQLPRLPELFETGRQLLDEVENTEPAGSRI VQEKVFKGLDLLEKAAEMLSQLDLESRNEDLEELASTDLKYLLV PAFQGALTMKQVMPSKRLDHLQRASPTLKYLLV PAFQGALTMKQVMPSKRLDHLQRAREHT INVLTQCHCYHVABFE LPKTMINSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLESIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPPILTRIMAQAKVFGA GYPSLIPTMTVSDWYSQHRKYGALPDQGIAKAAPBEFRKAAQQQE EQEEKEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG \$478 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHRQKFLFSLGVHINWVRCAKFSPDGRIJVSASDDKTVK LDMKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKW DVRTHRLLCHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSTGYFASGGSDEQVMVWKSNF DIGDHGEVTKVVRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP \$479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LDMKSSRECVHSYCEHGGFVTYVDFFPSGTCIAAAGMDNTVKW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTHHGHQGPATTVAFSRTGSYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPYATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP \$479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LDMKSSRECVHSYCEHGGFVTTVDFFPSGTCIAAAGMDNTVKW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTHGHQGPATTVAFSRTGSYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP \$480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKQC LENQQLIMQRATP LLEKEKULDGISSGKBQEEMKKQNQDQDQIQVLEQSI LRLEKERQDLEKAELQISTKERAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGBSTVLSSIPLPSDDFKGTGIKVYDDGG KSVYAVSSNHSAAYNGTSTVLSSIPLPSDDFKGTGIKVYDDGG KSVYAVSSNHSAAYNGTDAVVSEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFOSRIKKTNGLGIGVNESI	1	1	1	LQQDPEKRPSASSLLSHVFFKQMKEESQDSILSLLPPAYNKPSI
\$477 \$ 1044 RGNSRLRYSHEDELQLPRLPELFETGRQLLDEVENTEPAGSRI VQEKVFKGLDLLEKAAEMLSQLDLESRNEDLEELASTDLKYLLV PAFQGALTMKQVMPSKRLDHLQRASPTLKYLLV PAFQGALTMKQVMPSKRLDHLQRAREHT INVLTQCHCYHVABFE LPKTMINSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLESIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPPILTRIMAQAKVFGA GYPSLIPTMTVSDWYSQHRKYGALPDQGIAKAAPBEFRKAAQQQE EQEEKEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG \$478 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHRQKFLFSLGVHINWVRCAKFSPDGRIJVSASDDKTVK LDMKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKW DVRTHRLLCHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSTGYFASGGSDEQVMVWKSNF DIGDHGEVTKVVRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP \$479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LDMKSSRECVHSYCEHGGFVTYVDFFPSGTCIAAAGMDNTVKW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTHHGHQGPATTVAFSRTGSYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPYATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP \$479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LDMKSSRECVHSYCEHGGFVTTVDFFPSGTCIAAAGMDNTVKW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTHGHQGPATTVAFSRTGSYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP \$480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKQC LENQQLIMQRATP LLEKEKULDGISSGKBQEEMKKQNQDQDQIQVLEQSI LRLEKERQDLEKAELQISTKERAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGBSTVLSSIPLPSDDFKGTGIKVYDDGG KSVYAVSSNHSAAYNGTSTVLSSIPLPSDDFKGTGIKVYDDGG KSVYAVSSNHSAAYNGTDAVVSEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFOSRIKKTNGLGIGVNESI	1	{		SLPPVLPWTEPECDFPDEKDSYWEF
VQEKVFKGLDLLEKAAEMLSQLDLFSRNEDLEEIASTDLKYLLV PAFQGALTMKQVNPSKRLDHLQRAREHFINYLTQCHCYHVABFE LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPBEFFKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG 5478 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTTVDFHBSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTHGHQGPATTVAFSRTGEYFASGGSDBQVMWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGFATTVAFSRTGEYFASGGSDEQVMWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP LSHTGHQGFATTVAFSRTGEYFASGGSDEQVMWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEBELVKGRLQAITDKRKIQEBISQKRLKIEEDKLKH CHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKBIQDLEKABLQISTKEBAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGBTSLAPVEVEELLRQASERNSKSPTEYH EFFYANPFYRPTTPQRETVTPGPNFOSRIKIKTNGLGIGVNESI	E 477		3044	
PAFQGALTMKQVNPSKRLDHLQRAREHFINYLTQCHCYHVAEFE LPKTMNNSAENHTANSSMYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVRPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPBEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG 5478 2 835 KTVRIWYPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHLNWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQQPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRNEEABLVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKERIQDLEKABLQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSYYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EBYYANFFYRPTTPQRETVTPGPFFFQRETKIKTNGLGIGVNESI	34//	1 .	1011	
LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE HRLSAMKSAVESGQADDERVREYYLLHILQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPBEFRKAAQQQE EQEEKEEDDEQTLHRAREWDDWKDTHPRGYGNRQMMG 5478 2 835 KTVRIWPPVKGESTVFRAHTATVRSVHFGSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHCHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFIPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGSYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKTQEBISQKRLKIEEDKLKH QHLKKKALREKMLLDGISSGKRQEEMKKQNQQDQHQIQVLECSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKBINEEKEDDEQNR KALYAMBIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYAMPFYRPTTPQRETVTPGPNFORRIKIKTNGLGIGVNESI	.	1		
HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRINAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPBEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG 5478 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEBISQKRLKIEEDKLKH QHLKKKALREEKKILDGISSGKRQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYAMPFYRPTTPQRETVTPGPNFORRIKIKTNGLGIGVNESI	ì	1	1 .	
EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQG IAKAAPBEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQMMG 5478 2 835 KTVRIWYPNVKGESTVFRAHTATVRSVHFGSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNTLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNTLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWILDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPPYANPFYRPTTPQRETVTPGPRFQERIIKKTNGLGIGVNESI		· ·		
EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQG IAKAAPBEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQMMG 5478 2 835 KTVRIWYPNVKGESTVFRAHTATVRSVHFGSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNTLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNTLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWILDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPPYANPFYRPTTPQRETVTPGPRFQERIIKKTNGLGIGVNESI	1	1	1	HRLSAMKSAVESGOADDERVREYYLLHLORWIDISLEEIESIDO
GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPBEFRKAAQQQE EQEEKBEEDDEQTLHRAREHDDWKDTHPRGYGNRQNMG 5478 2 835 KTVRIWYPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLTTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRWEEAELVKGRLQAITDKRKIQEBISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKBQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLFKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSYYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTTEQPNFQERIKKIKTNGLGIGVNESI	1 .	-['		EIKILRERDSSREASTSNSSROERPPVKPFILTRNMAOAKVFGA
EQEEKEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG 5478 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVMKSNF DIGDHGGTYKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGETYKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKERAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDFRSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	1			
5478 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDBQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKBQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKERAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTIKVYDDGQ KSYYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANSFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	1		1	- · · · · · · · · · · · · · · · · · · ·
VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDBQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEABLVKGRLQAITDKRKIQEBISQKRLKIEBKLKH QHLKKKALREKWILDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEBAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLFKSYIPSRLRKBINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPPYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	L	<u> </u>	<u> </u>	
LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWILDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSYVAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	5478	2	835	
LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWILDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSYVAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	1			
DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKBQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAFLQISTKEBAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSYYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	1			
MEGRILYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEHISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	1	1	1	
DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEAELVKGRLQAITDKRKIQEHISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	1			
LENQQLIMQRATP 5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEAELVKGRLQAITDKRKIQEBISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKBQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	1			
5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKBQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKBINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	j	1	1	
VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKBQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKBINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI			1	
VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKBQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKBINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	5470	2	835	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT
LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSITSRMEEAELVKGRLQAITDKRKTQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKBQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEBAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	1	"	1 .	
DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRILYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSITSRMEEAELVKGRLQAITDKRKIQEBISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKBINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	1			
MEGRILYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSITSRMEEAELVKGRLQAITDKRKIQEBISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEBAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKBINEEKEDDEQNR KALYAMBIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	1	1		
DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKTQEBISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	1	1		
LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKTQEBISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	ì		1	
LENQQLIMQRATP 5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKTQEBISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	1	ł		DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC
5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEBISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	1			
QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	 		1000	
LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	5480	444	1952	
EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	1		1	
KALYAMEI KVEKDLKTGESTVLSSI PLPSDDFKGTGI KVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKS PTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKI KTNGLGIGVNESI	1	j		LRLEKEIQDLEKAELQISTKERAILKKLKSIERTTEDIIRSVKV
KALYAMEI KVEKDLKTGESTVLSSI PLPSDDFKGTGI KVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKS PTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKI KTNGLGIGVNESI		1	1	_ · · · · · · · · · · · · · · · · · · ·
KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	ł		(
EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI	i	1		
EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQQAEEKLHTPQKR	1	1		
HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQQAEEKLHTPQKR	1		ł	EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLG1GVNES1
	1	1		HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQQAEEKLHTPQKR

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
, NO.	location		Gidlamic Acid, F=Fhenylalanine, G=Glycine,
ſ		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
(amino acid	sequence	Codon, /=possible nucleotide deletion,
J	sequence] "	\=possible nucleotide insertion)
	 		LMTPWEESNVMQDKDAPSPKPRLSPRETIFGKSEHQNSSPTCQE
1	Į.	}	DEEDVRYNIVHSLPPDINDTEPVTMIFMGYQQAEDSEEDKKFLT
		•	
1.		i .	GYDGIIHAELVVIDDEEEEDEGEAEKPSYHPIAPHSQVYQPAKP
			TPLPRKRSEASPHEKHKS
5481	3	1422	NSPGSVCLCQCVCPSLLHCLPPLLLLLLLLLLHESPQPPALRV
1			VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFEPTVFRDTLV
1	1		QGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGSMLA
1	ł		PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIRRYK
1			YLEKAFEDEMKKLLLFLKAFSETEQTKLAMLSGILLGNGTLPAT
1			ILTSLFTDSLVKEGIAASFAVKLFKAWMAEXDANSVTSSLRKAN
		ļ	LDKRLLELFPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSLGTR
[1		
1	1		KELQKELQERLSQECPIKEVVLYVKEEMKRNDLPETAVIGLLWT
			CIMNAVEWNKKEELVAEQALKHLKQYAPLLAVFSSQGQSELILL
1	}		QKVQEYCYDNIHFMKAFQKIVVLFYKADVLSEEAILKWYKEAHV
L			AKGKSVFLDQMKKFVEWLQNAEEESESEGEEN
5482	1492	528	THVVMTGMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLSLRL
1]	,	EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPS
1			CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPA
1	1		LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAOCNVTLEVSTGP
			GAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDA
1	1		IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTP
1	j		TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVP
			VMVPAQSQAGSLV
5483	1	788	
3403	.	, 788	FFFFKGCRAGRGNESDYRKLEEMHQRFLVSERSKDDLQLRLTRA
1			ENRIKQLETDSSEEISRYQEMIQKLQNVLESERENCGLVSEQRL
			KLQQENKQLRKETESLRKIALEAQKKAKVKISTMEHEFSIKERG
1	[FEVQLREMEDSNRNSIVELRHLLATQQKAANRWKEETKKLTESA
]		EIRINNLKSELSRQKLHTQELLSQLEMANBKVAENEKLILEHQB
	1		KANRLQRRLSQAEERAASASQQLSVITVQRRKAASLMNLENI
5484	3	1997	IMADMEDLFGSDADSEAERKDSDSGSDSDSDQENAASGSNASGS
1	l '		ESDQDERGDSGQPSNKELFGDDSEDEGASHHSGSDNHSERSDNR
1	[SEASERSDHEDNDPSDVDQHSGSBAPNDDEDEGHRSDGGSHHSE
	<u> </u>		AEGSEKAHSDDEKWGREDKSDQSDDEKIQNSDDEERAQGSDEDK
	ļ. ·	•	LQNSDDDEKMQNTDDEERPQLSDDERQQLSEEEKANSDDERPVA
1	1		SDNDDEKQNSDDEEQPQLSDEEKMQNSDDERPQASDEEHRHSDD
1 .		•	EEEQDHKSESARGSDSEDEVLRMKRKNAIASDSEADSDTEVPKD
			NSGTMDLFGGADDISSGSDGEDKPPTPGQPVDENGLPQDQQEEE
1.			PIPETRIEVEIPKVNTDLGNDLYFVKLPNFLSVEPRPFDPQYYE
			DEFEDEEMLDEEGRTRLKLKVENTIRWRIRRDEEGNEIKESNAR
	•		IVKWSDGSMSLHLGNEVFDVYKAPLQGDHNHLFIRQGTGLQGQA
1			VFKTKLTFRPHSTDSATHRKMTLSLADRCSKTQKIRILPMAGRD
1			PECQRTEMIKKEEERLRASIRRESQQRRMREKQHQRGLSASYLE
[PDRYDEEEEGEESISLAAIKNRYKGGIREERARIYSSDSDEGSE
1	j		EDKAQRLLKAKKLTSDEVRPNLFNSRGLSCTQBPTALNEELTDO
]		AGTN
5485	161	1074	
3-03	707	1074	KRKILSSMMDSEAHEKRPPILTSSKQDISPHITNVGEMKHYLCG
1	1		CCAAFNNVAITFPIQKVLFRQQLYGIKTRDAILQLRRDGFRNLY
			RGILPPLMQKTTTLALMFGLYEDLSCLLHKHVSAPEFATSGVAA
1	{		VLAGTTEAIFTPLERVQTLLQDHKHHDKFTNTYQAFKALKCHGI
]	j		GEYYRGLVPILFRNGLSNVLFFGLRGPIKEHLPTATTHSAHLVN
] 1			DFICGGLLGAMLGFLFFPINVVKTRIQSQIGGEFQSFPKVFOKI
1 1	}		WLERDRKLINLFRGAHLNYHRSLISWGIINATYEFLLKVI
5486	1404	142	IPGSTISWSPAAARGLSVCRCCRLHPASAMDLFGDLPEPERSPR
1	-203	747	
	j		PAAGKEAQKGPLLFDDLPPASSTDSGSGGPLLFDDLPPASSGDS
1	[GSLATSISQMVKTEGKGAKRKTSEEEKNGSEELVEKKVCKASSV
]]	ļ	`	IFGLKGYVAERKGEREEMQDAHVILNDITEECRPPSSLITRVSY
į l			FAVFDGHGGIRASKFAAQNLHQNLIRKFPKGDVISVEKTVKRCL
1	ļ	ļ	LDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLG
	į.		DSRAILCRYNEESQKHAALSLSKEHNPTQYEERMRIQKAGGNVR
1	-		DGRVLGVLEVSRSIGDGQYKRCGVTSVPDIRRCQLTPNDRFILL

		77	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYEAAC
			NRLANKAVQRGSADNVTVMVVRIGH
5487	535	182	AVSLEQIRGLQTPAPVPLPLQPCPSNCDMERVTLALLLLAGLTA
		Į.	LEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK
	1		CKCKSSQKQHSPVPEKAIPLITPGSATTC
5488	1072	259	AMAASGEPQRQWQEEVAAVVVVGSCMTDLVSLTSRLPKTGETIH
]	j	GHKFFIGFGGKGANQCVQAARLGAMTSMVCKVGKDSFGNDYIEN
		į	LKQNDISTEFTYQTKDAATGTASIIVNNEGQNIIVIVAGANLLL
		Ì	NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGVKTL
			FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAADAGE
	ĺ		AALVLLKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVKAVD
	1	ł	TTVSFKI
5489	81	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETEPLK
	1	1	LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV
	1	1	LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD
			IAGDEDNRRWMRENVPGEKKPONGIPLPPQIFNEEQYCGDFDSF
			FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEDVG
İ	j		NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEEETAEGEEP
			GEDEDS
5490	81	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETEPLK
3430) ")	LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV
			LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD
ł	1		IAGDEDNRRWMRENVPGEKKPONGIPLPPQIFNEEQYCGDFDSF
<u>l</u>		ļ	FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEDVG
İ			NLPBAQEKNEEEGETATEETEEIAMEGAEGEAEEEEETAEGEEP
1			GEDEDS
5491	204	1194	GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEGRSE
3491	204	1194	QGDMASSFLPAGAITGDSGGELSSGDDSGEVEFPHSPEIEETSC
1			LAELFEKAAAHLQGLIQVASREQLLYLYARYKQVKVGNCNTPKP
Į			SFFDFEGKOKWEAWKALGDSSPSQAMQEYIAVVKKLDPGWNPQI
[•	PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCRENNIDH
ł			ITKAIKSKNVDVNVKDEEGRALLHWACDRGHKELVTVLLQHRAD
1			INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDGCLP
1			BEVTGCKTVSLVLQRHTTGKA
F402	 	1996	ASKNPLSAVCTTGIMSSLAVRDPAMDRSLRSVFVGNIPYEATEE
5492	3	1896	OLKDIFSEVGSVVSFRLVYDRETGKPKGYGFCEYQDQETALSAM
1		1	The state of the s
]	1	1	RNLNGREFSGRALRVDNAASEKNKEELKSLGPAAPIIDSPYGDP IDPEDAPESITRAVASLPPBOMFELMKOMKLCVQNSHQEARNML
<u> </u>	1		LONPOLAYALLQAQVVMRIMDPEIALKILHRKIHVTPLIPGKSQ
{			SVSVSGPGPGPGLCPGPNVLLNQONPPAPQPQHLARRPVKDI
}	1		PPLMQTPIQGGIPAPGPIPAAVPGAGPGSLTPGGAMQPQLGMPG
1	1		VGPVPLERGQVQMSDPRAPIPRGPVTPGGLPPRGLLGDAPNDPR
1]	1	GGTLLSVTGEVEPRGYLGPPHQGPPMHHASGHDTRGPSSHEMRG
1			GPLGDPRLLIGEPRGPMIDQRGLPMDGRGGRDSRAMETRAMETE
l			VLETRVMERRGMETCAMETRGMEARGMDARGLEMRGPVPSSRGP
]]		MTGGIQGPGPINIGAGGPPQGPRQVPGISGVGNPGAGMQGTGIQ
			GTGMQGAGIQGGGMQGAGIQGVSIQGGGIQGGGIQGASKQGGSQ
1	1		PSSFSPGQSQVTPQDQEKAALIMQVLQLTADQIAMLPPEQRQSI
L			LILKEQIQKSTGAS
5493	1	1876	RAPMMTKAVPEEPRKPGRLTQALNSPLTWEHVWICVPGGTPDCL
	1	1	TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH
			VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDFVRTLA
1			EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE
,]	}	EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM
	1		GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQGYVEW
}	1	1	SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL
)		HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL
	1	1	QAKADLEKELECAREGEEERREREEVLREEIQTLTSKLQELQEM
		1	KKEEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSEEGLPRP
	1		RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQAAFR

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
J	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	bequence	\=possible nucleotide insertion)
	1 44440000	 	GHLTRTKLLASKAHGSEPPSVPGLPDQSSPVPRVPSPIAQATGS
}			PVQEEAIVIIQSALRAHLARARHSATGKRTTTAASTRRRSASAT
}		ł	HGDASSPPFLAALPDPSPSGPQAVAPLPGDDVNSDDSDDIVIAP
	ļ]	SLPTKNFPV
5494	71	536	RSKAKIGTPTREVPSTDMKVRRESSSSLTHRPAPSPATPRLLGT
3.31	(-	1 336	RRVLLGVSEGTGCADAMELVLVFLCSLLAPMVLASAAEKEKEMD
· I		1	PFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKCSFNQKPRAP
			GDEEAQVENLITANATEPQKAEN
5495	273	2168	DSLLLIQVDTMPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAG
1 3133	2/3	2100	
			ELRPASLVVLPRSLAPAFERFCQVNTGPLPLLGQSEPEKWMLPP
ı			QGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFL
}		1	GCSFSLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCP
1			LVVTMRPIPKDKLEGLVRACCSLGGEQGQPVHMGDPELLGIKEL
			SKPAYGDAMVCPPGEVPVFWPSPLTSLGAVSSCETPLAFASIPG
j			CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQ
İ			KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSVLITT
ì		Í	GFPTHFNHEPPEETDGPPGAVALVAFLQALEKEVAIIVDQRAWN LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAFLCKNGDPQT
}			PRFDHLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLFLAAKK
			IPGISSTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVEADFA
	ľ		VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQA
1	1		WTQALPSVIKEEKMLGILVQHKVRSGVSGIVGMEVDGLPFHNTH
	1		AEMIQKLVDVTTAQV
5496	3	2408	QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWIDYEG
	1	. 2400	MKSGKGRPISFVDSFPLSIWICQPTRYAESQKEPQTCNQVSLNT
l	}		SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSDTFFR
1			FSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLILLSE
1			NLRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDOANTLK
			SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINRIRSVTVNH
ļ			MSDNRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYLSDKH
			LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVLNYRE
			DSNILSFDSDGNQNILSSTLTSKGNETIESIFKAEDLLPEAASL
			SENLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCVSYKN
1		· · · · ·	MKRSSSQMSLDTISLDSMILEEQLLBSDGSDSHMFLEKGNKKNS
			TTNYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHDDLMS
			VVVFKITGVNGEIDIRGEDTEICLOVNOVTPDOLGNISLRHYLC
	•		1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
}			NRPVGSDQKAVIHSKSSPEISLRFESGPGAVIHSLLAEKNGFLQ CHIKNFSTEFLTSSLMNIQHFLEDETVATVMPMKIQVSNTKINL
			KDDSPRSSTVSLEPAPVTVHIDHLVVERSDDGSFHIRDSHMLNT
	,		GNDLKENVKSDSVLLTSGKYDLKKQRSVTQATQTSPGVPWPSQS
			ANFPEFSFDFTREQLMEENESLKQELAKAKMALAEAHLEKDALL
			HHIKKMTVE
5497	1821	3308	SISKLLKRRSNIDAYLLSNSCAFFAPRLFSLASOIIREOOSPNV
1		5500	CFIYKYSGFPSLECQCHFVSPHSSCYINFFSFPPPFFVCFQLSN
			GFSHYSLSSESHVGPTGAGLFPHCLPASRLLPRVTSVHLPDYAH
l i			YYTIGPGMFPSSQIPSWKDWAKPGPYDQPLVNTLQRRKEKREPD
			PNGGGPTTASGPPAAAEEAORPRSMTVSAATRPGEEMEACEELA
			LALSRGLQLDTQRSSRDSLQCSSGYSTQTTTPCCSEDTIPSQVS
i i			
] .			DYDYFSVSGDQEADQQEFDKSSTIPRNSDISQSYRRMFQAKRPA STAGLPTTLGDAMUTDGVATIBETESTEDSVEDGTTGAGDTDIE
}			STAGLPTTLGPAMVTPGVATIRRTPSTKPSVRRGTIGAGPIPIK
1 1			TPVIPVKTPTVPDLPGVLPAPPDGPEERGEHSPESPSVGEGPQG VTSMPSSMWSGQASVNPPLPGPKPSIPEEHRQAIPESEAEDOER
j l			
			EPPSATVSPGQIPESDPADLSPRDTPQGEDMLNAIRRGVKLKKT TTNDRSAPRFS
5498	2434	1400	
0620	4434	1492	ILTHQEIFTGEKPCECGKASIQMSHLSQQKIYSGENPFACKVCG
[KVFSHKSNLTEHEHFHTREKPFECNECGKAFSQKQYVIKHQNTH
}	· ·		TGEKLFECNECGKSFSQKENLLTHQKIHTGEKPFECKDCGKAFI
j	[QKSNLIRHQRTHTGEKPFVCKECGKTFSGKSNLTEHEKIHIGEK
	1	ĺ	PFKCSECGTAFGQKKYLIKHQNIHTGEKPYECNECGKAFSQRTS
[]	1		LIVHVRIHSGDKPYECNVCGKAFSQSSSLTVHVRSHTGEKPYGC
1 1			NECGKAFSQFSTLALHLRIHTGKKPYQCSECGKAFSQKSHHIRH

		T 5 32 4 4	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	 		QKIHTH
5499	324	926	GFGQIGRGHKITTYPFSPRKSGRKGMAQSQGWVKRYIKAFCKGF
	· ·	\	FVAVPVAVTFLDRVACVARVEGASMQPSLNPGGSQSSDVVLLNH
		1	WKVRNFEVHRGDIVSLVSPKNPEQKIIKRVIALEGDIVRTIGHK
]	Į.	NRYVKVPRGHIWVEGDHHGHSFDSNSFGPVSLGLLHAHATHILW
i		Ì	PPERWOKLESVLPPERLPVQREEE
5500	1978	1286	KPDWRLONLPPRLYLWRSSRFGFGHLKKRLQMDFKIEHTWDGFP
5500	1310	1235	VKHEPVFIRLNPGDRGVMMDISAPFFRDPPAPLGEPGKPFNELW
			DYEVVEAPFLNDITEQYLEVELCPHGQHLVLLLSGRRNVWKQEL
Ì	1	1	PLSFRVSRGETKWEGKAYLPWSYPPPNVTKFNSFAIHGSKDKRS
ļ			YEALYPVPQHELQQGQKPDFHCLEYFKSFNFNTLLGEEWKQPES
İ	-	1	1
			DLWLIEKCDI
5501	2927	2226	CRPPVSARVAPGHQGAVGGSGRRPARVEVVDAAARPSSRPFSLP
		1	AAIMLALISRLLDWFRSLFWKEEMELTLVGLQYSGKTTFVNVIA
			SGQFSEDMIPTVGFNMRKVTKGNVTIKIWDIGGQPRFRSMWERY
1			CRGVNAIVYMIDAADREKIEASRNELHNLLDKPQLQGIPVLVLG
			NKRDLPNALDEKQLIEKMNLSAIQDREICCYSISCKEKDNIDIT
			LQWLIQHSKSRRS
5502	3	824	NSAFPVWVPERTALLTCPLGAAPGSSREAPGIAGPPNSTAMSKL
1			GKFFKGGGSSKSRAAPSPQEALVRLRETEEMLGKKQEYLENRIQ
	į		REIALAKKHGTONKRAALQALKRKKRFEKQLTQIDGTLSTIEFQ
1			REALENSHINTEVLRNMGFAAKAMKSVHENMDLNKIDDLMQEIT
ŀ		i	EQQDIAQEISEAFSQRVGFGDDFDEDELMAELEELEQEELNKKM
1			TNIRLPNVPSSSLPAQPNRKPGMSSTARRSRAASSQRAEEEDDD
1			IKOLAAWAT
5503	216	654	KGVRRRGRVRSDSEDSHLGYFKMSFLLPKLTSKKEVDQAIKSTA
5503	210.	0.74	EKVLVLRFGRDEDPVCLQLDDILSKTSSDLSKMAAIYLVDVDQT
Į.	1		AVYTQYFDISYIPSTVFFFNGQHMKVDYGGEDPALRSIKAVRRT
1	1		SPAGTLGEKPVNS
	<u> </u>		QLSFSFQAPVTFDDITVYLLQEEWVLLSQQQKELCGSNKLVAPL
5504	58	3563	GPTVANPELFRKFGRGPEPWLGSVOGORSLLEHHPGKKQMGYMG
}			EMEVQGPTRESGQSLPPQKKAYLSHLSTGSGHIEGDWAGRNRKL
1	İ	440	EMEVOGPTRESGOSLPPOKKAYLISHIS IGSGHIEGDWASKNAKI
1	1	<u>.</u>	LKPRSIQKSWFVQFPWLIMNEEQTALFCSACREYPSIRDKRSRL
		}	IEGYTGPFKVETLKYHAKSKAHMFCVNALAARDPIWAARFRSIR
1		1	DPPGDVLASPEPLFTADCPIFYPPGPLGGFDSMAELLPSSRAEL
1	· · · · ·	1	EDPGGDGAIPAMYLDCISDLRQKEITDGIHSSSDINILYNDAVE
		İ	SCIQDPSAEGLSEEVPVVFEELPVVFEDVAVYFTREEWGMLDKR
	1	1 .	QKELYRDVMRMNYELLASLGPAAAKPDLISKLERRAAPWIKDPN
]]		GPKWGKGRPPGNKKMVAVREADTQASAADSALLPGSPVEARASC
1		1	CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQFPWLVIDPKETKL
1		1	FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV
1		1	NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN
1			DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILED
]	1		VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP
			LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR
	Į.	ł	GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH
			IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR
	1		RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF
]			VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES
1			LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV
1			LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI
1.			
1			LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL
1			AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL
			SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT
1	1		CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL
	•		KDCIMEPPERLLYPHTSQEAPGMS
5505	3312	1219	NCSPRSLSAAKMSNRNNNKLPSNLPQLQNLIKRDPPAYIEEFLQ
j			QYNHYKSNVEIFKLQPNKPSKELAELVMFMAQISHCYPEYLSNF
1			POEVKOLLSCNHTVLDPDLRMTFCKALILLRNKNLINPSSLLEL
ł		1	FFELFRCHDKLLRKTLYTHIVTDIKNINAKHKNNKVNVVLQNFM

Deginning nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, t=Deutsi	C 690	I Dec 37	T W	
No: nucleotide corresponding to first amino acid trist amino acid trist amino acid residue of residue of amino acid residue of amino acid sequence	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
location				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Laleucine, M-Methionine, N-Asparagine, peridue of amino acid residue of amino acid sequence Paperoline, Q-Galutamine, ReAsparagine, peridue of amino acid sequence Servine, T=Threonine, V-Valine, watching of amino acid sequence Valing of the period of amino acid sequence Valing of the period of amino acid sequence Valing of the period of t	NO:		1	Giutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid amino acid sequence seq	1			H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence sequence (amino acid sequence sequence) sequence (better the sequence sequence) sequence (better the sequence) se	}		1	
residue of amino acid sequence Martyptophan, Y=Typtophan, Y=Typtophan, Y=Stop Codon, /=possible nucleotide delection				
amimo acid sequence Codon, /-possible nucleotide insertion VPMLSDSNATAARNSLDWMLELYRENINNDAKTVAVITTACES VPMLINDANTAARNSLDWMLELYRENINNDAKTVAVITTACES VPMLINDANTAARNSLDWMLELYRENINNDAKTVAVITTACES VPMLINDANTAARNSLDWMLELYRENINNDAKTVAVITTACES VPMLINDANTAARNSLDWMLELYRENINNDAKTVAVITTACES VPMLINDANTAARNSLDWMLELYRENINNDAKTVAVITTACES KKSSKNKKLEKANKVLKKHRKKKEPEVRNSAITLIHDPOOPS KKSSKNKKLEKANKVLKKHRKKKEPEVRNSAITLIHDPOOPS FLOPHOREVITKILIFAADASHILVPPIIJGLIMTVARMFUTRIN NSGEVITVGINAIKETTACPLANTRELLQDLDAVKHRKONWM MSARTLIHLIFATLANPOMLOKKFRCKPTEAS IERRUGURGHIVON SSDEEQOEISKKLNSHPWEERRAKAAATSTSRVLTQBDPQKIRN AMARKEDAARPOKKRYTEEDBEEPRGELLSINGIREHKK PKSDEKTRIATAMAKKTDRKEPVRKTKTNTPSSSTIKEEKKKOK NPMMMYSONNSKOKRYTEEDBEEPRGELLSINGIREHKK PKSDEKTRIATAMAKKTDRKEPVRKTKTNTPSSSTIKEKKKOK NPMMMYSONNSKOKRSTEENDLANDALLKKKKOK NPMMMYSONNSKOKRSTEENDLANDALLKKKKOK NPMMMYSONNSKOKRSTEENDLANDALLKKKKOK NPMMMYSONNSKOKRSTEENDLANDALLKKKKOK NPMMMYSONNSKOKRSTEENDLANDALLKKKKOK NPMMMYSONNSKOKRSTEENDLANDALLKKKOK NPMMMYSONNSKOKRSTEENDLANDALLKKKKOK NPMMMYSONNSKOKRSTEENDLANDALLKKKKOK NPMMMYSONNSKOKRSTEENDLANDALLKKKKOK NPMMMYSONNSKOKRSTEENDLANDALLKKKKOK NPMMMYSONNSKOKRSTEENDLANDALLKKKKOK STASLSVULSSNCQTBALKSVSTITUSULSCULCORPHYRMAVV LLAVYTAPDSTTSSNCHLISTISTUSTISTISTISTISTISTISTISTISTISTISTISTISTIS	1	1		
Sequence Appossible nucleotide insertion				
YTMLKDSNATAAKNSLDVMLELYRRIINNDAKTVAVITTACES VTELLVAALTFELGEDERGOSSEDEDOPTARDLUQYATO KKSSKNIKKLEKAMKVLKGRIRKKKCPVPNSSAILLHDPOODS BKLKJQLECCKERFEVRMIMALLISKJVOITHEELFFYFYFLOR FLQPHQREVTKILLFAQASHHLVPPSIIGSLIMTVANNFVTUR NSGEWITVGINAIKEITARCHANTELQUOJENTYPTFTOR NSGEWITVGINAIKEITARCHANTELQUOJENTAVANNFVTUR NSGEWITVGINAIKEITARCHANTELQUOJENTAVANNFVTUR NSGEWITVGINAIKEITARCHANTELQUOJENTAVANNFVTUR NSGEWITVGINAIKEITARCHANTELQUOJENTAVANNFVTUR NSGEWITVGINAIKEITARCHANTELQUOJENTAVANNFVTUR NSGEWITVGINAIKEITARCHANTELQUOJENTAVANNFVTUR AMARICHANTAVANAGKTDREFVEKKTKTNFFSSSTIKEKKKK NPAMMYSQNNRSKORKYTEITDSGEPGGELISKINGIRGHKKKK NPAMMYSQNNRSKORKYTEITDSGEPGGELISKINGIRGHKKKK NPAMMYSQNNRSKORKSFFERDLAGPORS AMARICHANTAVANAGKTDREFVEKKTKTNFFSSSTIKEKKKK NPAMMYSQNNRSKORKSFFERDLAGPORS NPAMMYSQNNRSKORKSFERDLAGPORS AMARICHANTAVANAGKTDREFVEKKTKTNFFSSSTIKEKKKKK NPAMMYSQNNRSKORKSFFERDLAGPORS NPAMMYSQNNRSKORKSFERDLAGPORSTIKEKKKKK NPAMMYSQNNRSKORSFERDLAGPORSTIKEKKKKK NPAMMYSQNNRSKORSFERDLAGPORSTIKEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	i	amino acid	sequence	Codon, /=possible nucleotide deletion,
VTKILIVAALTFFLGNDEDERGODSBSEEDDDPTARDLIJUTGYATO KKSSKNKKLEKRIKKUKKRIKKKKPKPWYNSTANILIHDFOORS EKLIKOLBCCKERFEVYMMINALISIKUGIHELIFLFHYFFFLOR FLOPPIOREVTKILIFAAQASHILIVETAAQASHILIVETAAQASHILIVETAAQASHILIVETAAQASHILIVAANPYTDE NSGEWITVGINALKEITARCPLANTEELLQULAGVKTHKONNW MSARTLIHLIPETURMOKKKRIKPETSIGILIMTVANIPVTDE NSGEWITVGINALKEITARCPLANTEELLQULAGVKTHKONNW MSARTLIHLIPETURMOKKKRIKPETSIGILIMTVANIPVTDE SEDEOGEISKKINSHPEDERGUAAATSTRULTQATOKUKKIN AOMRKELDAAPGKSOKRKIFETDEBESTSILISEEDDAGGEHIDVOK PROBLEGGETETTPURMOKKTIKTETSIGILISERDILIKKKKONK NPMMHINSONNASIKKRIFFERKOLARDALIKKKKONK NPMMHINSONNASIKKRIFFERKOLARDALIKKKKONK PROBLEGGGGEETPTTPURSPLEGGGDELAPRIPYTERFERKLICKORS 1 1531 FRODLEGGGGGSGSARMPAPHIPPEREREERELOPERS CSGGGGETPTTTPURSPLEGGGDELAPRIPYTERFERKLICKORS LUQVERRINVLISTGRGILEPTURACVENERPRASIDEVELAPPE EAARTPURMOLAKLECATICLOVETRIVAVLORSEWINTEESVATA TSPGRETTSOSPIVUMINTVALAUVAGISCULCKOOPRIGAPHYTRY SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE SPASISAVILSINGUPAALIKSCALIVOVALARSVENYEVE LAVADORDEPPREPRODOLOVALVYTKINONOMPERACILIARSVENYEVE KASENYILIVOVARVORBELISAVIPYISACATIONOPERACILIARSVENYEVE VANDAPSTITMOYOGRILIARSVENYEVE VANDAPSTIMMOYOGRILIARSVENYEVE VANDAPSTIMMOYOGRILIARSVENYEVE VANDAPSTIMMOYOGRILIARSVENYEVE VANDAPSTIMMOYOGRILIARSVENYEVE VANDAPSTIMMOYOGRILIARSVENYEVE VANDAPSTIMMOYOGRILIARSVENYEVE VANDAPSTIMMOYOGRILIARSVENYEVE VANDAPSTIMMOYOGRILIARSVENYEVE VANDAPSTIMMOYOGRILIARSVENYEVE VANDAPSTIMMOYOGRILIARSVENYEVE VANDAPSTIMMOYOGRILIARSVENYEVE VAN	L	sequence	J	\=possible nucleotide insertion)
KKSSKNKKLBERANKVLKKRIKKKEPEYNFSAILLHIDPODDR BELLKULDLECCKERFEVROMIMALISKUNDHIELFIFYFFICOR FLOPHOREVTKILLFAADASHHLVPPSIJOSILMTVANNFVTBE NSGEWTVGINAIKETTARCPLANTFELLOPLAD,VCHIKOKNW MSARTLIHLFRITAMPOMLOKKFRCKPTBAS IERRUGFSVEHLDAN DYIPGABVLEVEKERANDNEGORUS SISLESEEDADGRWIDVOM SSDEEGOGISKKANSHWEBERRAKAAAISTSRVITORDROKKING AMMRELDAAPIGKOKKFRCKFTBAS IERRUGRORFWIDVOM SSDEEGOGISKKANSHWEBERRAKAAAISTSRVITORDROKKING NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKOK NPMMRYSONNASKKSPERENGLEDALKKKOK NPMMRYSONNASKKSPERENGLEDALKKKOK NPMMRYSONNASKKSPERENGLEDALKKKOK NPMMRYSONNASKKSPERENGLEDALKKKOK NPMMRYSONNASKASSERPADAJAIPEREREERALCPORS LARPSELANDASKOCHOWSPERENGLEDALKKYSPERVENGADV LARPSELANDASKOCHOWSPERENGLEDALKYSPERVENGADV SPASLSNILSSNCCIPALKYSSET PUTWAADSCYLCKOPRINGADINY SPASLSNILSSNCCIPALKYSSET PUTWAADSCYLCKOPRINGADINY SPASLSNILSSNCCIPALKYSSET PUTWAADSCYLCKOPRINGADHINY SPASLSNILSSNCCIPALKYSSET PUTWAADSCYLCKOPRINGADHINY SPASLSNILSSNCLATATUS STORMAN SVOMPONINGSCHATUS CARA SKRISTEMBYLLTATUS STORMAN SVOMPONINGSCHATUS CARA LAQVIAROBININGSALATUS CARACT				YTMLRDSNATAAKMSLDVMIELYRRNIWNDAKTVNVITTACFSK
KKSSKNKKLBERANKVLKKRIKKKEPEYNFSAILLHIDPODDR BELLKULDLECCKERFEVROMIMALISKUNDHIELFIFYFFICOR FLOPHOREVTKILLFAADASHHLVPPSIJOSILMTVANNFVTBE NSGEWTVGINAIKETTARCPLANTFELLOPLAD,VCHIKOKNW MSARTLIHLFRITAMPOMLOKKFRCKPTBAS IERRUGFSVEHLDAN DYIPGABVLEVEKERANDNEGORUS SISLESEEDADGRWIDVOM SSDEEGOGISKKANSHWEBERRAKAAAISTSRVITORDROKKING AMMRELDAAPIGKOKKFRCKFTBAS IERRUGRORFWIDVOM SSDEEGOGISKKANSHWEBERRAKAAAISTSRVITORDROKKING NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKKOK NPMMRYSONNASKKSPERENGLEDALKKKOK NPMMRYSONNASKKSPERENGLEDALKKKOK NPMMRYSONNASKKSPERENGLEDALKKKOK NPMMRYSONNASKKSPERENGLEDALKKKOK NPMMRYSONNASKKSPERENGLEDALKKKOK NPMMRYSONNASKASSERPADAJAIPEREREERALCPORS LARPSELANDASKOCHOWSPERENGLEDALKKYSPERVENGADV LARPSELANDASKOCHOWSPERENGLEDALKYSPERVENGADV SPASLSNILSSNCCIPALKYSSET PUTWAADSCYLCKOPRINGADINY SPASLSNILSSNCCIPALKYSSET PUTWAADSCYLCKOPRINGADINY SPASLSNILSSNCCIPALKYSSET PUTWAADSCYLCKOPRINGADHINY SPASLSNILSSNCCIPALKYSSET PUTWAADSCYLCKOPRINGADHINY SPASLSNILSSNCLATATUS STORMAN SVOMPONINGSCHATUS CARA SKRISTEMBYLLTATUS STORMAN SVOMPONINGSCHATUS CARA LAQVIAROBININGSALATUS CARACT	1	,	1	VTKILVAALTFFLGKDEDEKQDSDSESEDDGPTARDLLVQYATG
FLOPHOREVTKILLFAROASIHLTVPETI IGILLMTVANNFYTEN NSGEWTYGINAIR SETARCELAMTERLELDIALAMTERLELDIALAMTERLELDIALAMTERLELDIALAMTERLELDIALAMTERLELDIALAMTERLELDIALAMTERLEND	1			KKSSKNKKKLEKAMKVLKKHRKKKKPEVFNFSAIHLIHDPODFA
NSGEWMYVGINAIKBITAGCHLAMTEELLODLAQYKTHRUSUM MSARTLIHE, PERKOVETAS I EARNOBYGELDAK DYY PCABVLEVEKERANDEDOMBSTSLEERDADDEWIDD SSDEDOOLS IKKLINGMMERIKKADALSEKROPTOSTOKITO SSDEOOLS IKKLINGMMERIKKADALSEKROPTOKITOKITOK PKODETYLLATAMOKTORKEY YKKITUMPSE JOEDENLIKK PKSDEYTELATAMOKTORKEY YKKITUMPSE JOEDENLIKKEKOK PKSDEYTELATAMOKTORKEY YKKITUMPSE JOEDENLIKKEKOK PKSDEYTELATAMOKTORKEY YKKITUMPSE JOEDENLIKKEKOK PKSDEYTELATAMOKTORKEY YKKITUMPSE JOEDENLIKKEKOK NPMMERYSONVESIOKKES FIRKOLALRALLIKKKEMI SGOGGET PETTY PUNSPLEGOGDELIKEN YVRPYPYRMAVV LAAFSILGAGGET PEAP PESNYTOLMPER PLYVRPYPYRMAVV LAAFSILGAGGET PEAP PESNYTOLMPER PLYVRPYPYRMAVV LAAFSILGAGGET PEAP PESNYTOLMPER PLYVRPYPYRMAVV LAAFSILGAGGET PEAP PESNYTOLMPER PLYVRPYPYRMAVV SRRSYEMWS LITHAROKIC PLUMPKYLALVAGUGE WYMTSY SAFALSANUSSNOCYSBALKEYS PYTOLARASKY I PUNMKYL SRRSYEMWS LITHAROLIS CONSUMPTION ARGAKY I PUNMKYL SRRSYEMWS LITHAROLIS CONSUMPTION ARGAKY I PUNMKYL SRRSYEMWS LITHAROLIS CONSUMPTION ARGAKY I PUNGKY PATALOLIS CONSUMPTION ARGAKY I PUNKTY VORGEN AND ARGAY SPASLASNUSSNOCYSBALKEYS PYTOLARASKY I PUNKTY VORGEN AND ARGAY SRRSYEMWS LITHAROLIS CONSUMPTION ARGAY I PUNKTY VORGEN AND ARGAY SRRSYEMWS LITHAROLIS CONSUMPTION ARGAY I PUNKTY VORGEN AND ARGAY SPASLASNUSSNOCYSBALKEYS PYTOLARASKY I PUNKTY VORGEN AND ARGAY SPASLASNOS AND ARGAY ARGAY AND ARGAY ARGAY VAVADOVOPORM PRIODOLOVIL LUPYTKOPOCH ARGAY VAVADOVOPORM PRIODOLOVIL LUPYTKE DOLONG GORGANGER KISSENTI VIGUVYR VORDELS SVANDEN I SAFTET SVENOR SKRSK KISSENTI VIGUVYR VORGEN AND ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION AND ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION	Ì	\$	{	EKLLKOLECCKERFEVKMMLMNLISRLVGIHELFLFNFYPFLOR
NSGEWMYVGINAIKBITAGCHLAMTEELLODLAQYKTHRUSUM MSARTLIHE, PERKOVETAS I EARNOBYGELDAK DYY PCABVLEVEKERANDEDOMBSTSLEERDADDEWIDD SSDEDOOLS IKKLINGMMERIKKADALSEKROPTOSTOKITO SSDEOOLS IKKLINGMMERIKKADALSEKROPTOKITOKITOK PKODETYLLATAMOKTORKEY YKKITUMPSE JOEDENLIKK PKSDEYTELATAMOKTORKEY YKKITUMPSE JOEDENLIKKEKOK PKSDEYTELATAMOKTORKEY YKKITUMPSE JOEDENLIKKEKOK PKSDEYTELATAMOKTORKEY YKKITUMPSE JOEDENLIKKEKOK PKSDEYTELATAMOKTORKEY YKKITUMPSE JOEDENLIKKEKOK NPMMERYSONVESIOKKES FIRKOLALRALLIKKKEMI SGOGGET PETTY PUNSPLEGOGDELIKEN YVRPYPYRMAVV LAAFSILGAGGET PEAP PESNYTOLMPER PLYVRPYPYRMAVV LAAFSILGAGGET PEAP PESNYTOLMPER PLYVRPYPYRMAVV LAAFSILGAGGET PEAP PESNYTOLMPER PLYVRPYPYRMAVV LAAFSILGAGGET PEAP PESNYTOLMPER PLYVRPYPYRMAVV SRRSYEMWS LITHAROKIC PLUMPKYLALVAGUGE WYMTSY SAFALSANUSSNOCYSBALKEYS PYTOLARASKY I PUNMKYL SRRSYEMWS LITHAROLIS CONSUMPTION ARGAKY I PUNMKYL SRRSYEMWS LITHAROLIS CONSUMPTION ARGAKY I PUNMKYL SRRSYEMWS LITHAROLIS CONSUMPTION ARGAKY I PUNGKY PATALOLIS CONSUMPTION ARGAKY I PUNKTY VORGEN AND ARGAY SPASLASNUSSNOCYSBALKEYS PYTOLARASKY I PUNKTY VORGEN AND ARGAY SRRSYEMWS LITHAROLIS CONSUMPTION ARGAY I PUNKTY VORGEN AND ARGAY SRRSYEMWS LITHAROLIS CONSUMPTION ARGAY I PUNKTY VORGEN AND ARGAY SPASLASNUSSNOCYSBALKEYS PYTOLARASKY I PUNKTY VORGEN AND ARGAY SPASLASNOS AND ARGAY ARGAY AND ARGAY ARGAY VAVADOVOPORM PRIODOLOVIL LUPYTKOPOCH ARGAY VAVADOVOPORM PRIODOLOVIL LUPYTKE DOLONG GORGANGER KISSENTI VIGUVYR VORDELS SVANDEN I SAFTET SVENOR SKRSK KISSENTI VIGUVYR VORGEN AND ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION AND ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION ARGAY ARGAY NELLOLE POEVSOLKAR CONSUMPTION	-]]	FLOPHOREVTKILLFAAOASHHLVPPEIIOSLIMTVANNFVTDK
MSARILHIFERILAPOMLOKKFERGAPTEAS IRANQEYVEGLEDGER IDVOM SSDEBOOD 15 KKILASHOMBERKARAALSTSEVIJOGDOPGUNDA AQMAKELDAAP GAKOKKKYIR INDSDEPRGELISLEDIEFILHKK PROMERISANDA VERKSOKRKYIR INDSDEPRGELISLEDIEFILHKK PROMERISANDA VERKSOKRKYIR TENDSDEPRGELISLEDIEFILHKK PROMERISANDA VERKSOKRKA PRAHPIPERREREALCOPGRS CSGGGGETTGTTEVWS PIEGGGDELIRPTYVEPSYRMANUN LAAPPSLGAGGETTEATTEVWS PIEGGGDELIRPTYVEPSYRMANUN LAAPPSLGAGGETTEATTEVWS PIEGGGDELIRPTYVEPSYRMANUN LAAPPSLGAGGETTEAPPESWITCHSPROVAGVASFAWPOPY LUVOY PREKNYLLETGROLOPFILVACVYGREPKASDEVPLAPATT EARETTEMMOALKLECATIGLOVSTLINFUNCKASTASPAWPOPY LUVOY PREKNYLLETGROLOPFILVAGVYGREPKASDEVPLAPATT EARETTEMMOALKLECATIGLOVSTLINFUNCKASTASPAWPOPY SPASISJAVIJSSKOCYPALKYPSYPTOVLARASKYNMY SPASISJAVIJSSKOCYPALKYPSYPTOVLARASKYNMY SPASISJAVIJSSKOCYPALKYPSYPTOVLARASKYNMY SPASISJAVIJSSKOCYPALKYPSYPTOVLARASKYNMY SRRSYEHWEYLITATLIS IGVSMPLIJSGOCHCKOPRIGAPHYYX SPASISJAVIJSSKOCYPALKYBSYOMMY SOMPHONYMINKLY SRRSYEHWEYLITATLIS IGVSMPLIJSGOCHCKOPRIGAPHYYX SPASISJAVIJSSKOCYPALKYBSYOMMY SOMPHONYMINKLY SRRSYEHWEYLITATLIS IGVSMPLIJSGOCHCYPTYVGSC GAAVPTI INTERGOPALISCICLICHYTTYVGGGCHTAVYTORAL LUVYARGRIKARVYBSPVOKY 15507 3704 1271 PROFTROMOANDA SOMPHONYMINKLY SRRSYEHWEYLITATLIS IGVSMPLIJSGOCHCYPTAGAGK VAYADAVOPOPMERIOOLOVILLYPTKEDNOCHGPCRACEKAGKK VAYADAVOPOPMERIOOLOVILLYPTKEDNOCHGPCRACEKAGKK VAYADAVOPOPMERIOOLOVILLYPTKEDNOCHGPCRACEKAGKK VAYADAVOPOPMERIOOLOVILLYPTKEDNOCHGPCRACEKAGKK VAYADAVOPOPMERIOONOCHVELTYRINGINGACY NELLOLIFOTATUR VERKORINGAN SOMPHONYMINACY NELLOLIFOTATUR VERKORINGAN SOMPHONYMINACY NELLOLIFOTATUR VERKORINGAN SOMPHONYMINACY NELLOLIFOTATUR VERKORINGAN SOMPHONYMINACY NELLOLIFOTATUR VERKORINGAN SOMPHONYMINACY NENKALATILITANO ON THE PROFT TO THE NITRO ON TH	1	ļ		
DYTPOARVLEVEKEENANDEDOMESTISLEEEDADOEM IDVING SSDEEOOOT SKKLNSMMEERKAAAATSTSEVOEPOKTINA AQMEKELDAPOKSQIKKYIEIDSDEEPROELLSLEDIELEKKEKKIK PKRODEFTRATAMAGKTDEKEFYKKKTCHPPSSTTKEKKKKK PKRODEFTRATAMAGKTDEKEFYKKKTCHPPSSTTKEKKKKK NPMMRYSONVESIONKSSERKOLALRALLKKKKRIK 1531 FREDLICGGREGEADERGGSAMPAPAHPLEERERELGFERE CSGGGGETPGTTPVMSPLEGGGDEELRENPYVRPPYRMAVVV LAAFPSLLAGGETPEAPPSSMTQLAFFRYVRAAGYASTMYEL LAAFPSLLAGGETPEAPPSSMTQLAFFRYVRAAGYASTMYEL LAAFPSLAGGETPEAPPSSMTQLAFFRYVRAAGYASTMYEL LAAFSTALGAGGETPEAPPSSMTQLAFFRYVRAAGYASTMYEL LAAFSTALGAGGETPEAPPSSMTQLAFFRYVRAAGYASTMYEL LAAFSTALGAGGETPEAPPSSMTQLAFFRYVRAAGYASTMYEL LAAFSTALGAGGETPEAPPSSMTQLAFFRYVRAAGYASTMYEL LAAFSTALGAGGETPEAPPSSMTQLAFFRYVRAAGYASTMYEL LAAFSTALGAGGETPEAPPSSMTQLAFFRYVRAAGYASTMYEL LAAGYIAPDSTSMNQDALFAKKSVQMMGVNFFSCLETVGSL LEQGALLEETREMGRISEFAAHLLISGSDEPPSSPATTLSGLIL LAGYIAPDSTSMNQDALFAKKSVQMMGVNFFSCLETVGSL LEQGALLEETREMGRISEFAAHLLISGSDEPPSSPATTLSGLIL LAVVARAGRIKKGRKAVPVSSPVGKV VAVADOVGPOMPHIOLOGVULVYTKEDONCGSGCGAGKAGKK VAVADVOVGPOMPHIOLOGVULVYTKEDONCGSGCGAGCKAGKK CTVTTERAQAVLACFLIKHHDII IIDHRNPRQLDABALCESIRSS KIJSENTIVIGVVRVORUELSIVAPPTSAGGGGGTAAGKK KASENTIVIGVVRVORUELSIVAPPTSAGGGGAGKAGKKAV NISHAGKAGAVATAGAATATAAGAATATAAGAATATAAGAATATAAGAATATAAAAAA	1		}	
SSDEROCEISKILINEMPMERRAXAAISTSRVLTQEDOPKIEM AOMRELDARPGKSQKKYLTEIDSDERPERGLENDETELIKKE PKBUKETELATAMAGKTDREEVERKTKINDPSSSTNIKEKKOK NPMMRYSOVINSKIKSSPERGOLALDETALLIKKENKE NRMMRYSOVINSKIKSSPERGOLALDETALLIKKENKE STOOL 1531 FRODLCGGROSAPGEGSSAWPAPAHFLPEREREREALCPGRS CSGGGGETT CTEVWSPLEGGGDELRENPTYVEFEYRWAVV LAAFBELGAGGETTEAPTENGOLALPENGLAKSTEVOVINAGYARSKEWSPE LAAFBELGAGGETTEAPTENGOLALPENGASSAWPEYLAPRI CSGGGGETT CTEVWSPLEGGGDELRENPTYVEFEYRWAVV LAAFBELGAGGETTEAPTENGOLALPENGASSAWPEYLAPRI EAARTTEMMGARILLEGVSTLTWALGEKVLOPENGASSAWPEYLAPRI EAARTTEMMGALALLALGVSTLTWALGEKVLOPENGASSAWPEYLAPRI TSPGERFTIDSQFLVLWMRVLAALIVAGISCVLCKOPPREGAPHYXY SPASLSVLUSSKOCYPELKEVSFTOVOLAKSKYI PVMLMKKUL SRRSTEHWEVLTATLI SIGUSMPILLSSGEPERSSPATTISGILL LAGVIALDSTAMMSVAMPGWSPFSCLFTVGSL LAGVALLEGTFRWGRHSEPAAHALLISIGSACGLFITYTTGGF GAAVPTITMTAQAPAILLSGLCLYGHTVYUNGWSPFSCLFTVGSL LAGVALLEGTFRWGRHSEPAAHALLISIGSACGLFITYTTGGF GAAVPTITMTAQAPAILLSGLCLYGHTVYUNGWSPSCLFTVGSL LAGVALLEGVARRAKSKONDOLALVASSGEPSSPATTAGLKI LAGVAARGELKGRGKKAVPVESPVQKV PROTRECERSPROCHERSPROCHERSCHGAVVETALGRANDLINGSGLCKERAGKK CTYTTERQAAVLACPLDHEHD II TIDHENNGGVAVFALGKSIST NELLGLEFGGFVASGLKURACMSVETALGNSSGALCKSTRSSC KLEENTVIVGVVRRVDREELSVMPFISAGFTRRYVENDRITUSTIST RELIGIBERGE GORGENSTAMPTISAGFTRRYVENDRITUSTIST GEMGGIYYAKKANGONIQONNKII EVIGGGKIRRYVSI INCC NOMNKAKEKISECVOSDITHONTOKKKIDERKSGADDLINGSDELRELSG NEYVLISTKNTQWSSNITPISLODUPPRILARMENERVPDPI FELBAATHRIPTGYGGELICKAGASGLALIVNINIAAGESSMEVTEA LDRVLEILKTETLSVSPOFGAKODDPHANDLYGSHDALLREN EVSSGRRHSSMARHSNTIEAPITICAGSGLALIVNINGSDELKRICHE NEYKADUKURAAPATARASKATURSHALARAKSETIRSMIQITE ANYHSSNPYHNSTHSADVLHARAYPISKERIKETLDPIDEVAAL LAATHHOVDHORTNISTLCHAGSSLALIVNINSHDLINKEHTALKP CALTUSHOPPINSTICHAGSSLALIVNINSHTLIKKRHIL KCADUSHPCRPLQVCISWAARISEETSSOTDERKOGGLPVWMV FERNYSSIKPRAGGGSFPVERGREGAGGAGKRESTIRSMIQITE ANYHSSNPYHNSTHSADVLHARAYPISKERIKETLDPIDEVAAL KVWSINKPLATALESNEETDHONGSVINTHALUSSHHAALKP CALTUSHAMPATAVAKURSHALARAKSERDPYPEOGERSKYM KVRSOLIDHPURARTHVURKNINGKARAKSGAY VIKKVLUDGLANSASGARAAAAATAWAKCHEBODDHOLBA CKRSOLIDHOVARAFVURKRYLOKGREGAGAASGARREKERGL		· ·		
AGMRELDAAPGKSORRKYTEIDSIDEPRGELLSLROPTERHIKK PRINDETELLAMAGKUTDREPVEKTIKTINPSSITINEIKKUK NYMMRYSQNVESKNIKSFREKULALDALLIKKKURM TRODICEGGGSSAPGEGGSANDAPAPHIPEREREALCPGES CSGGGGETETTTWISPIEGGGGELIRNPYVEFPYRMNYV LAAFPSLGAGGETPEAPPENTQLIFFREVVALAGKASFWPEY LLVQYFRRINYLETGRELGCFPLVKACVCFGAPHSSGAPDEGGGSAPWEY LLVQYFRRINYLETGRELGCFPLVKACVCFGAPHSSGAPWEY LLVQYFRRINYLETGRELGCFPLVKACVCFGAPHSSGAPWEY LLVQYFRRINYLETGRELGCFPLVKACVCFGAPHSSGAPWEY LLVQYFRRINYLETGRELGCFPLVKACVCFGAPHSSGAPHS TSPGRFTIDSGYLLVMRWYLALIVAGISCVLCKOPRHGAPMYYK SPASLSHVLSSWCYRALKVSFPTOVLAKASKVI EVMIMSKLV SRRSTEHWEITTATLI SIGVSPFLSSMPLSSGAPTTSGALL LAGYIAFDS TSINMGDALPAYMSSVOMMFGWIPFSCLFTVGSL LEGGALLEGFTMGHBEPSAPATALLIL ICACYLCKOPRHGAPMYYK SPASLSHVLSSWCYRALKVSFPTOVLAKASKVI EVMIMSKLV SRRSTEHWEITTATLI SIGVSPFLSSSPPSSPATTLSGLIL LAGYIAFDS TSINMGDALPAYMSSVOMMFGWIPFSCLFTVGSL LEGGALLEGFTMGHBEPSAPATALLIL ICACYLCKOPRHGAPMYYK SPASLSHVLSSWCYRALKVSFPTOVLAKASKVI EVMIMSKL LAGYIAFDS TSINMGDALPAYMSSVOMMFGWIPFSCLFTVGSL LEGGALLEGFTMGHBEPSAPATALLIL ICACYLCKOPRHGAPMYYK SPASLSHVLSGAPTLATLIN SPASLSHVLSTAFT SPASLSHVLSTAGAPHSALLIL SALLAFTALIN SPORGAPARATALLIL LAGYIAFDS TSINMGDALPAYMSSVOMMFGWIPSCLFTVGSL LAGYIAFDS TSINMGDALPAYMSSVOMMFGWIPSCLFTVGSL LAGYIAFDS TSINMGDALPAYMSSVOMMFGWIPSCLFTVGSL LAGYIAFDS TSINMGDALPAYMSSVOMMFGWIPSCLFTVGSL LAGYIAFDS TSINMGDALPAYMSSVOMMFGWIPSCLFTVGGG GAAVPTITMTLQAPATALLSCLLOCHTVGOCHTPTTGCACCKAGFK CTVTTKEAQAVALCTLEKTDALPAYMSLALLACHT II DIDHAPARALACHAGASKA KSERTUTUVGVVRRVDEELSWMPFISAGFTRRVVSINNINGC NEXTANAMAGNALACHAGAPATALACHAGAPACHAG	1	1		7 1
PRIBRETELATAMAGKTDREEFVERKTKINPPSSSTNIKEKKOK NPMMAYSON/SKIKKSPERGOLALEDALKKKINK NPMMAYSON/SKIKKSPERGOLALEDALKKKINK 1531 FRODLCGCRGGSAPGEGSSAWPAPAPHIPEREREREALCPGRS CSGGGGETTER PERENCLALEDALKKKINK LAAFSLIAGGETPEAP PERENCLALEDALKKKINK LAAFSLIAGGETPEAP PERGOLDERLENPYVEFFYRMAVV LAAFSLIAGGETPEAP PERWOLMFERVVARAGYASSMYPGY LLVQYFREKNYLETTGREICFPLVRACVFGNEPKASDEVELAPET EARAETTMWOALKLIPCATGLOYSLITMCHVARAGYASSMYPGY LLVQYFREKNYLETTGREICFPLVRACVFGNEPKASDEVELAPET EARAETTMAGALKLIPCATGLOYSLITMCHVARAGYASSMYPGY LLVQYFREKNYLETTGREICFPLVRACVFGNEPKASDEVELAPET EARAETTMAGALALGUSCYLLCKOPHERABDEVELAPET TSPGERFTDSQFLUMMRVLAALIVAGLISCYLCKOPHERABPHYRY SPASISNVLSSKCOYPALKEVSPFTOVALAGUSTVENMINGKUL SRSSTEWBEVLTATLISIGVSMPLLSSGPEPSSPATTLSGLIL LAQYIAFDSTSMODALLAPYKNSSYOWMPFSCLETTVSGLIL LAQYIAFDSTSMODALLAPYKNSSYOWMPFSCLETTVSGLIL LAQYIAFDSTSMODALLAPYKNSSYOWMPFSCLETTYSGLIL LAVYARGRIKAGRIKAQPVESTVAKSVOWMPFSCLETTSGLIL LAVYARGRIKAGRIKAQPVESTVAKSVOWMPFSCLETTSGGGTATAGKK VAVADVOQFGMAFHODOLOVLLVETKERDQCGGCRACKAGRK CTVTTERQAVLACTILDHHDIIIIDHENPRQLDAEALCRSTRSS KLSENTYUUSVAVRVENEELSSWMPTISAGFVENNINMACY NELLOLEFGEVSSOLKARACNSVETJALENSBATETTSBDPTO YANPAFSTTRYGYGGSELIKGEGBVPINKRVENNINMACY NELLOLEFGEVSSOLKARACNSVETJALENSBATETTSBDPTO YANPAFSTTRYGYGGSELIKGEGBVPINKRULDITUNSCHILT GKENGGIYYAKKNADHIOVNKII PVIQGGKTRHYVSIITVC NORNKARKISECVSSDTHTONUTGKHKKORRKSILDUTMSLATIROV RUMANAGANARAT BUSSQRHISBARATHSVITEADITVSLUMTIKAAGESSPMPVTES LDRVLEILKTTELYSPQGGAKDODPHANDLVGGIMSDGLRRLGG NEYVLISTKOTHONUSNNIITTI SLDUVPPRIAMERESYMPDTI LAATHHVOHDFORTNSFLCNAGSELALILVNIDTAVLESHHALAP OLTTODAKCHI KRIMENDIYATRAQUTSLOGTHUMBERSYMDPTI PRIMTSIS PRAGTISFLCNAGSELALILVNIDTAVLESHHALAP OLTTODAKCHI KRIMENDIYATRAQUTSLOGTHUMBERSYMDPTI KAMUSSAYBANSTISAOVARRAGYUTRAQUTSLATATHTHFEHMIN KEVNSI HKPLAATLEBNOETDKNOSVIITMLLATTENTHITHSMIL KCADVSNPCRPLQYCIENAARISEEYSGOTESHICHTHONUTYLSVL KWENJUSKYMANATATAYAYSKORGFLUKAGYOTYONAGCHRACHARACHA KEVNSI SHIPHATTITATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTISTATAYTI		}		
NPMMRYSONVESKNIKSFREKOLALDALLIKKKIMK	1	!		
1531 FRODLEGGRGSSAMPAPAHHLPERERERALCORG CSGGGETPTTYWSPLEGGDELRNPYVRFPYRMAVW LAAPSLGAGGETPEAPPESWTQLWFRPVVRFPYRMAVW LAAPSLGAGGETPEAPPESWTQLWFRPVVRAGVAGVASFWPGY LLVQYFRRKNYLETTGRGLCFFLVKACVGGNEPKASBVPLAPRT EARSTTYMWQALKLIPCTGGLCYFLVKACVGGNEPKASBVPLAPRT EARSTTYMWQALKLIPCTGGLCYFLVKACVGGNEPKASBVPLAPRT SPASLSNIVLSSWCQYBALKFVSFPTOVLKMSVLQEWMGSWFSCLFTVGGL SPASLSNIVLSSWCQYBALKFVSFPTOVLKMSKLVI LOWNIMGKLV SRRSYEHWEYLTATLISIGVSMFLLSGGPERSSPATTISGLIL LAGYIAFDSFTSMWQDALPAYKNSSVOWMGFWFFSCLFTVGGL CARAVETI INTELGOAPHILSCLLYGHTVTVGGGGVAVVPAALL LRVYARGRLKQRGKKAVPVESPVQKV DROTTERCHFAGRASRRARRFPFCGFAAPGSLEIGGFGTAGKK VAVADVQFGMRRHCDQCVJLLVFTTERDNCONGFCRACEKAGFK CTVTKEAQAVLACFLDKHHDIIIIDHRNPRQLDAEALCRSIRSS KLSENTVIVGVWRVDRESLGSVMPTJALBNSEDAIBITSDRFTQ VANDAPGFTTMGYGGGELIGKELBEV HENDCONGFCRACEKAGFK CTVTTEAQAVLACFLDKHHDIIIIDHRNPRQLDAEALCRSIRSS KLSENTVIVGVWRVDRESLGSVMPTJALBNSEDAIBITSDRFTQ VANDAPGFTTMGYGGGELIGKELBEV HENDCONGFCRACEKAGFK CTVTTEAQAVLACFLDKHHDIIIIDHRNPRQLDAEALCRSIRSS KLSENTVIVGVWRVDVARESLSVMPTJALBNSEDAIBITSDRFTQ VANDAPGFTTMGYGGGELIGKELBEV HENDCONGFCRACEKAGFK CTVTTEAQAVLACFLDKHHDIIIDHRNPRQLDAEALCRSIRSS KLSENTVIVGVWRVTQVRRESLSVMPTJALBNSEDAIBITSDRFTQ VANDAPGFTTMGYGGGELIGKELBEV HENDCONGFCRACEKAGFK CTVTTEAQAVLACFLDKHHDIIIDHRNPRQLDAEALCRSIRSS KLSENTVIVGVWRVTQVRRESLSVMPTJALBNSEDAIBITSDRFTQ GREWGGIYYAKKNIGNIQONVXIIFVVQGGGKIRHVYSIIRVCI GREWGGIYYAKKNIGNIQONVXIIFVVIGAGRABUDVATAVARSKNITHRVSIIRVCI GREWGGIYYAKKNIGNIQONVXIIFVVIGAGRABUDVATAVARSKNITHRVSIIRVCI GREWGGIYYAKKNIGNIQONVXIIFVITISCHERUSHVYDFI GREWGGIYYAKKNIGNIQONVXIIFVITISCHERUSHVYDFI GREWGGIYYAKKNIGNIQONVXIITISCHERUSHVYDFI GREWGGIYYAKKNIGNIQONVXIITISCHERUSHVYDFI GREWGGIYYAKKNIGNIQONVXIITISCHERUSHVYDFI GREWGGIYAKKNIGNIAFTSCHERUSHIVATISCHERUSHVATAVATAVATAVATAVATAVATAVATAVATAVATAVAT	1			
CSGGGETPOTTPWSSILEGGGDELRRNPYVRFPYRRMAVWY LAAPPSLGAGGTTPEAPPESWTQLWFFRFWAWASPAFWRPYV LLVQYFRRRNYLETGGGCFFLVKACVFGNEPKASDEVPLAPRT EAAETTPRWQALKLECATGLOVSYLTWGVLGGRWAFSTGADEVPLAPRT TSPGERFTDGGFLVMANVLALIVAGLCVKOPRHOAPMYRY SPASLSNVLSSWCOYEALKFVSFPTOVLAKASKVIEVMLMCKLU SRRSVEHWEYLTATLISIGGVSMFLLSSGCGQLFIFYTIGGL LAGYIAFDSFTSNWQDALFAYKWSSVQMMFGWFFSCLFTVGSL LAGYLAFDSFTSNWQDALFAYKWSSVQMMFGWFFSCLFTVGSL LAGYLAFDSFTSNWQDALFAYKWSSVQMMFGWFFSCLFTVGSL LEQGALLEGTRFWGRRSEFAAHALLISICSACGQLFIFYTIGGF GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL LRVYARGGLKQRKKAVPVSSPVQKV PROTRECFRAGRASRRRARRPFPCFGFAAPGSLEIGGFGTAAGKK VAVADVQFGMRRHODOLQVLLWFTKEDDNCONFFCACKAGFK CYTYKEAQAVLACFLJKKHDIIIDHRNFRQLDAEALCRSIRSS KLSENTVIVGVVRRVDRSELSVWPFISAGFTRYVENDNIMACY NELLQLEFGSWSGLKLRACNSVFTALENSBALEITTSEDRFYQ NELLQLEFGSWSGLKLRACNSVFTALENSBALEITTSEDRFYQ NELLQLEFGSWSGLKLRACNSVFTALENSBALEITTSEDRFYQ NANAFETIMGYQSGELIGKELGEVPINEKKADLLDTINSCIRI GKEWGGIYYAKKKNGDNIQONVKIIFVIGGGGKIRHYSGIRKG NEYVLSTKNTOMYSSNITTPISLDDVPPRIARAMENESYMPPTIS LOPVLEILITTELYSSFGRAKDDPHANDLWGGLMSDGLKRLGS NEYVLSTKNTOMYSSNITTPISLDDVPPRIARAMENESYMPPTI FURLATIMFRULIVIGLEMFARFGICEFURSSTLASHVQJIE ANYHSSNPYHNSTHSADULHATAYPLSKERIKETLDPIDEVAAL LAATIHDVDHPGRTRSFLCAASSELAILYNDTAVLESSTLASHVQIIE ANYHSSNPYHNSTHSADULHATAYPLSKERIKETLDPIDEVAAL LAATIHDVDHPGRTRSFLCAASSELAILYNDTAVLESSTLASHVQIIE ANYHSSNPYHNSTHSADULHATAYPLSKERIKETLDPIDEVAAL LAATIHDVDHPGRTRSFLCAASSELAILYNDTAVLESSTLASHVQIIE KCADUSNB CEPHLQYCIEKARARIGEETGERGGGDFWVMPV FORNCSIPKSGUGKIFKAMENDVTRTAGGIIDWALATEMTCHFEHN KEVNSINKPLATLEENGETDKNOBVINTMLRTERNTLIKMULI KCADUSNB CEPHLQYCIEKARARIGEETGERGGOGDEEKGKGM VUKKVLUDQUVASPLLGWHPTLGLGLEGGTVGESCGLEEKFM PTYRDMCVWPAAGFVWLFLVPPGFRAVYINGLTLGMDTTLSTL KYMSCLUBMALANILAGRAPATAGETGLACGGCLEEKFM PTYRDMCVWPAAGFVWLFLVPPGFRAVYINGLECLOFVTASSFCRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM ESPYWDDSKIKRRVLEFNRECRGTVAGREGGLAGSGAPGRSM AGGERQPPPDSSEERAPPATON FI FKKSITHVDRWINGKKRSQAY ERDQFRYWSAGKARAALIKKULEFTENSEGLELCDFYTLASAPGRR AGGERQPPDSSEERAPPATON FI FKKSITHVDRAGGGWCLDDDFWLFFUNDR ETPPDDQDFSEGNKAYRTWYAKLDERARNILADRUFTLANDR	5ENE		1631	
LAAPPSLCAGGETPEAPPESSHTOLMFFRPVNNAAUAFASHVPEV LLVQVFRRKYNLETGRGLCPPLVARCVEGNEPKASDEVPLAPET EAAETTPMWQALKLLFCATGLQVSYLTWGVLQERVMTRSYGATA TSPGGRFTDSQFLVLMNRVLALLTVAGLSCVLCKQPHGAPMYRY SFASLSNVLSSWCQYBALKVSYPTQULKASKVIPVMLMGKLV SRRSYEHMEVLTATLISIGVSMPLLSSGPEPRSSPATTLSGLIL LAGYIAPPSSTSNWQDALAFAYKMSSVQWSPSFCSPFSFTTGGG GAAVFII TIMTRQAPAILLSCLLYGHTVVGJGFVAVYFALL LRVYARGELKQRKKAVEVSPYQKV PRGTRRCRFAGRASRRARRRPFCFGFAAPGSLEIGGFGAAGKK VAVARVGGFMRFHCDOLQVLLVPTTEDNCCNGFCRACKKAGKK CTVTKEAQAVLACFLDKHHDIIIIDHRNPRQLDAEALCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSS KLSENTVIVGVWRRVDREISVAPTALENSGALIRSCRIPTSVINGTIGH GEWGGIYYAKKKNGDNIQONVIIPVGGGGKIRFVVYSIRVIG VANDAFFITMOYGGGGLIGKELGBV HINGAGRASALLCRSIRSS KLSENTVIVGVWRRVDREELSVMPFISARALLCRSIRSSMPVISCHELSSWPPITAR LDRVLEITRUCYGGGRUFTUNGCINGCLARSCRIPTSCHIPSITS	2508	i	1231	-
LLVOYFRENYLLETGRGLCFPLIVACVEGNEPHASDRVPLAPET EARAETPHWQDAILLIPACHGGVSYLLVQRVMTRSYGATA TSPGERFTDSQFLVLMRRVLALIVAGLSCVLCKQPRHGAPMYRY SPASLSRVLSSNCQYEALKFVSFPTQVLAKASKUT IVVALMGKKUV SRRSTEHMEVILATLIS ISGVSMFLLSSGEPERSSPATTLSGLIL LAGY1AFDSTSSNWQDALFAYKMSSVQMMFCVWFFSCLFTVGSLIL LAGY1AFDSTSSNWQDALFAYKMSSVQMMFCVWFFSCLFTVGSLIL LAGY1AFDSTSSNWQDALFAYKMSSVQMMFCVWFFSCLFTVGSLIL LAGY1AFDSTSSNWQDALFAYKMSSVQMMFCVWFFSCLFTVGSLI LERVYARGELKQRKKKXDVPSSPVGKV VAVADVQFGMRRHQDGLQVLLVGTTUTVVGGLGVAVVFAALL LRVYARGELKQRKKKXDVPSSPVGKV VAVADVQFGMRRHQDGLQVLLVFTTEDDNCCNFFCACEKAGFK CTVTTEAQAVLACFLJKHHDIII IDHENFRQLDAEALCRSIRSS KLSENTVIVGVVRRVDREELSVWFISAGFTRRYVENDNIMACT NGLLQLEFGRYSGLKLARACNSVFTLAEDALITSCSIRST KLSENTVIVGVVRRVDREELSVWFISAGFTRRYVENDNIMACT NGLKQLEFGRYSGLKLARACNSVFTLAEDALITSCSIRST KLSENTVIVGVVRRVDREELSVWFISAGFTRRYVENDNIMACT NGLKALEFGRYRSGLKARACNSVFTLAEDALITISCIRI GKRWGGIVYAKKKNGDNIQQNVKII IPV IQQGCKIRHYVSII IRVC NGNNKAEKISECVQSDTRTDNOTGRHKDRKGSLDVKAVASRAT BYSSQRRHSSMARIHSMTIEAPITKV INI INAAGESSMPVTEA LDRVLEI LARTTELYSFGPGAKDDDFHANDLVGGLMSDGLRRLGG NEYVLSTRNTQWYSSNITTPI SLDDVPPRIARAMENERYMPFOI FELBAATIMPDLIVIGLKMRARRGICERSSTLSSWLQITE ANYHSSNPVINSTHSADVLHATAYLSKERIKETLDPIDBVAAL LAATHDVDHDFGTTNSFLCAAGSELALIVATVLASERHAALAP QLTTQDDKCNIFKNMERNDYRTLRGGII IDMVLATEMTKHEHUN KEVNS INKPLATLESNGETDKNQSVINTMLRTPERMTLIKKMLII KCADVSNPCRPLQYCIEMARATISESTFSQTDERKQGLPVVMVV FPRNTCSIPRSGISFIDVFTTTMDFAMDAFVOLPPINGHLDNNF KYMKLLDEMKINNLRPPPB S508 1151 691 LSSVSKRSASMRAVGCSMGPFHWYLSLDRLPPAGGLRGFNW VULKKULVDQLVASPILLGWYPLGGLCLEGGTVGGSCQELREKW BPYKADMCVWPAAQFVUFLFVPPQRVTYINGLTIGMDTTLSYL KYRSVPLTPPGCVALDTRAD SFROGONALSASGFPAAAAAA IMVKKLKFHEQKLLKQVDFLNNE BPYKADMCVWPAAQFVUFLYPPQRVTYINGLSRAMGRIARRIADLP EPTYDDQPSRFGNKAYRTWYAKLGERGEGLGASGSAPGRSKM ABGRQPPPDSSEGRAPPATON FI FKKE INTUDNICH EPTPPUDQPSRFCNKAYRTWYAKLGERGELGASGSAPGRSKM ABGRQPPPDSSEGRAPPATON FI FKKE INTUDNICH EPTPPUDQPSRFCNKAYRTWYAKLDERARRILDRNILDRW DETPPUDQPSRFCNKAYRTWYAKLDERARRILADRWILDRWID ETPPUDQPSRFCNKAYRTWYAKLDERARRILADRUTLDRWID ETPPUDQPSRFCNKAYRTWYAKLDERARRILADRUTLDRWID ETPPUDQPSRFCNKAYRTWYAKLDERA		ļ		
EAAETTPMMQALKILECATGLQVSYLTWGVLQERWTESYSCATE TSPGERFTDSQFLVLMMRVLALIVAGLSCVLCKQPRHGAPMYRY STASISNVLSSWCQYBALKFVSFFTQVLARASKVIPVMLMGKLV SRRSYEHWEYLTATLISIGVSMPFLUSSGPPBRSSPATTLSGLIL LAGYIAFDSFTSMNQDALPAYMMSSVQMMFGWFFSGCFTVGSL LEQGALLBETFFMGRHSFPAHALLILSICSCGQLFYFYTTIGG GAAVFTIITMTRQAPAILISGLIVSVQMMFGWFFSGCFFTVGSL LEQGALLBETFFMGRHSFPAHALLILSICSCGQLFYFYTTIGG GAAVFTIITMTRQAPAILISGLIVATVVTVGGLGWAVVFAALL LRYYARGRLKQRGKKAVPVESPVQKV 5507 3704 1271 PRGTRRCRPAGRASRRARRRPGCEGPAAPGSLEIGGFGTAAGKK VAVADVQFGMMFHGDOLQVLLVFTKEDNQCNGFCRACEKAGFK CTVTKEAQAVLACFLDKHHDIIIIDHENDRQLOKGFCRACEKAGFK CTVTKEAQAVLACFLDKHHDIIIIDHENDRQLOKGFCRACEKAGFK CTVTKEAQAVLACFLDKHHDIIIIDHENDRGLDABALCSIRSS KJESHTVIVGVVRRVDYRELSWMPFISAGSTRRYVENBPNIMACY NELLQLEFGBWSQLKIRACNSVFFALENSBDAIBITSEDPFYO YANPAFETTMGYQSGELIGKBLGBVPINEKKADLLDTINSCIRI GKEMGGIYYAKKNGDNIQQNVKIIFVIGGGKIRHVYSIIRVC NGMNRAEKIBECVQSDTHTDMGTCKHIDRRKADLLDTINSCIRI GKEMGGIYYAKKNGDNIQQNVKIIFVIGGGKIRHVYSIIRVC NGMNRAEKIBECVQSDTHTDMGTCKHIDRRKADLLDTINSCIRI GKEMGGIYYAKKNGDNIQQNVKIININAQESSBPVTEA LDRVLEILRTTELYSQGGAKDDDPHANDLUGGKISDGLRLSG MYBVLSITNOTMYSSNIITPISLDDVPRIAAMMERYDDPDI FELBAATHNRPLIYLGLRMPARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYINSTHSADVLHATAYFISKERIKETLDPIDEVAAL LAATIHDVDHGRTNSFICANGSBLALLVNDTAVLESHPALAF QLTTGDDRCNIFRNMERNDYRTLRGGIIDMVLATTMTKHTEHTN KFVNSINNFLATLEEGEGDTNNGSVIHALTPTJERDTLIKMLI KCADVSNPCRPLOYCTEMAARISEEYSOTDEBKQGGLPVVMVV FDRNTCSIPKSQISFIDYFITMMFTPENFRITIKMLI KCADVSNPCRPLOYCTEMAARISEEYSOTDEBKQGGLPVVMVV FDRNTCSIPKSQISFIDYFITMMFTPENFRITIKMLI KCADVSNPCRPLOYCTEMAARISEEYSOTDEBKQGGLPVVMVV FDRNTCSIPKSQISFIDYFITMWFTPENFRITIKMLI KCADVSNPCRPLOYCTEMAARISEEYSOTDEBKQGGLPVVMVV FDRNTCSIPKSQISFIDYFITMWFTPENFRITIKMLI KCADVSNPCRPLOYCTEMAARISEEYSOTDEBKQGGLPVMVV FDRNTCSIPKSQISFIDYFITMWFTPENFRITIKMLI KCADVSNPCRPLOYCTEMAARISEEYSOTDEBKQGGLPVMVV FDRNTCSIPKSQISFIDYFITMWFTLRQGIIDDVLARHUNDTYLSYL KYRSVPUTANAACHULARVYACLUBERPROBLEADVTNYNQLSRAVRELARRIDLDP EPTYADMVVDSSKIKRHULAVRUSELCDFVTNASSFCRR LETVLILKRANAQHILQANAFVQGHVRVQGDVVTDPAFLVTRSM EPTYTWVDSSKIKRHULAVRUSERLECDFVTNASSFCRR EPTYLVDSSKIKRHULAVRNSCHLORGEBLLODV				-
TSSGERFIDSOFL/LAMRYLALIVAGISCVILCKOPRHGAPMYRY SPASISNIVISSMCQTSELKFVSFPOULARSKYLPWHIMGKIU SRRSTEHMEYLTATLISIGVSMFLLSSGPEPRSSPATTLSGLIL LAGYIAFDSFTSNWQDALFAYKMSSVQMMGVWFFSCLFFVGSLIL LAGYIAFDSFTSNWQDALFAYKMSSVQMMGVWFFSCLFFVGSLIL LEQGALGETFFWGRISFPAAHALICSACQULFTYTIGGE GAAVFTIIMTIRQAFAILLSCLLYGHTVTVUGGLGVAVVPAALL LERVYARGELKORGKKAVPUSSPVQXV 1271 PRGTRRCRFAGRASRRARRRFPCGFAAPGSLEIGGFGTAAGKK VAVADVQFGPMRFHQDDLQVLLVFTKEDNQCMSGCRACEKAGFK CTVTKEAQAVLACFLKHHDIIIIDHNPRQLDAFALCRSIRSS KLSENTVIVGWURRVDREELSVMPFISAGFTRRYVENPNIMACY NELLQLEFGBWRSQLKJRACNSVPTALENSEDALISTISEDRFIQ VANPAFETTMGYQSGELIGKELGSVPINSKKADLLDTINSCIRI GKEWGGIYYAKKNGENIQQOWKKIIPPIGGKHTYVSINICK NGNNKABELISECVQSTHTDMOTGKHKDRKKSLDVKAVASRAT BVSSQRRHSSNARIHSMTIFAPITKVINIINAAQESSPMPVTEA LDRVLEILERTFELYSPOFGAKDDPHADLVGGLMSGCLKRLGS NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEVWDFDI FELBAATHNRPLİYLGLKHFARFGICSFLHCSESTLRSMLQIIE ANYHSSNPYINSTHSADVLHATAVFLSKRIKETLDPIDVAAL IAATHDDDHFGRTNSFLCNAGSSLAILNDTAVLESHHAALAF QUITTGDDOKCHIFKNMERDVPRILGGLEKGIGEVIMVU FPRINTCSIFNSQISFIDYFITDMOTGRAKGKILEVKHEHIN KPVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNBCRPLQYCIENAARISESYSSOTDESKQQLEVVMPV FPRINTCSIFNSQISFIDYFITOMFIDADAFVULPDIMGHLDNNF KYWKGLDEMKLIRNLRPPPB 5508 1151 691 LSSVBSRSJNBAVGCONG PFLHYWYLSLDRLPPASGLRGPPN VLKKULVDQLVASPLLGVWYPLGLGCLEGQTVGESCGELREKFW EFYKADMCVWPAAQFVNELFYPPGFRVTYINGLTIGMDTYLSYL KYRSVPLTPPGCVALDTRAD SKRSGCONALSASGPAAAAAA IMWRKLKFHEGKLLKQVDFLNBE EFDTYWDVSSKIKRHVLENNERDDFDLEA ADYIGSTLTPROGUSTAVRELARRLDLP ERDOFRVRASAALIDKLALGLVPTRGSLELCDFVTASSFCRRR LDTVLLKLRNAGHLQAAVAFVEQCHWRVGPDVTDPAFLVTRSM EFFTYWDSSKIKRHVLENNERDDFDLEA ADYIGSTLTPROGUSTAVRENDERDFLEA ADYIGSTLTPROGUSTAVRELARRLRDLP ERDOFRVRASAALIDKLALGLVPTRGSLELCDFVTASSFCRRR LDFVLVUNDSSKIKRHVLENNERDDFDLEA ADYIGSTLTPROGUSTAVRENDERDFDLEA AGGERQPPPDSSEEAPPATON FI I PKKE IHTVPDMGKWKRSQAY ADYIGSTLTLTRIGVENSKKKLYTEYRYESAERELVALLINTLDRWID ETPPUDQPSRFGKKAYRTWYAKLDEERELUAVLINTLDRWID ETPPUDQPSRFGKKAYRTWYAKLDEERELUAVLINTLDRWID ETPPUDQPSRFGKKAYRTWYAKLDEERELUAVLINTLDRWID ETPPUDQPSRFGKKAYRTWYAKLDEERELUAVLINTLDRWID ETPPUDQPS	1		,	
SPASISNVLSSWCQYEALKFVSFPTQVLAKASKY1PVMLMGKLV, SRRSYEHWEYLTATL IS IGVSMPLSGPPRSS PATTLSGLIL LAGYIAFDSFTSNWQDALFAYKMSSVQMMFGVNFFSCLFTVGSL LEQGALLEGTTFMGRHSEFAAHALLISICSACGQLFIFYTIGGF GAAVFTI IMTIRQAPALLISCILYGHTVTVVGGLGVAVVPAALL LRVYARGRLKGRGKKAVPVESPVGKV 5507 3704 1271 PROTRECREAGRASRERREPCPEOGPAAPGSLEIGGFGTAAGKK VAVADVQFPMRFHQDQLQVLLVFTKEDNQCNGFCRACEKAGFK CTVTKEAQAVLACFLEKHHDI II IDHENPRQLDAEALCRSIRSS KISENTVIVOVVRRVDYRELSWMF1 SAGFTRRYVEMPNIMACY NSLLQLEFGBVRSQLKLRACNSVFTALENSBDAISITSBDRFIQ VANDAFETTMGVOSGELIGKEIGBVF ISAGFTRRYVEMPNIMACY NSLLQLEFGBVRSQLKLRACNSVFTALENSBDAISITSBDRFIQ VANDAFETTMGVOSGELIGKEIGBVF ISAGFTRRYVEMPNIMACY NSLLQLEFGBVRSQLKLRACNSVFTALENSBDAISITSBDRFIQ VANDAFETTMGVOSGELIGKEIGBVF ISAGFTRRYVEMPNIMACY NSLLQLEFGBVRSQLKLRACNSVFTALENSBDAISITSBDRFIQ VANDAFETTMGVOSGELIGKEIGBVF ISAGFTRRYVEMPNIMACY NSLLQLEFGBVRSQLKRACNSVFTALENSBDAISITSBDRFIG VANDAKKRISECVQSDTHTDNOTGKHKDREKADLLDTINSCIRI GREWGGIYYAKKNGDINGONVKIIPVIGGGKIRHYVSIIRVC NGNINKAEKISECVQSDTHTDNOTGKHKDREKGSLDVKAVASRAT BVSSGRRISSMARIHSMTIEAPITKVINIINAAGESSMPVTEA LDRVLEILRTTELYSPGFGAKDDDPHANDLVGGMSDCLRRLSG MFSVLISTROTIMVSSNIITPISLODVPPRIRARMSMERVBVDFII FELBAATTNRPLIVLGLIKMFARFGICFFLHCSESTLRSWLQIIE ANYHSSNYHNSTHSADAVLHARAYFLCGFILGCSBSTLRSWLQIIE ANYHSSNYHNSTHSADAVLHARAYFLCGFILGCSBSTLRSWLQIIE ANYHSSNYHNSTHSADAVLHARAYFLCGFILGCSBSTLRSWLQIIE ANYHSSNYHNSTHSADAVLHARAYFLCGFILGCSBTLRSWLQIIE ANYHSSNYHNSTHSADAVLHARAYFLCGFILGCBHAMALAF QLITTADDKCNIFKNMERNDYRTLRQGIIDMTATMTKHHEHVN KEVNSINKINFLATLEEGETDKINGDVINTMILRTPERRTLIKRMLI KCADUSNPCRPLQYCLEWARAISEEYSOTDERKQGGLPVVMPV FRONTCSI FLYSQIISFIDYBTTOMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNIRPPPP 5508 1151 691 LSSVFSRRSARBRAVGCSMGFFLHYWLSLDRLPFABGLRGFFN VLKKULVDQLVASPILGHWYPLGGCLEGQTVGBSCQGLEKFW EFYKADMCVMPAAQFVNILFYPPQFRVTINGLTLGWDTYLSYL KYRSVPUTPOGCWALDTAD VLKKULVDQLVASPILGHWYPLGGCLEGQTVGBSCQGELEEKFW EFYKADMCVMPAAAGANAAIMVKLKFHEQKLLKQVUTPAFLVTRSM EFYTADMVDSSKIKRHULVENDERDDFDLRA 5509 1238 619 RKSRGCONALSASGPAAAAAIMVRLKKLEFPDRDLRA BEPOTUVDSSKIKRHULVENDERDDFDLRA EFYDPUDQSRFGRKAYRTWAKLDEFRELVCLCKICUVRDDQ ADYLOFI IITLINEC	1.			
SRRSYEHMEYLTATLISIGUSMAILSGEPERSSPATTLEGLIL LAGYIAFDS FTSNWQDALFAYKMS VOXMMFGVNFFSCLFTVGSL LEQGALLEGTEFMGRHSEFAAHALLISICSACGQLFIFYTIGGE GAAVFTIMTURQAFAILLSCLLYGHTVTVGGEGVAVVPAALL LRVYARGELKORGKKAVPVESPVKV 5507 3704 1271 PROTRECEPAGRASERARREPECEGBAPGSLEIGGFGTAAGKK VAVADVQFGPMFHQDQLQVLLVFTKEDNQCMGFCRACEKAGFK CTVTKEAQAVLACFLDKHHDIIIDHRNFRQLDAEALCRSIRSS KLSENTVIVGVRRVDREELSVMFFISAGFTRRYVENPHIMACY NEILQLEFGBVRSQLKLRACHSVATLENSBDAIETISBERFIG YANPAPETTMGVQSGELIGKELGBVPINSKKADLLDTINSCIRI GKEWQGIYYAKKKNGDNIQQNVKIIPVIQGGKKRHCVSILSVC NGNNKABKISECVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT BVSSQRRISSNARIHSMTIEAPITKVINIINAQESSPMPVTEA LDRVLEILRTTELKSPOFGAKDDDHANDLVGGIMSGGLRELSG NEVVLSTKNTOMVSSNIITPISLDDVPPRIARAMENBERVDPDI FELBAATHNPLIVIGLKMFARFGIGEFHLCSESTLRSNLQIIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDBVAAL IAATHHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKMEENDYRTLAGIIDMATKKHEHWM KEYNSINKPLATLEENGETDKNQBVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEMAARISEEYFSQTBEBKQGLEVVMPV FORNTCSIPKSGISFIDYFITDMFDAMDAFVULDPLMQHLDNNF KYWKGLDBMKLRNLRPPPB 5508 1151 691 LSSVSRRSAGHRAVGCSMGPFLHYWYLSLDELFPASGLEGPPN VLKKVLVDQLVAS PLLGVWYFLGLGCLEGQTVGESCQELREKFW BPYKADMCVWPAAQFVMFLVPPQFRVTYINGLILGMDTYLSYL KYRSVPLTPPGCVALDTRAD 5509 1238 619 RKSGCGONALSASGGPAANAA MVKKLKFHEKKLLKGVDFLNNE LYVLKLLKLAMQHLQAAVAFVEQGIMVRGPDVTDAFFLYTRSM LETVLLKLRWAQHLQAAVAFVEQGIMVRGDPLARRINDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCERR LETVLLKLRWAQHLQAAVAFVEQGIMVRGDPLARRINDLP ERDGFRVWDOSSKIKHVLEYNEERDDFDLEA APIGFILTLEGVKGKKLTFFEYRYSEAIEKLVALLNTLDRWID ETPPUDQPSRRGNKAYRTWYAKLDERAFAHLCCLKCKGVURNDOD LATVFKVPNRYLESWRKLGKTYRMPBAGSQGWGLDDFQFLPFI WGSSQLIDHPYLEFRIPVDEKAVNENHKDMTATVTPTHLAAAVP EKAYSVLESSVOLSTET IDYGTGBAFAFLCCLCKGTVURNDOD LATVFKVPNRYLESWRRLGKTYRMPBAGSGGWGLDDFQFLPFI WGSSQLIDHPYLEFRIPVDEKAVNENHKDMTHECLIFITEMKT GFFABHSNQLMINSANPSSKVNOCALIKMYLACLEKFFVIQHF UGSSQLIDHPYLEPRIPVDEKAVNENHKDMFLECLIFITEMKT GFFABHSNQLMINSANPSSKVNOCALIKMYLACLEKFFVIQHF		.		
LAGYIAFDS FTSNMQDALFAYKMSSVQMMFGVMFFSCLFTVGSL LEQGALLEGTRFMGRHSEFAAHALLLS ICSACGQLFTFTYTIGF GAAVFTIIMTLRQAFAILLSCLIVGHTVTVVGGLGVAVVPFAALL LRVYARGELKQRGKKAVPUSSPVQKV 5507 3704 1271 PROTRECREAGESRARRREPGCPGAPAGSLEIGGFGTAAGKK VAVADVQFGPMRFHQDQLQVLLVFTKEDNQCMGFCRACEKAGFK CTVTKEAQAVLACFLDKHHDIIIDHRWPGLDAEALCRSIRSS KLSENTVIUGVVRVDREELSVMPFISAGFTRRYVEMPIMACV NELLQLEFGEVRSQLKLRACNSVPTALBNSBDAIETISEBRFTQ YANPAFETTMGYQSGELIGKELGBVPINEKKADLLDTINSCIRI GKEWGGIYYAKKNGDNIQONVKIIPVIGQGKTRHVVSIIRVC NGMNKAEKISECVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT EVSGGRHISSMAR HISSTIFEBTVINIINNAQESSPMPVTEA LDRVLEILRTTELYSPQPGAKDDDPHANDLVGGLMSDGLRRLSG MEYVLSTRNTQMVSSNIITPISLDDVPPLRARAMENEETVDFDI FELBAATHNRELIVLGKMPARFGICEFLHCSESTLESWQOILE ANYHSSNPYHNSTHSADVLHATAYPLSKERIKETLDPIDBVAAL LAATIHDUHDHGRINFSLCNAGEGILIVNDTAVLSHHAALAF QLTTGDDKCNIFKNMERNDYRTLRGGILDMVLATEMTKHPEHVN KEVNSINKPLATLEENGETDKNQEVITMLETPENRTLIKRMLI KCADVSNPCRFLQVCIEWAAR ISALILVNDTAVLSHHAALAF QLTTGDDKCNIFKNMERNDYRTLRGGILDMVLATEMTKHPEHVN KEVNSINKPLATLEENGETDKNQEVITMLETPENRTLIKRMLI KCADVSNPCRFLQVCIEWAAR ISALILVNDTAVLSHHAALAF QLTTGDDKCNIFKNMERNDYRTLRGGILDMVLATEMTKHPEHVN KYWKGLDEMKLRNLRPPBB 5508 1151 691 LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLPPASGLRGPPN VLKKVLVDQLVASPLLGVWYPLGLGCLGSQTVQESCGELERFW EPYKADWCUWBAAQFVNFLEVPBGVTYYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCQNALSASGPAABAAIMVRKLKFHEQKLLKQVDFLNWE EPYKADWCUWBAAQFVNFLEVPBTYTYNGLISCAUGHTVASFSCRR LPTVLLKLRMAQHLQAAVAFVEQGHVVGPDVVTDPAFLVTRSM EPFYWVDSSKIKRHVLENNEERDDFDLEA FERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRR LPTVLLKLRMAQHLQAAVFVEQGHVVGPDVVTDPAFLVTRSM EPFYWVDSSKIKRHVLENNEERDDFDLEA AGGERGPPPDSSEREAPPATONT IKKSHIHTVPDMWKWKSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLINTLDRWID ETPPVDQPSRFGRKAYRTWYAKLDEEABNLATVVPTHLAAAVP EVAVYLKSSVONSTRIDYTGTGBLAFFAAFLCCLCKIGVURVDDQ AGGERGPPPDSSEREAPPATONT KRISHITHVTAMATUTVVPTHLAAAVP EVAVYLKSSVONSTRIDYTGTGBLAFFAAFLCCLCKIGVURVDDQ VGSQLIDHPYLEPRHFVDEKAVNTAKLDEEABNLATVTVPTHLAAAAVP EVAVYLKRSVONSTRIDYTGTGBLAFFAAFLCCLCKIGVURVDDQ VGSQLIDHPYLEPRHFVDEKAVNGGLIRMYKAECLEKFFVIGHF UGSSQLIDHPYLEPRHFVDEKAV	1			<i>}</i>
LEGGALLECTRFMGRHSEFAAHALLISICSAGGQLPTPYTIGOF GAAVPTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVPAAL LRVYARGELKGRGKKAVPVESPVQKV 5507 3704 1271 PRGTRRCRFAGRASRRARRPFCCPGPAPGSLEIGGFGTAAGKK VAVADVQFGPMRFHDOLGVLULVFTEDDOCMGFCRACEKAGFK CTVTKEAQAVLACFLDKHHDIIIIDHNPRQLDAEALCRSIRSS KLSENTVLUGVRRVDREELSVMPFISAGFTRRVVENFNIMACY NELLQLEFGBVESQLKIRACNSVFTALENSBDALETISBERFJG VANPAPETTMGYGSGELIGKLEGBVPINSKADLLDTINSCIRI GERWGGIYYAKKANGDNIQONVKIIPVIGGGKURHVSIIRVC NGNNKAEKISECVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT BVSSQRRISSNARIHSNTIEAPITKVINIINAAGESSPMVTFA LDRVLEILRTTELLSFOPGAKDDHNDLVGGIMSGGLRFLSG NEVVLSTKNTOMVSSNIITPISLDDVPPRIARAMENEEVMOPDI FELBAATHNRDLIVIGLKMPARGEFLANDLOLIE ANYHSSNPYHNSTHSADVLHATAYPLSKERIKETLDPIDEVAAL IAATHHDVDHBGRTNSFLCNAGSELAILVNTAVLESHHAALAF QLITTGDDKCNIFKMEENDYRTLGGLHOWLTKKHEHVN KFYNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADUSNPCRFLQVCIENAARIESTSGTDEBKQQIEDVMPV FFRNTCSIPKSQISFIDYFITDMFDAMDAFVDLPDLMQHLDNNF KWMCLDEMKLRNLRPPPB 15508 1151 691 LSSVSRRSAMFRAVGCSMGPFLHYWYLSLDRLPPASGLRGPPN VLKKVLVDQLVASPLLGUWYPLGLGCLBGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTVINGLTLGWDTYLSYL KYRSVPLTPGGCVALDTAA 5509 1238 619 RKSGCGONALSASGPAAAAA MVKKLKFHEGKLLKGVDFLNWE LETVLLLKLRWAQHLQAAVAFVEGGHVRGPDVVTDAFFLVTRSM EFYKADWCVWPAAQFVNFLFVPQGGHVRGPDVVTDAFFLVTRSM EFYKADWCVWPAAGFVVRFLYRLQREDPDVTDAFAFLTRSM LETVLLKLRWAQHLQAAVAFVEGGHVRGDEGQASGSAPGRRM LETVLLKLRWAQHLQAAVAFVEGGHVRGDEGQASGSAPGRRM LETVLLKLRWAQHLQAAVAFVEGGHVRGDEGASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKSELLCDFVTASSFCRR LETVLLKLRWAQHLQAAVAFVEGGHVRGDFOLDEA AEGERGVPPDSSEEAPPATQNFIIPKSKEIFLVDDMCKWKRSQAY ADYIGFIILTLEGVKGKKLTFFYRYSEAIEKLVALLNTLDRWID ETPPDUQPSRFGRKAVRTWYAKLDEEABNLUATVVPTHLAAAVP EVAVYLKSSVOLSTETIPTGTGGTAFAAFLCCLCKGTVUKNDOD IATVFKVPNRYLESWRRLGKKLTFFRYRSEAIEKLVALLNTLDRWID ETPPDUQPSRFGRKAVRTWYAKLDEEABNLUATVVPTHLAAAVP EVAVYLKSSVOLSTETI DYTGTGBAFAFLCCLCKGTVUKNDOD IATVFKVPNRYLESWRRLGKKUTFFRYNGALIEKLVAULNDTUD ETPPDUQPSRFGRKATTNYAKLDEEABNLUATVVPTHLAAAVP EVAVYLKESVONSTETI DYTGTGBAFAFALCCLCKGTVUKNDOD GFFAEHSNQLWNISAVPSNSKVNGGLIRMYLAECLEKFFVIQHF UGSSQLIDHPLEERHFVLOKKEVNSCHKNONGLIRMYLAECLEKFFVI				
GAAVFII IMTLRQAPAILLSCLLYGHTVTVUGGLGVAVVFAALL LRVYARGRLKQRKKAVPUSSPUGUT FRÖTRRCRPAGRASRRARRPPCEGPAAPGSLEIGGFGTAAGKK VAVADVOFGPMRFHODOLQVLLVPTKEEDNCNGFCRACEKAGKK CTVTKBAQAVLACFLDKHHD II IDHRNPRQLDABALCRS IRSS KLSENTVIUGVVRRVDREELSVMPFISAGFTRRYVENPNIMACY NELLQLEFGEVRSQLKLRACNSVFTALENSEDAIETTSEDRFIQ YANPAPETTMGYGSGELIGKELGBVPINEKKADLLDTINSCIRI GKEWQGIYYAKKKNGENIQQNVKIIPVIGQGKIRHVSVIIRVC NGNNKAEKISECVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT LDRVLEILRTTELYSPGFGAKDDDPHANDLUGGIMSGIRRLSG NEVVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEVMDPDI FELEAATHNRPLIYIGLKMFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAVFLSKERIKETLDPIDEVAAL LAATHHDVHPGGTNSFLCNAGSISAILAILYNDTAVLSHHHALAF QLTTGDDKCNIFKNMERRDYRTLRGGIIDMVLATEMTKHFEHVN KPVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLII KCADVSNECRFLQYCIERAARISESEYSGTDEBKQGGLEVVMPV FPRNTCSIFKSGISFIDVFITDMFDAMDAFVDLPDIMQHLDNNF KWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRRSSMFAVGCSMGPFLHYWYLSLDRLFPASGLRGPPN VLKKVLVDQLVASPLLGWYPLGLGCLEGGTVGESCGELREKFW EFYKADMCVWPAAQFVNLFLYPGFRVTYINGLILGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKILKQVDFLNWE VTCHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQRFVRASAALLDKLYALGLVPTRGSLBLCDFVTASSFCRR LPTVLLKLMAQHLQAAVAFVEGGVRVKGERGLAASSAFGRKM BEDFYTWVDSSKIKRRVLEYNEREDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVPERGRVGRRVKGERGLAASSAFGRKM AGGERQPPPDSBERAPPATOR IPKKEIHTVPDMGKWRSQAY ADYIGPILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETTPPVDOPSRRGNKAYRTWYAKLDEREARUNATVVPTHLAAAVP EVAVYLKESVORSTRIDYGTGHEAAFFAFLCCLCKTGVLRVAVDD UAIVFKVFNRYLEWRRLQKTYRREAGSGGWGGDDPGFLEFI WGSSQLIDHPYLEPRHPUEKAVNENHKDYMFLEGLIFITEMKT TAIVFKVFNRYLEWRRLQKTYRREAGSGGWGGDDPGFLEFI WGSSQLIDHPYLEPRHPUEKAVNENHKDYMFLEGLIFITEMKT 1AIVFKVFNRYLEWRRLQKTYRREAGSGGWGGDDPGFLEFI WGSSQLIDHPYLEPRHPUEKAVNENHKDYMFLEGLIFITEMKT 1AIVFKVFNRYLEWRRLQKTYRREAGSGGWGGDDPGFLEFI WGSSQLIDHPYLEPRHPUEKAVNENHKDYMFLEGLIFITEMKT 1AIVFKVFNRYLEWRRLQKTYRREAGRGUVRGLECKFFVUGHF	-			l
LRVYARGRLKQRGKKAVPVESPVQKV				, · · ·
PRGTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGGGTAAGKK VAVADVQPGPMRFHODOLQVLLVETIKEEDNCCNGFCRACEKAGFK CTVTKEAQAVLACFIDKHHD II IDHRNPRQLDAEALCRSIRS KLSENTVIVGVVRVDREELSVMPFISAGFTRRYVENPNIMACY NELLCLEFGEVRSOLKLRACNSVFTALENSEDAIETTSENFTQ YANPAPETTMGYGSGELIGKELGBVPINEKKADLDTINSCIRI GKEWQGIYYAKKKNGENIQQNVKIIPVIGQGKIRHVVSIIRVC NGNNKAEKISECVQSDTHTDNQTGKHKDRKKGSLDVKAVASRAR EVSSQRRHSSMARIHSMTIEAPITKVINIINAQESSPMPVTEA LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRLSG NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDPDI FELEBATHNRPLIVIGLKMFARPGICEFLHCSESTLRSWQIIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL LAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLITTGDDKCNIFKMERRDVRTLRQGIDMVLATEMTKHFEHVN KFVNSINKPLATLEENGSTDKNQSVINTMLRTPENRTLIKRMII KCADVSNPCRPLQYCIEWAARISEYFSQTDEBKQQGLPVVMPV FFDRNTCSIPKSGISFIDYFITDMPDAMDAVOLPDLMQHLDNNF KVWKGLDEMKLRNLRPPBE S508				GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL
VAVADVQFGPMRFHQDQLQVLLVFTKEDNQCNGFCRACEKAGFK CTVTKEAQAVLACFLDKHHDIIIIDHRDRQLDAEALCRSIRSS KLSENTVIVGVVRVDREELSVMPFISAGFTRYVVENPHIMACY NELLQLEFGBVRSQLKLRACNSVFTALENSBDAIETTSEDRFIQ YANDAFETTMGYGSGELIGKELGEVPINEKKADLLDTINSCIRI GKEWQGIYYAKKKNGDNIQONVXIIPVIGGGKIRHYVSIIRVC NGNNKAEKISECVGSDTHTDNQTGKKKDRKKGSLDVKAVASRAT EVSSQRRHSSMARIHSMTIEAPITKVINIINAQESSPMPVTĒA LDRVLEILRTTELLYSPQFGAKDDDPHANDLVGGLMSDGLRRLSG NEVLISTKNTQMYSSNITTPISLDDVPPRTARAMENEEVMDPDI FELBAATHNRPLIYLGIKMFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYPLSKERIKSTLDPIDEVAAL IAATHBUVDHPGRTNSFLCNAGSELAILVNDTAVLESHHAALAF QLITGDDKCNIFKNMERDVPTLRQGIIDWLALTEMKHFEHNN KFVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEETFSOTDEBKQGGLEVVMPV FDRNTCSIPKSQISFIDYITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRSSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFFN VLKKVLVDQLVASPLLGWYPFLGGLEGGTVGESCGELREKFW EFYKADWCWPAAQFNNFLFVPPGCVALDTRAD VLKKVLVDQLVASPLLGWYPFLGGLEGGTVGESCGELREKFW EFYKADWCWPAAQFNNFLFVPPGFVTYINGLTLGWDTYLSYL KYRSFVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCONALSASGPAAAAAAMVRKLKFHEGKLLKQVDFLNWE ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRR VTDHILHELRVLRRYRLQREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRR VTDHLHELRVLRRYRLQREDYTRYNGLSRAVRELARRLRDLP ERDQFFVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRR SERGCONALSASGPAAAAAMAYFVEGGHVVAOPDVVTDPAFLVTRSM EDFFVLWVDSSKIKRHVLEYNEERDDDDLEA ARGERQPPPDSSERAPPATQNFIIPKKGRGGAGSAGGSKFM ARGERQPPPDSSERAPPATQNFIIPKKGRGGAGAGGSAGGSKFM ARGERQPPDSSERAPPATQNFIIPKKGERGLVASGVSAGAAAAA PAYLGFILTINGGVKGKKLTFFYRYSEATEKLVALLINTLDRWID ETPPVDVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLGEVRRKLQKTYRMBEAGSGGWGGLDDFCFLFFI MGSSQLIDHPYLEPRHFVDEKANVENHKYDMFLECILFITEMKT GFFABHSNQLMNISAVPSMSKVNQGLIRNYKAECLEKFPVIQHF			_	LRVYARGRLKQRGKKAVPVESPVQKV
CTUTKEAQAVLACFLUKHHDIIIIIIRRDPRQLDAEALCRSIRSS KLSENTVIVGVVRVDREELSVMPFISAGFTRRYVENPNIMACY NELLQLEFGEVRSQLKLRACNSVPTALENSBDAIEITSEDRFTQ YANPAFETTMGYQSGELIGKELGEVPINEKKADLLDTINSCIRI GKEWQGIYYAKKNGDNIQQNVKIIPVIGGGKIRHYVSIIRVC NGRNKAEKISECVQSDTHTDNOTGKHKDRKKADLLDTINSCIRI GKEWQGIYYAKKNGDNIQQNVKIIPVIGGGKIRHYVSIIRVC NGRNKAEKISECVQSDTHTDNOTGKHKDRKGSLDWKAVASRAT EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRISG NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEPWDPDI FELEAATHNRPLIYLGLKMPARGGIGEFLHICSESTLRSNLQIIE ANYHSNPYHNSTHSADVLHATAYPLSKERIKETLDPIDEVABA LAATIHDVDHPGRTNSFLCNAGSELAILVNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN KPVNSINKPLATLEENGETDKNQGVINTMLRTPENRTLIKRHLII KCADUSNPCRPLQYCIEMARISEEYFSOTDEBKQQGLEVVMPV FORNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDIMQHLDNNF KYWKGLDEMKLRNLRPPPB S508 1151 691 LSSVFSRRSASMFAVGCSWGPFLHWYLSLDRLPPASGLRGFPN VLKKVLVDQLVASPLLGVWYFLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPGFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTHAD 5509 1238 619 RKSRGCQNALSASGPAAAAAAMVRKLKFHEQKLLKQVDFLNWE VTDHNIHELRVLRRYRLQRREDYTBYQGLSRAVRELARRIRDLP ERDQFRVRASAALIDELVARGEDYTANSFCRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EFFYUNDSSKIKRHVLENDERDDFDLEA AEGERQPPPDSSEEAPPATQNFIIPKKELGKUAGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKELTATVPDMGKWKRSQAY ADYIGFILTINGGVKGKKLTFEYRVSAIERKLVATVPTHLAAAVP EVAVYLKESVGNSTRIDVGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVNRKLQKTYRMBEAGSQGWGLDDFQFLFFI WGSSQLIDHPYLEPRHFVDEKAVNENHKNDYMFLECILFITEMKT GPFABHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	5507	3704	1271	PRGTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGGFGTAAGKK
KLSENTVIVGVVRRVDREELSVMPFISAGFTRRYVENPNIMACY NELLQLEFGBVRSQLKURACNSVYTALBINSBDAIETTSEDRFIQ YAMPAFFTTMGYQSGELIGKELGBVPIMEKKADLIDTINSCIRI GKEWQGIYYAKKKNGDNIQQNVKIIPVIQQGGKIRHYVSIIRVC NGNNKABKISECVQSDTHTDNGYGGKHKDRRKGSLDVKAVASRAT EVSSQRHSSMARIHSMTIEAPITKVINIINAQBESSPMPVTBA LDRVLEILRTTELYSPQFGAKDDDFHANDLVGGLMSDGLRRLSG NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEVWDFDI FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL IAATHEVDHPGBRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN KFVNSINKPLATLEENGETDKNQEVINTMLRTPERRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEBKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KVWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLPFASGLRGFPN VLKKVLVDQLVASPLLGVWFYLGGCLEGQTVGESCQELREKFW EFYKADWCVMPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCONALSASGPAAAAAAINWKLKFHEQKLLKQVDFLNWE EFPKADWCVWPAAQFVAHVKKKFHEQKLLKQVDFLNWE EPDVEVWDSKIKRHVLLYAGGLUPTRGSLELCDEVTASSFCRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPERGREVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATONFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLINEGVKGKKLIFETWSEALEKLVALLNTLDRWID ETPPPVDDPSFRGNKAVAKLDEEABRULATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRWPAGSQGVWGLDDPGFLFFI WGSSQLIDHFYLEPRHFVDEKANNEHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSSKVNQGLIRMYKABECLEKFPVIQHF		,		VAVADVQFGPMRFHQDQLQVLLVFTKEDNQCNGFCRACEKAGFK
NELLQLEFGEVRSQLKLRACNSVFTALENSEDAIETTSEDRFIQ YANPAFETTMGYQSGELIGKELGBVPINEKKADLLDTINSCIRI GKEWQGIYYAKKKNGBUNQOWKIIPYUGQGKIKHYVSIIRVC NGNNKAEKISECVQSDTHTDNQTGKHKDRKGSLDVKAVASRAT EVSSQRRHSSMARIHSMTIEAPITVINIINAAQESSEMPYTEA LDRVLEILRTTELYSPOPGAKDDDPHANDLVGGMSDGLRRLSG NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDPDI FELEAATHNRPLTYLGLKMPARFGIGEFLHCSESTLRSWLQIIE ANYHSSNPYNINSTHSADVLHATAYPISKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLRGGIIDMVLATEMTKHFEHVN KFWNSINKPLATLESHGEDKNQSVINTMLRTPERRTLIKRNLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEBKQQGLPVVMPV FFRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KVWKGLDEMKINLIRPPEN FSNMTCSIPKSQISFIDYFTTDMFDAWDAFVDLPDLMQHLDNNF KVKKGLDEMKINLIRPPEN FSNMTCSIPKSQISFIDYFTTDMFDAWDAFVDLPDLMQHLDNNF KVRKGLDEMKINLIRPPEN FSNMTCSIPKSQISFIDYFTTDMFDAWDAFVDLPDLMQHLDNNF KVRKGLDEMKINLIRPPEN EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLIGGWFPN VLKKVLVDQLVASFLLGWWYFLGIGGLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLIGWDTYLSYL KVRSPVPLTPPGCVALDIRAD **STSGCONALSASGPAAAAAAINVKLKFHEQKLLKQUDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVELARRLRDLP ERDQFRVRASAAALDKLYALGUVPTRGSLELCDFVTASSFCRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDFDFLEA **STSGCONALSASGSFPLVEFGRGRVGARVKGERGIQASGSAPGRSKM AEGERQPPPDSSEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPPUDOPSFRGRKVARKLDEKERGLUATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFRRYLESVMRKLQKTYRMPAGSQGVWGLDDPGFLFFI WGSSQLIDHPYLEPRHFVDEKANNHKDYMFLECILFITEMKT GPFABHSNQLWNISAVPSMSKVNQGLIRMYKABECLEKFPVIQHF				CTVTKEAQAVLACFLDKHHDIIIIDHRNPRQLDAEALCRSIRSS
YANPAFETTMGYQSGELIGKELGBVPINEKKADLLDTINSCIRI GKEWQGIYYAKKNGDNIQQUNKIIPVIGGGKIRHYVSIIRVC NGNNKABKISECVQSDTHTDNQTGKHKDRRGSDLVKAVASRAT EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTËA LDRVLEILRTTELYSPQFGAKADDDPHANDLVGGLMSDGIRRLSG NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDPDI FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN KFVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEBKQQGLPVMPV FORNTCSIPKSQISFIDVPITDMDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGVWYPLGLGCLEGQTVGESCQELREKFW EFYKADWCVMPAAQFVNELFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCONALSASGPAAAAANATMVRLKFHEQKLLKQVDFLNWE ERDQFRVRASAALDKLYALGLVPTRGSLELCDFVTASSFCRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVTTDPAFLVTRSM EDFVTWDDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRGARVKGERGLQASGSAPGRSKM AGGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKKKRSQAY ADYIGFILTLNEGVKGKKLTFFYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEBAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMPSPAGSGGWGLDDFGFLFFI WGSSOLIDHPYLEPRHFVDEKAVNENHKDYMFLEGLIFITEMKT GGPFAEHSNQLWNISAVPSWSKUNGGLIRLYKABCLEEFFPUQHF				KLSENTVIVGVVRRVDREELSVMPFISAGFTRRYVENPNIMACY
GKEWQGIYYAKKNGDNIQONWIIPVIGQGGKIRHYVSIIRVC NGNNKAEKISECVQSDTHTDNQTGKHKGRAGDDVKAVASRAT EVSQQRHSSMARIHSMTIEAPITKVINIINAQGSSMPYVTEA LDRVLEILRTTELYSPQPGAKDDDPHANDLVGGIMSDGLRRLSG NEYVLSTKNTQNVSSNIITPISLDDVPPRIARAMENERYWPPDI FELEAATHNRPLITVIGKMFARRGIGEFHLHGSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL IAATHDVDHBGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKMENDYRTLRQGIIDWVLATEMTKHFEHVN KEVNSINKPLATLEENGETDKNQGVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEBKQQGDVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRRSASMFAVGCSMGPFTHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGVWYPLGLGGLEGGTVGESCQELREKFW EFYKADWCVWPAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCONALSASGPAAAAA MWRKLKFHEQKLLKQVDFLNWE ERDQFRVRASAALDKLVALGLVPTRGSLELCDFVTASSFCRR LPTVLLKLRNAQHLQAAVAFVEQGHVRVGPDVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEEDDFDLEA FAGAHLSSGSSEPLVFPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTINEGVKGKKITFFYRVSEAIEKLVALLINTLDRWID ETPPVDQPSRFSNKANAYRWYAKLDEERENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMSPAGSGGWGLDDFGFFFI WGSSQLUIDHPYLEPRHFVDDEKAVNENHKDYMFLECILFITEMKT GGFFAEHSNQLWNISAVPSWSKVNQGLIRNYKAECLEKFPVLQHF				NELLQLEFGEVRSQLKLRACNSVFTALENSEDAIEITSEDRFIO
GKEWQGIYYAKKNGDNIQONWIIPVIGQGGKIRHYVSIIRVC NGNNKAEKISECVQSDTHTDNQTGKHKGRAGDDVKAVASRAT EVSQQRHSSMARIHSMTIEAPITKVINIINAQGSSMPYVTEA LDRVLEILRTTELYSPQPGAKDDDPHANDLVGGIMSDGLRRLSG NEYVLSTKNTQNVSSNIITPISLDDVPPRIARAMENERYWPPDI FELEAATHNRPLITVIGKMFARRGIGEFHLHGSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL IAATHDVDHBGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKMENDYRTLRQGIIDWVLATEMTKHFEHVN KEVNSINKPLATLEENGETDKNQGVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEBKQQGDVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRRSASMFAVGCSMGPFTHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGVWYPLGLGGLEGGTVGESCQELREKFW EFYKADWCVWPAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCONALSASGPAAAAA MWRKLKFHEQKLLKQVDFLNWE ERDQFRVRASAALDKLVALGLVPTRGSLELCDFVTASSFCRR LPTVLLKLRNAQHLQAAVAFVEQGHVRVGPDVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEEDDFDLEA FAGAHLSSGSSEPLVFPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTINEGVKGKKITFFYRVSEAIEKLVALLINTLDRWID ETPPVDQPSRFSNKANAYRWYAKLDEERENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMSPAGSGGWGLDDFGFFFI WGSSQLUIDHPYLEPRHFVDDEKAVNENHKDYMFLECILFITEMKT GGFFAEHSNQLWNISAVPSWSKVNQGLIRNYKAECLEKFPVLQHF				YANPAFETTMGYQSGELIGKELGBVPINEKKADLLDTINSCIRI
NGNNKAEKISECVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT BVSSQRRHSSMARIHSMIT LAPITIVUTINIAAQESSPMPVTEA LDRVLETLRTTELYSPQFGAKDDPHANDLVGGLMSDGLRRISG NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDPDI FEILBAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL IAATIHDVDHGGRTNSFLCNAGSELAILVNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN KEVNSINKPLATLEENGETDKNOEVINTMLRTJENRTLIKRMLII KCADVSMPCRPLQYQTUSMAARISEYFSOTDEKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KVWKGLDEMKLRNLRPPBG 5508 1151 691 LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGVWYFLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCQNALSASGPAAAAAIWVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRIRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYMEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATONFIIPKKSHTVPDMGKWKRSQAY ADYIGFILTLNEGVVGKKLTFEYRVSEAIEKLVALLNTLDRWID ETTPPVDQPSRRGNKAYRTWYAKLDEEABNLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVWRKLQKTYRWPAGSQGWGLDDFQFLPFI WGSSQLIDHPYLLEPHVDEKAVNENHKDYMFLECLLFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	1			
EVSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA LDRVLEILRTTELYSPOPGAKDDDPHANDLVGGIMSDGLRRISG NEYVLSTKNTQMYSSNIITPISLDDVPPRIARAMENEEYWDPDI FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCRAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLRGGIIDMVLATEMTKHFEHVN KFVNSINKPLATLEENGETDKNQEVINTMLRTEENRTLIKRMLI KCADVSMPCRPLQYCLEWAARISEEYFSQTDEBKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGVWYPLGIGCLEEGTVGESCQELREKFW EPYKADWCVWPAAQFVNPLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCONALSASGPAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQREDYTRYNQLSRAVRELARRLRDLP ERDGFRVRASAALLDKLYALGLVPTTRGSLELCDFVTASSFCRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVQPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA ABGERQPPDSSEBAPPATQNFIIPKKSHTVPDMKKWKRSQAV ADYIGFILTLNEGVKGKKLTFEYRYSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLGKTYRMEPAGSQGWGLDDFQFLFFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	•	,	:	,
LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRLSG NEYVLSTKNTQMYSSNIITPISLDDVPPRIARAMENEEYWDPDI FELBAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIE ANYHSSMPYHNSTHSADVLHATAYPISKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLAITMYKHFBHVN KFWNSINKPLATTLBENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRRSASMPAVGGCSMGPFLHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGVWYFLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVMFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD KYRSPVPLTPPGCVALDTRAD RESEGCONALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMCKKKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLINTLDRWID ETTPVDQPSRFGNKAYRTWYAKLDEREARLAATVVTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMSPAGSQGVWGDDDFQFLPFI WGSSQLIDHPYLEPRHPVDEKKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	1 . 1		- •	
NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDFDI FELEAATHNRPLIVICLKWFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYPLSKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN KFYNSINKPLATLEENGETDKNQEVINTMLRTPERRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEBKQQGLPVVMPV FORNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRRSASMFAVGCSMGPFLHWYLSLDRLPPASGLRGFPN VLKKVLVDQLVASPLLGVWYPLGLGCLEGGTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCQNALSASGPAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRR LPTVLLKLRMAQHLQAAVAFVEQCHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSFPLVEFGRGRVGARVKGERGLQASGSAPGRSKM ABYGFILTILNEGVKGKKLTFEYRVSEAIEKLVALINTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDVGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	1			_ '
FELEAATHNRPLTYLGLKMFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYYLSKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKMMERNDYRTLRQGIIDMVLATEMTKHFEHVN KFVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEBKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSREASMFAVGCSMGPFLHYWYLSLDRLPPASGLRGFPN VLKKVLVDQLVASPLLGVWYPLGLGCLEGQTVGESCQELREKFW EPYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCQNALSASGPAAAAAIMVRKLKFHEQKLLKQVDFLNWE ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFYTWVDSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVURVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFIPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	1	·		l ·
ANYHSSNPYHNSTHSADVLHATAYPLSKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILVNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN KFVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCTEWAARISEEYFSQTDEBKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB S508 1151 691 LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLPPASGLRGFPN VLKKVLVDQLVASPLLGVWYPLGLGCLEGQTVGESCQELREKFW EPYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCQNALSASGPAAAAAIMVRKLKFHEQKLLKQVDFLNWE ERDQFRVRASAALLDKLYALGLVPTRCSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGRQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDFQFLPFI WGSSQLIDHPYLEVRRKLQKTYRMEPAGSQGVWGLDFQFLPFI WGSSQLIDHPYLEVRRKVDRNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	e 0 = 0	a i inga at the annual construction	garaga a lagra a lagra a series	
IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMERRDYRTLRQGIIDMVLATEMTKHFEHVN KFYNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEBKQQGLPVVMPV FDRNTCSIPKSQISFIDVFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGWWYFLGLGCLEGQTYGESCQELREKFW EPYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEBEARNLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IANVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVMENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF				
QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN KFVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEBKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLPPASGLRGFPN VLKKVLVDQLVASPLLGWWYPLGLGCLEGQTVGESCQELREKFW EPYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCQNALSASGPAAAAAAIWVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	1 1			1
KFVNSINKPLATLEENGETDKNOEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEBKQQGLPVVMPV FORNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGVWYPLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDGFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEERENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECTLFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	j .			
KCADVSNPCRPLQYCIEWAARISEEYFSQTDEBKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRRSASMFAVGSMGPFLHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGVWYFLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RESRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRRLARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFI 1PKKEIHTVPDMCKWKRSQAY ADYIGFILTLNEGVKKKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF			1	
FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGVMYFLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCQNALSASGPAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	} I			
KYWKGLDEMKLRNLRPPPB 5508 1151 691 LSSVFSRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGVWYFLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCQNALSASGPAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETTPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	1			
S508 1151 G91 LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN]			
VLKKVLVDQLVASPLLGVWYPLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNPLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCQNALSASGPAAAAA IMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF) EEOO			
EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCQNALSASGPAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	2208	1151	691	
KYRSPVPLTPPGCVALDTRAD 5509 1238 619 RKSRGCQNALSASGPAAAAA IMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	1 1		i	· ·
5509 1238 619 RKSRGCQNALSASGPAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF				
VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	L			
ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	5509	1238	619	RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE
LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF				
LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	1			ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR
EDFVTWVDSSKIKRHVLEYNEERDDFDLEA 5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF				
5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	1 1			f
AEGERQPPPDSSEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	5510	96	1195	
ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF]			1
ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	1			
EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	1	1		•
IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	1 . 1	ĺ		·-
WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF] [-
GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	[
	1 1	j	ł	•
	1 [The state of the s
				IN GOLDI THE VIOL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
			L=Leucine, M=Methionine, N=Asparagine,
}	corresponding	to first	
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
j	sequence	_	\=possible nucleotide insertion)
5511	276	1980	KLSRVLNLPPENLITSISAVPISOKEEVADFOLSVDSLLEKDND
) 3322	1	1	HSRPDIQVQAKRLAEKLRCDTVVSEISTGQRTVNFKINRELLTK
	l	{	TVLOOVIEDGSKYGLKSELFSGLPQKKIVVEFSSPNVAKKFHVG
}	1	ļ	HLRSTIIGNFIANLKEALGHQVIRINYLGDWGMQFGLLGTGFQL
	i		
}	1	ł	FGYEEKLQSNPLQHLFEVYVQVNKEAADDKSVAKAAQEFFQRLE
ļ			LGDVQALSLWQKFRDLSIEEYIRVYKRLGVYFDEYSGESFYREK
}	}		SQEVLKLLESKGLLLKTIKGTAVVDLSGNGDPSSICTVMRSDGT
1			SLYATRDLAAAIDRMDKYNFDTMIYVTDKGQKKHFQQVFQMLKI
}	}	ł	MGYDWAERCQHVPFGVVQGMKTRRGDVTFLEDVLNEIQLRMLQN
ļ	l .		MASIKTTKELKNPQETAERVGLAALIIQDFKGLLLSDYKFSWDR
1		1	VFQSRGDTGVFLQYTHARLHSLEETFGCGYLNDFNTACLQEPQS
ļ		1.	VSILOHLLRFDEVLYKSSQDFQPRHIVSYLLTLSHLAAVAHKTL
ł	Į.	1 .	OIKDSPPEVAGARLHLFKAVRSVLANGMKLLGITPVCRM
	 	1035	DPSLLLTITVTGVTVLVLVLKSMNSRRREPITLQDPEAKYPLPL
5512	120	1015	
			IEKEKISHNTRRFRFGLPSPDHVLGLPVGNYVQLLAKIDNELVV
1			RAYTPVSSDDDRGFVDLIIKIYFKNVHPQYPEGGKMTQYLENMK
1			IGETIFFRGPRGRLFYHGPGNLGIRPDQTSEPKKTLADHLGMIA
1	[GGTGITPMLQLIRHITKDPSDRTRMSLIFANQTEEDILVRKELE
1 '	i .	,	BIARTHPDQFDLWYTLDRPPIGWKYSSGFVTADMIKEHLPPPAK
Ì	ĺ		STLILVCGPPPLIQTAAHPNLEKLGYTQDMIFTY
5513	2	837	ARWRLPSDSPRIPPAGAETPGRGSCRNYLPSSSPPPPEPSSFPS
1 3323	["	1	PPTSRGGPGSRDTMSDSEEESQDRQLKIVVLGDGASGKTSLTTC
	J		FAOETFGKOYKOTIGLDFFLRRITLPGNLNVTLQIWDIGGQTIG
1	ţ		
			GKMLDKYIYGAQGVLLVYDITNYQSFENLEDWYTVVKKVSEESE
1		ļ	TQPLVALVGNKIDLEHMRTIKPEKHLRFCQENGFSSHFVSAKTG
ì	1	}	DSVFLCFQKVAAEILGIKLNKABIEQSQRVVKADIVNYNQEPMS
	İ	Į.	RTVNPPRSSMCAVQ
5514	1295	449	VNRPSWIMGNFRGHALPGTFFFIIGLWWCTKSILKYICKKQKRT
	1		CYLGSKTLFYRLEILEGITIVGMALTGMAGEQFIPGGPHLMLYD
l .	l	1	YKQGHWNQLLGWHHFTMYFFFGLLGVADILCFTISSLPVSLTKL
	\		MLSNALFVEAFIFYNHTHGREMLDIFVHQLLVLVVFLTGLVAFL
1	i		EFLVRNNVLLELLRSSLILLQGSWFFQIGFVLYPPSGGPAWDLM
	1 -	,	DHENILFLTICFCWHYAVTIVIVGMNYAFITWLVKSRLKRLCSS
1	,		EVGLLKNAEREOESEEEM
		0.00	
5515	1572	260	FVRLVGRGDCDPLLSVCLTTMPLYEGLGSGGEKTAVVIDLGEAF
1	Programme and the	A	TKCGFAGETGPRCITPSVIKRAGMPKPVRVVQYNINTEELYSYL
[KEFIHILYFRHLLVNPRDRRVVIIBSVLCPSHFRETLTRVLFKY
j			FEVPSVLLAPSHLMALLTLGINSAMVLDCGYRESLVLPIYEGIP
	1	1	VLNCWGALPLGGKALHKELETQLLEQCTVDTSVAKEQSLPSVMG
1	1	1	SVPEGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGNNERPSPPP
1		1	NVDYPLDGEKILHILGSIRDSVVEILFEQDNEEQSVATLILDSL
	}	1	IQCPIDTRKQLAENLVVIGGTSMLPGFLHRLLAEIRYLVEKPKY
1		!	KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE
1		1	YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK
		 	
5516	3	735	NSREPPQAGPGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES
1			IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGPTWAG
1		1	KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW
		1	DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR
1	1	1	YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY
1	1	1	PLEEPTTEPPVNLTYSANSPVGR
5517	246	499	SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA
1		1	TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK
F63.6	 	1275	DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA
5518	3	1375	
1			FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP
j	1	1	EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR
1			IHIMPSMNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY
1	J	1	NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA
1			TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN
1	,		GVTNGYSWYPLQGGMQDYNYIWAQCFEITLELSCCKYPREEKLP
	i .	1	A THE STATE OF THE
			SFWNNNKASLIEYIKQVHLGVKGQVFDQNGNPLPNVIVEVQDRK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ľ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1 1	sequence	sequence	\=possible nucleotide insertion)
 	sequence		HICPYRTNKYGEYYLLLLPGSYIINVTVPGHDPHITKVIIPEKS
1		1	QNFSALKKDILLPFQGQLDSIPVSNPSCPMIPLYRNLPDHSAAT
5519	87		KPSLFLFLVSLLHIFFK
2213	0/	477	IKSKLNQQVEVQESEWRLTEAKGPTMGKESGWDSGRAAVAAVVG
	<u> </u>		GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIANGGGVA
	 	<u> </u>	AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLGSPPSS
5520	117	943	PTEGRQKVLKTFTVPRSALAMTKTSTCIYHFLVLSWYTFLNYYI
		Ì	SQEGKDEVKPKILANGARWKYMTLLNLLLQTIFYGVTCLDDVLK
			RTKGGKDIKFLTAFRDLLFTTLAFPVSTFVFLAFWILFLYNRDL
1 1		f	IYPKVLDTVIPVWLNHAMHTFIFPITLAEVVLRPHSYPSKKTGL
j !]	TLLAAASIAYISRILWLYFETGTWVYPVFAKLSLLGLAAFFSLS
ļ 1	,	Į.	YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFQWPDWKS
<u> </u>		L	PAKHQLVKNIR
5521	546	911	KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGNPQPSEE
1 1		1	GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRGVDELER
	:		LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP
5522	1224	637	GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYITNYSRRF
1		,	WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVGKEEEVK
1 1		ł	AYLDFREKGGYRTTTVIFYPKDPTTKPFSVLLYIGTCDNPDYLG
1			PAPLEDIAEQIFNAAGPSGRNTEYLFELANSIRNLVPEEADEHL
			FALEKLVKERLEGKQNLNCI
5523	3	1280	SKGKKRMGSSMSAATARRPVFDDKEDVNFDHFQILRAIGKGSFG
	,	,	KVCIVQKRDTEKMYAMKYMNKQQCIERDEVRNVFRELEILQEIE
1 1			HVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQFSEDTV
1 1			RLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI
1 1			ATIIKDGERATALSGTKPYMAPEIFHSFVNGGTGYSFEVDWWSV
			GVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEM
1 1			VALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPG
1			FVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRD
1 (SSQSENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPES
1 1			RDAAEPVEDEAERSALPMCGPICPSAGSG
5524	85	2318	RERERDHRPGESSQGQSGAGGCFPSPTMELRCGGLLFSSRFDSG
1			NLAHVEKVESLSSDGEGVGGGASALTSGIASSPDYEFNVWTRPD
1 (٠.	CAETEFENGNRSWFYFSVRGGMPGKLIKINIMNMNKQSKLYSQG
.]]			MAPFVRTLPTRPRWERIRDRPTFEMTETQFVLSFVHRFVEGRGA
	en de annie, de la decembra de		TTFFAFCYPFSYSDCOELLNOLDORFPENHPTHSSPLDTIYYHR
1			ELLCYSLDGLRVDLLTITSCHGLREDREPRLEQLFPDTSTPRPF
			RFAGKRIFFLSSRVHPGETPSSFVFNGFLDFILRPDDPRAQTLR
1 1			RLFVFKLIPMLNPDGVVRGHYRTDSRGVNLNRQYLKPDAVLHPA
	· ·		IYGAKAVLLYHHVHSRLNSQSSSEHQPSSCLPPDAPVSDLEKAN
1 1			NLQNEAQCGHSADRHNABAWKQTEPAEQKLNSVWIMPQQSAGLE
1 }			ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE
1			NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV
] }			AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA
] [FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL
, ,			RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE
1			NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFPFHGSRPAGL
j j	ļ		PGLGSSTQKVTHRVLGPVRGKPVWEPLOHVFGCLGHCWGK
5525	105	834	SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS
			LTYEEFLGRVAELNDVTAKVASGOEKHLLFEVOPGSDSSAFWKV
1			" -
}		•	VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ
i .			SSTSEEPDENSSSVTSCQASLWMGRVKQLTDEEBCCICMDGRAD
1 1			LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP
1 1	ļ		· · · · · · · · · · · · · · · · · · ·
			TEDDMANYILNMADEAGQPHRP
5526	3	853	TEDDMANYILMMADEAGQPHRP RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT
5526	3	853	TEDDMANYILMADEAGQPHRP RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR
5526	3	853	TEDDMANYILMADEAGQPHRP RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR LDDDPPPSTLLKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI
5526	3	853	TEDDMANYILMADEAGQPHRP RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR LDDDPPPSTLLKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYEBHLEKHRKDK
5526	3	853	TEDDMANYILMADEAGQPHRP RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR LDDDPPPSTLLKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI

SEQ Predicted predicted end nucleotide location nucleotide location corresponding to first amino acid residue of amino acid segment containing signal properties amino acid residue of amino acid sequence sequenc	d, E= cine, =Stop PKQSSCG PYQLVS KIKLKKS TTSENLV PQKADVS KLDILGA PGETTTE PRAKTGGT PKEQTEN HIDAVAR ELIKEKH
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence sequ	EStop PKQSSCG PYQLVS KIKLKKS MTSENLV QKADVS KLDILGA PGETTTE RAKTGGT DKEQTCN HIDAVAR ELIKEKH
location corresponding to first amino acid residue of amino acid sequence 5527 3225 565 Larry Larr	EStop PKQSSCG PDYQLVS KIKKS MTSENLV DQKADVS KLDILGA PGETRTE RAKTGGT DKEQTGN HIDAVAR ELIKEKH
Corresponding to first amino acid residue of residue of amino acid sequence P=Proline, Q=Glutamine, R=Arginine,	ESTOP PKOSSCG PDYOLVS KIKLKKS KIKLKKS KIKLKKS KIKLKS KIKLGA PGETRTE RAKTGGT DKEOTGN HIDAVAR ELIKEKH
to first amino acid residue of amino acid residue of amino acid sequence 5527 3225 565 LIRKYLHONPLILERHOPNETCISFSATMKLKDTKSRE KPQTKGIKVVGKWKEVKIDPNMFADGQMDDLVCFEELT PAKNPSSLFSKEAPKRKAQAVSEEEEEEGGKSSSPKKE KNVATEGTSTQKEPEVKDPELEAQGDDMVCDDPEAGEN AWGDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDE AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPE AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEAE VSDQALLFGDDDAGEGPSSLIREKPVPRQNENEEENLI LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQE FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWI YHLRNLRQLRCLVVDEADRNVEKGHFAELSQLLEMLNI RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLI RGKPKVIDLTRMEATVETLTETKIHCETDEKDFYLYY RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIP	ESTOP PKOSSCG PDYOLVS KIKLKKS KIKLKKS KIKLKKS KIKLKS KIKLGA PGETRTE RAKTGGT DKEOTGN HIDAVAR ELIKEKH
amino acid residue of amino acid sequence RRNPDSPAKAIPKTLKDSQ LLRKYLLHQNPLLLRHQPNRTCISFSATMKLKDTKSRE KFQTKGIKVVGKWKEVKIDPNNFADGQMDDLVCFEELT PAKNPSSLFSKEAPKRKAQAVSEEEEEEEGKSSSPKKE KNVATEGTSTQKEFEVKDPELEAQGDDMVCDDPEAGEN QTAPKKKKNKGKKGLEPSQSTAAXVPKKAKTWIPEVHI AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDE AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEAE VSDQALLFGDDDAGEGPSSLIREREVPKQNENEEEENLI LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQE PTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWI YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNI RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLI RGKPKVIDLTRNEATVETLTETKIHCETDBKDFYLYY RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIP	PKQSSCG PTYQLVS KIKLKKS ATSENLV DQKADVS KLDILGA PGETRTE RAKTGGT DKEQTGN HIDAVAR ELIKEKH
residue of amino acid sequence	PKQSSCG PTYQLVS KIKLKKS ATSENLV DQKADVS KLDILGA PGETRTE RAKTGGT DKEQTGN HIDAVAR ELIKEKH
amino acid sequence Codon, /=possible nucleotide deletion, -possible nucleotide insertion)	PKQSSCG PTYQLVS KIKLKKS ATSENLV DQKADVS KLDILGA PGETRTE RAKTGGT DKEQTGN HIDAVAR ELIKEKH
=possible nucleotide insertion	PKQSSCG PKQSSCG PKQSSCG REVQLVS KIKLKKS ATSENLV PQKADVS KLDILGA PGETRTE RAKTGGT DKEQTGN HIDAVAR ELIKEKH
RRNPDSPAKAIPKTLKDSQ 5527 3225 565 LLRKYLLHQNPLLLRHQPNRTCISFSATMKLKDTKSRE KPQTKGIKVVGKWKEVKIDPNMFADGQMDDLVCFEELT PAKNPSSLFSKEAPKRKAQAVSEEEEEEEGKSSSPKKE KNVATEGTSTQKEPEVKDPELEAQGDDMVCDDPEAGEM QTAPKKKKNKGKKGLEPSQSTAAKVPKKAKTWIPEVHI AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDE AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPE AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEAE VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLI LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQE FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWI YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNI RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLI RGKPKVIDLTRNEATVETLTETKIHCETDBKDFYLYY RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE	TDYQLVS KIKLKKS MTSENLV DQKADVS KLDILGA PGETRTE RAKTGGT DKEQTGN HIDAVAR ELIKEKH
5527 3225 565 LLRKYLLHQNPLLLRHQPNRTCISFSATMKLKDTKSRE KFQTKGIKVVGKWKEVKIDPNMFADGQMDDLVCFEELT PAKNPSSLFSKEAPKRKAQAVSEEEEEEEGKSSSPKKE KNVATEGTSTQKEFEVKDPELEAQGDDMVCDDPEAGEM QTAPKKKKNKGKKGLEPSQSTAAKVPKKAKTWIPEVHI AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDE AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPE AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEAE VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLI LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQE FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWI YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNI RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLI RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYY RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE RTARATNEGLSLMLLIGPEDVINFKKIYKTLKKDEDIP	TDYQLVS KIKLKKS MTSENLV DQKADVS KLDILGA PGETRTE RAKTGGT DKEQTGN HIDAVAR ELIKEKH
KFQTKGIKVVGKWKEVKIDPNMFADGQMDDLVCFEELT PAKNPSSLFSKEAPKRKAQAVSEEEEEEEGKSSSPKKE KNVATEGTSTQKEFEVKDPELEAQGDDMVCDDPEAGEN QTAPKKKKNKGKKGLEPSQSTAAKVPKKAKTWIPEVHI AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDE AETGSGKTLAPAIPMIHAVLQWQKRNAAPPPSNTEAPE AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEAE VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLI LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQE FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWI YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNI RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLI RGKPKVIDLTRNEATVETLTETKIHCETDBKDFYLYY RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE	TDYQLVS KIKLKKS MTSENLV DQKADVS KLDILGA PGETRTE RAKTGGT DKEQTGN HIDAVAR ELIKEKH
PAKNPSSLFSKEAPKRKAQAVSEEEEEEEGKSSSPKKK KNVATEGTSTQKEPEVKDPELEAQGDDMVCDDPEAGEN QTAPKKKKNKGKKGLEPSQSTAAKVPKKAKTWIPEVHI AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPATRDE AETGSGKTLAPAIPMIHAVLQWQKRNAAPPPSNTEAPE AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEAE VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLI LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQE FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWI YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNI RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLI RGKPKVIDLTRNEATVETLTETKIHCETDBKDFYLYY RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE	KIKLKKS MTSENLV DOKADVS KLDILGA PGETRTE RAKTGGT DKEQTGN HIDAVAR ELIKEKH
KNVATEGTSTQKEPEVKDPELEAQGDDMVCDDPEAGEM QTAPKKKKNKGKKGLEPSQSTAAKVPKKAKTWIPEVHI AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDE AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPE AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEAE VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLI LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQE FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWE YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNE RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLE RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYY RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQE FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE	MTSENLV DOKADVS KLDILGA PGETRTE RAKTGGT DKEQTGN HIDAVAR ELIKEKH
QTAPKKKNKGKKGLEPSQSTAAKVPKKAKTWIPEVHI AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDE AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPE AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEAE VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEEENLI LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQE FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWE YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNE RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLE RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYY RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQE FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSEE RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIP	OQKADVS KLDILGA PGETRTE RAKTGGT DKEQTGN HIDAVAR ELIKEKH
AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDE AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPE AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEAE VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLI LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQE FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWI YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNI RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLI RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYY RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE	CLDILGA PGETRTE RAKTGGT DKEQTGN HIDAVAR ELIKEKH
AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPE AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEAE VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLI LKQELDDKSATCKAYPKRPLIGLVLTPTRELAVQVKQE FTGIKTAILVGGMSTQKQQRMLNRRPEIVATPGRLWI YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNI RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLI RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYY RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE	PGETRTE RAKTGGT DKEQTGN HIDAVAR ELIKEKH
AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEAE VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLI LKQELDDKSATCKAYPKRPLIGLVLTPTRELAVQVKQI FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWI YHLKNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNI RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLI RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYY RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE	RAKTGGT OKEQTGN HIDAVAR ELIKEKH
VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLI LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQI FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLMI YHLKNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNI RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLI RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYYI RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIP	OKEQTGN HIDAVAR ELIKEKH
LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQI FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWI YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNI RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLI RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYYY RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE: RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIP	HIDAVAR ELIKEKH
FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWI YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNI RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLI RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYYI RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSEI RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIP	ELIKEKH .
YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNI RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLI RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYYI RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSEI RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIP	SQYNPK STIKEKH
RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLI RGKPKVIDLTRNEATVETLTETKIHCETDBKDFYLYY) RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE: RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIP	JSQYNPK
RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYY) RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE: RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIP	
RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQI FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIP	JMQKIGM
FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSE RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIP	FLMQYPG
RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIP:	RLRNLEQ
RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIP	IYVHRSG
	LFPVQTK
YMDVVKERIRLARQIEKSEYRNFQACLHNSWIEQAAA.	ALEIELE
EDMYKGGKADQQEERRRQKQMKVLKKELRHLLSQPLF	resoktk
YPTQSGKPPLLVSAPSKSESALSCLSKQKKKTKKPK	SPQPEQP
QPSTSAN	
5528 3 895 GPFLSACRMWGACKVKVHDSLATISITLRRYLRLGAT	MAKSKFE
YVRDFEADDTCLAHCWVVVRLDGRNFHRFAEKHNFAK	PNDSRAL
QLMTKCAQTVMEELEDIVIAYGQSDEYSFVFKRKTNW	FKRRASK
FMTHVASQFASSYVFYWRDYFEDQPLLYPPGFDGRVV	VYPSNQT
LKDYLSWRQADCHINNLYNTVFWALIQQSGLTPVQAQ	GRLQGTL
AADKNEILFSEFNINYNNEPPMYRKGTVLIWQKVDEV	MTKEIKL
PTEMEGKKMAVTRTRTKPCKPSHLPRAPCLRWL	
5529 48 640 TFRLVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVK	MQRVSGL
LSWTLSRVLWLSGLSEPGAARQPRIMEEKALEVYDLI	RTIRDPE
KPNTLEELEVVSESCVEVQEINEBEYLVIIRFTPTVP	HCSLATL
IGLCLRVKLQRCLPFKHKLEIYISEGTHSTEEDINKQ	INDKERV
AAAMENPNLREIVEQCVLEPD	
FE20 4541 2606 AOTVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLT	DFGFSNK
FOPGKKITTSCGSLAYSAPEILLGDEYDAPAVDIWSL	GVILFML
VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDL	ITRMLQR
DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKN	LSEEEHN
SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLA	ERILREK
QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDL	TATPLSH
ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAG	PALSTVP
PASLKPTASGRKCLFRVEEDEEDBEDKKPMSLSTQV	VLRRKPS
VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKL	SRLKMNI
ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRR	LDKDSGF
TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKAS	PSENNAG
GGSPSSGSGNPTNTSGTTRRCAGPSNSMQLASRSAG	ELVESLK
LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTW	KMCISST
GNAGQVPAVGGIKFFSDHMADTTTBLERIKSKNLKNN	WLOLPLC
EKTISVNIQRNPKEGLLCASSPASCCHVI	~ ~ ~ ~ ~
THE PROPERTY OF THE PROPERTY O	TITATITY
5531 24 515 GSQPRAPRPRDSMERPEPELIRQSWRAVSRSPLEHGT ALEPDLLPLFQYNCRQFSSPEDCLSSPEFLDHIRKVM	MACULATI
ALEYDILIPLEQINCKQFSFELLISSFELLILIARVE	TAMTERU.
TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESI	THERE
LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE	T DODDAD
5532 3395 1402 SDWMVVGKRKMIIEDETEFCGEELLHSVLQCKSVFDV	MIDDED CAG
RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFT	NEKUSYG
KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAI	GEGMILK
GPNDFKLEDFYSASSELFRPYYGEGGIDGDGDITRP	INISAFRN
FVLDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLI	THE THE
LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFERVC RPANSERYVVCKGLKVGIDDVRDYLFAVNIKLNQLRI	TEKETIS
	THID COLUMN

<u> </u>	15		
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
I NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of		S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence	 	\=possible nucleotide insertion)
i			VVPLEVIKGDHEFTDYMIRSNESHCSLQIKALAKIHAFVQDTTL
1	1	ļ	SEPRQAEIRKECLRLWGIPDQARVAPSSSDPKSKFFELIQGTEI
			DIFSYKPTLLTSKTLEKIRPVFDYRCMVSGSEQKFLIGLGKSQI
1	1		YTWDGRQSDRWIKLDLKTELPRDTLLSVEIVHELKGEGKAQRKI
			SAIHILDVLVLNGTDVREQHFNQRIQLAEKFVKAVSKPSRPDMN
1			PIRVKEVYRLEEMEKIFVRLEMKIIKGSSGTPKLSYTGRDDRHF
1			VPMGLYIVRTVNEPWTMGFSKSFKKKFFYNKKTKDSTFDLPADS
Ì			IAPFHICYYGRLFWEWGDGIRVHDSQKPQDQDKLSKEDVLSFIQ
5535	<u> </u>		MHRA
5533	94	789	MKERRAPQPVVARCKLVLVGDVQCGKTAMLQVLAKDCYPETYVP
			TVFENYTACLETEEQRVELSLWDTSGSPYYDNVRPLCYSDSDAV
1	Į.		LLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTD
1			LSTLMELSHQKQAPISYEQGCAIAKQLGPEIYLEGSAFTSEKSI
1	1		HSIFRTASMLCLNKPSPLPQKSPVRSLSKRLLHLPSRSELISPT
F-53-	ļ <u></u>		FKKEKAKXCSIM
5534	3	605	LVRGRARAANPGRVGAMDGLRQRVEHFLEQRNLVTEVLGALEAK
]		TGVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIK
1			AIESPSKDDDTVWLTYWVVYALFGLAEFFSDLLLSWFPFYYVGK
1			CAFLLFCMAPRPWNGALMLYQRVVRPLFLRHHGAVDRIMNDLSG
			RALDAAAGITRNVKPSQTPQPKDK
5535	1029	332	KSFMDSEARLCSLVELSDTQDETQKSDSENEDLKIDCLQESQEL
))		NLQKLKNSERILTEAKQKMRELTVNIKMKEDLIKELIKTGNDAK
			SVSKQYTLKVTKLEHDAEQAKVELTETQKQLQELENKDLSDVAM
		li .	KVKLQKEFRKKVDAAKLRVQVLQKKQQDSKKLASLSIQNEKRAN
			ELEQSVDHMKYQKIQLQRKLQEENEKRKQLDAVIKRDQQKIKVI
			LSYIPAKYNMKC
5536	942	282	AAATAASLSPRGCRLRTPSSDVSPSRAPPPSAAPLPTGRAQMSP
			SGRLCLLTIVGLILPTRGQTLKDTTSSSSADATIMDIQVPTRAP
1	}	*	DAVYTELQPTSPTPTWPADETPQPQTQTQQLEGTDGPLVTDPET
1			HKSTKAAHPTDDTTTLSERPSPSTDVQTDPQTLKPSGFHEDDPF
			FYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNHCR
5537	3	2391	RARVSSPOLRVFRSGRPRRLRVLRINRTSVALRLAGTGRFVAKT
			PGHPGSWEMGLLTFRDVAVEFSLEEWEHLEPAQKNLYQDVMLEN
1			YRNLVSLGLVVSKPDLITFLEQRKEPWNVKSEETVAIQPDVFSH
1	· l		YNKDLLTEHCTEASFQKVISRRHGSCDLENLHLRKRWKREECEG
			HNGCYDEKTFKYDOFDESSVESLFHQQILSSCAKSYNFDQYRKV
1)		FTHSSLLNQQEEIDIWGKHHIYDKTSVLFRQVSTLNSYRNVFIG
l .	[EKNYHCNNSEKTLNQSSSPKNHQENYFLEKQYKCKEFEEVFLQS
	1		MHGQEKQEQSYKCNKCVEVCTQSLKHIQHQTIHIRENSYSYNKY
			DKDLSQSSNLRKQIIHNEEKPYKCEKCGDSLNHSLHLTQHQIIP
			TEEKPYKWKECGKVFNLNCSLYLTKQQQIDTGENLYKCKACSKS
			FTRSSNLIVHQRIHTGEKPYKCKECGKAFRCSSYLTKHKRIHTG
	,		EKPYKCKECGKAFNRSSCLTQHQTTHTGEKLYKCKVCSKSYARS
	·		SNLIMHQRVHTGEKPYKCKECGKVFSRSSCLTQHRKIHTGENLY
]		KCKVCAKPFTCFSNLIVHERIHTGEKPYKCKECGKAFPYSSHLI
	[RHHRIHTGEKPYKCKACSKSFSDSSGLTVHRRTHTGEKPYTCKE
		•	CGKAFSYSSDVIQHRRIHTGQRPYKCEECGKAFNYRSYLTTHQR
			SHTGERPYKCEECGKAFNSRSYLTTHRRRHTGERPYKCDECGKA
		!	FSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHQRSHTR
		· · · · · · · · · · · · · · · · · · ·	EKL
5538	926	161	HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG
]		,	IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP
[GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI
1			NVPLRRDQTIRFDHVITNMNNNYEPRSGKFTCKVPGLYYFTYHA
i	,		SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ
L			GENVFLQATDKNSLLGMEGANS I FSGFLLFPDMEA
5539	38	1258	HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG
			IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK
			DEIYGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCS
L			SDSFNEDIAAFAKQVRSERPLFSSNPELDNLVIQAIQVLRFHLL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
(location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
{	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
]	- Sequence		ELEKVHDLCDNFCHRYITCLKGKMPIDLVIEDRDGGCREDFEDY
ł			PASCPSLPDONNMWIRDHEDSGSVHLGTPGPSSGGLASOSGDNS
1			
1	[SDQGDGLDTSVASPSSGGEDEDLDQERRRNKKRGIFPKVATNIM
1			RAWLFQHLSHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIV
1			QPMIDQSNRTGQGAAFSPEGQPIGGYTETQPHVAVRPPGSVGMS
			LNLEGEWHYL
5540	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
1	l		PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
1			GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI
			YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
1	[1	FNEDNTAFAKOVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDONNIWIRDHED
1	(SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
1			EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
1			
I			LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
		<u> </u>	QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5541	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
			PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
		}	GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI
1	1		YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
	,		FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
	j	ļ	SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
1		•	EDLDOEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
ļ			LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
1	f	ļ ·	OPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
F-10-			PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWROHRG
5542	148	1440	1
}]	,	PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDBLPHYPGIVD
ł .	İ	1	GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI
1			YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
1	1	1	FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
1	,	1	KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
1 .	i	l ·	SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
ļ		}	EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
1		1 .	LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
1.27 2.2	la grammada sa	La La Caracteria de la composición della composición della composición della composición della composición della composición della composición della composición della composición della composición della composición della composición della composi	QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5543	2405	665	RWVREOPWPLRTSEAVKTPALRPFPGPRGVSPFPKPDWGKSPAP
1		1	KRPFSDSGAFWSPERRPGVLEAPRRRPVPASFRAVPPKPTRVHG
1	1	1	SSASRDRVIARTMIVADSECRAELKDYLRFAPGGVGDSGPGEEO
	1	}	RESRARRGPRGPSAFIPVEEVLREGAESLEQHLGLEALMSSGRV
1	1	1 .	DNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLASSWRHYIAIMAA
j.		1	ARHOCSYLVGSHMAEFLOTGGDPEWLLGLHRAPEKLRKLSEINK
1		1	
1	1]	LLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSLS
{	ſ	1	SFVFGCGILPEGDADGSPAPQAPTPPSEQSSPPSRDPLNNSGGF
j.	1		ESARDVEALMERMQQLQESLLRDEGTSQEEMESRFELEKSESLL
1	1		VTPSADILEPSPHPDMLCFVEDPTFGYEDFTRRGAQAPPTFRAQ
1]	1	DYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYSLTYNTIAMHSGV
ĺ	[DTSVLRRAIWNYIHCVFGIRYDDYDYGEVNQLLERNLKVYIKTV
	1	1	ACYPEKTTRRMYNLFWRHFRHSEKVHVNLLLLEARMQAALLYAL
1	1	1	RAITRYMT
5544	1895	514	LGGLLGRORLLLRMGAGRLGAPMERHGRASATSVSSAGEQAAGD
5544	-3,5		PEGROEPLRRRASSASVPAVGASAEGTRRDRLGSYSGPTSVSR
l l	1	1	ORVESLRKKRPLFPWFGLDIGGTLVKLVYFEPKDITAEEEEEEV
1	İ	1	1 7:
1	1	1	ESLKSIRKYLTSNVAYGSTGIRDVHLELKDLTLCGRKGNLHFIR
			FPTHDMPAFIQMGRDKNFSSLHTVFCATGGGAYKFEQDFLTIGD
	}	1	LQLCKLDELDCLIKGILYIDSVGFNGRSQCYYFENPADSEKCQK
		1	LPFDLKNPYPLLLVNIGSGVSILAVYSKDNYKRVTGTSLGGGTF
			FGLCCLLTGCTTFEEALEMASRGDSTKVDKLVRDIYGGDYERFG
1		Į.	LPGWAVASSFGNMMSKEKREAVSKEDLARATLITITNNIGSIAR
			1
		1	MCALNENINQVVFVGNFLRINTIAMRLLAYALDYWSKGQLKALF

SEQ	Drodietod	Drediated and	Amino acid segment containing signal peptide
ID	Predicted beginning	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
]	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
Į.	sequence		\=possible nucleotide insertion)
5545	802	131	GAMWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVL
			KLLNTHHRVRLHSHDIKYGSGSGQQSVTGVEASDDANSYWRIRG
1			GSEGGCPRGSPVRCGOAVRLTHVLTGKNLHTHHFPSPLSNNOEV
Į.			SAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVT
1			GEOYGSPIRGOHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAGH
)			DEL
5546	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
ł	i		RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
			LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
1			SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
			NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
			KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
1			AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
1			FVSKTEEELQAILEAKBKKLRLKAQRQAQQAQNVQRKQEQREAH
	}		RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDBQEDDDI
	,	:	EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
L			CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRFGKRVA
5547	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
(!		RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
		,	LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
1			SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
}			NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
			KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
1			AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
ì			FVSKTEEBLQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH
[RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
ļ			EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRPGKRVA
5548	1	2153	DOTGPPETIAFTFPRSTMEPLCPLLLVGFSLPLARALRGNETTA
2240		21,33	DOIGE BITTE IT ENDING FOR DOLONG THE CAME IN
1 1	_	ı	DONFORT TO COUNTRY CONTRACTOR AND A CONT
			DSNETTTTSGPPDPGASQPLLAWLLPLLLLLLLVLLLAAYFFRF BKOBKAWAGTSDKKMBNGILEEOFOORWALLSBSDSGDKKYPPDT
<u> </u>	. ·		RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI
			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN
			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK
			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN
is days - Was in	الله والمواد الإساسة المارة المارة	Constitute stars o approximate	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY
	ه بعد و در داد در رسی در باد در داد. ه بعد و در داد در در رسی در باد در در در در در داد در در در در در در در در در در در در در	The other store or segment of the	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR
	ه بعد و در داد در رسال در باد در	The state of the company of the	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC
	n in British was a straight and was as	The state of the community of	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKPLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ
	n in Berne was per the level as an	The state of the community of	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW
		Tanada sance agences	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI
		The state of the company of the state of the	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKPLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG
		The state of the commence of the	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLEDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL
		The state of the community of the	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ
		Tax other times our engineers	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITTEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK
5549	915	256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ
5549		256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME
5549		256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWBWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF
5549		256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEFRKLTNVRIMKENMTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWBWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPABGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD
	915		RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPABGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL
5549		256	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEFRKLTNVRIMKENNRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPABGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV
	915		RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEEFRKLTNVRIMKENNRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI
	915		RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKPLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPABGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ
	915		RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKPLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPABGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQEEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN
	915		RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFFKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQEEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN
	915		RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMXYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN FSHRIDHLSFGELVPAIINPLDGTEKIAIDHNQMFQYFITVVPT
	915		RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWBWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVVEPTVFDLSPQQKEWQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN FSHRIDHLSFGELVPAIINPLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTHQFSVTERBRIINHAAGSHGVSGIFMKYDLSSL
	915		RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGFKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWBWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITTEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPABGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMTTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN FSHRIDHLSFGELVPAIINPLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTHQFSVTERBRIINHAAGSHGVSGIFMKYDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC
	915		RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK IGLEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWBWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ DFIDIFSDYANFK FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI TVAMKCQYVGADVLDLAETMVASADGLVVEPTVFDLSPQQKEWQ RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN FSHRIDHLSFGELVPAIINPLDGTEKIAIDHNQMFQYFITVVPT KLHTYKISADTHQFSVTERBRIINHAAGSHGVSGIFMKYDLSSL

CEO.	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location		H=Histidine, I=Isoleucine, K=Lysine,
1		corresponding to first	L=Leucine, M=Methionine, N=Asparagine,
Į	corresponding to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}]		
-	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			WFVFRRYAEFDKLYNTLKKQFPAMALKIPAKRIFGDNFDPDFIK
]		QRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSDPSEDE
1	ĺ		DERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKV
)		LLAKRKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKH
			PFLVGLHYSFQTTEKLYFVLDFVNGGELFFHLQRERSFPEHRAR
j			FYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTDFGLC
l	Ì	' I	KEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTVDWWCLGAVLY
			EMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSILEELL
1			EKDRONRLGAKEDFLEIONHPFFESLSWADLVOKKIPPPFNPNV
1			AGPDDIRNFDTAFTEETVPYSVCVSSDYSIVNASVLEADDAFVG
İ			FSYAPPSEDLFL
5552	2748	930	LGPAAGAAMGKKHKKHKAEWRSSYEDYADKPLEKPLKLVLKVGG
			SEVTELSGSGHDSSYYDDRSDHERERHKEKKKKKKKKKSEKEKHL
	1		DDEERRKRKEEKKRKREREHCDTEGEADDFDPGKKVEVEPPPDR
			PVRACRTQPAENESTPIQQLLEHFLRQLQRKDPHGFFAFPVTDA
			IAPGYSMIIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNA
			MTYNRPDTVYYKLAKKILHAGFKMMSKQAALLGNEDTAVEEPVP
1	1		EVVPVQVETAKKSKKPSREVISCMFEPEGNACSLTDSTABEHVL
1			ALVEHAADEARDRINRFLPGGKMGYLKRNGDGSLLYSVVNTAEP
ı		•	DADEEETHPVDLSSLSSKLLPGFTTLGFKDERRNKVTFLSSATT
1	ł ·		ALSMONNSVFGDLKSDEMELLYSAYGDETGVQCALSLQEFVKDA
ì			GSYSKKVVDDLLDQITGGDHSRTLFQLKQRRNVPMKPPDEAKVG
1	į į		DTLGDSSSSVLEFMSMKSYPDVSVDISMLSSLGKVKKELDPDDS
1			HLNLDETTKLLQDLHEAQAERGGSRPSSNLSSLSNASERDQHHL
1			GSPSRLSVGEQPDVTHDPYEFLQSPEPAASAKT
5553	74	1095	LGREAVYLVSRMDGPVAEHAKOEPFHVVTPLLESWALSQVAGMP
2553	/4	1032	VFLKCENVQPSGSFKIRGIGHFCQEMAKKGCRHLVCSSGGNAGI
	1		AAAYAARKLGIPATIVLPESTSLQVVQRLQGEGAEVQLTGKVWD
1			EANLRAQELAKRDGWENVPPFDHPLIWKGHASLVQELKAVLRTP
1	•	·	PGALVLAVGGGGLLAGVVAGLLEVGWQHVPIIAMETHGAHCFNA
1]		-
1	·		AITAGKLVTLPDITSVAKSLGAKTVAARALECMQVCKIHSEVVE
1			DTEAVSAVQQLLDDERMLVEPACGAALAAIYSGLLRRLQAEGCL
			PPSLTSVVVIVCGGNNINSRELQALKTHLGQV
5554	166	2318	CSGRTGGRGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL
1			GRSFFWVLPPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQ
Jan. mar.	ra managan nga ngangan namangan na ang ang ang ang ang ang ang ang	and the second section of the section of the second section of the section of the second section of the section of th	WVRDSCRKLSGLLRQKNAVDNKLKTAIGAVEKDVGLSDEEKLFQ
			VHTFEIFQKELNESENSVFQAVYGLQRALQGDYKDVVNMKESSR
			QRLEALREAAIKEETEYMELLAABKHQVEALKNMQHQNQSLSML
1	• .		DEILEDVRKAADRLEEBIEEHAFDDNKSVKGVNFEAVLRVEEEE
1			ANSKQNITKREVEDDLGLSMLIDSQNNQYILTKPRDSTIPRADH
1			HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN
}	1	1	SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC
1			YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM
1			GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS
1			ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK
1	1	}	LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL
		[VSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL
1	1	į	TVLVFLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV
[SEFSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI
]	1	ļ	TRCVPRPERRSSL
5555	212	1425	LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR
)	j	}	GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK
İ	Į.		KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY
1		j	DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR
1	1		GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE
1			MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD
1			GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV
		J	TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL
1			PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGŞVQK
		j	VYNGLQGY
5556	5835	3346	RTRGMSKNCVPMEFEEYLLRMFQGTFYLLQKITKDNNAHTVKSR
	1 3333	1 2220	WINGS THE PROPERTY OF THE PROP

SEQ	Predicted	Predicted end	Their said second containing signal world
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
I NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
Ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			LEELDESYIEKFTDFLRLFVSVHLRRIESYSQFPVVEFLTLLFK
ł			YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNRYE
ĺ			DALVLLLTEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYLR
	1		QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSGS
	j		GHRLNITAENDCRRLHCSLRDLSSLLOAVGRLAEYFIGDVFAAR
			FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHAQ
1	}		SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIST
			KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDASA
1	1		
1	J		LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVRSINHASLI
	ľ		SALSRDYRNLKPSAVAPQRKMPLDDTKLIIHQTLSVLEDIVENI
1	ł		SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFFL
1			TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGCR
ł			VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERPS
1	}		PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIABEQMENEP
	Į.		QFSAIMQAFGQSFLQPDIHLFKQNLFYLBTLNTKQKLYHKKIFR
:			TAMLFQFVNVLLQVLVHKSHDLLQEEIGIAIYNMASVDFDGFFA
1			AFLPEFLTSCDGVDANQKSVLGRNFKMDRVRRERGRAKRRAEWA
			RKPGTCAARRGHIEASGRGLCPPCSLAAAHEMPADLVL
5557	1712	491	VILGAGLRDKDMWIPVVGLPRRLRLSALAGAGRFCILGSEAATR
1			KHLPARNHCGLSDSSPQLWPBPDFRNPPRKASKASLDFKRYVTD
			RRLAETLAOIYLGKPSRPPHLLLECNPGPGILTOALLEAGAKVV
1	ľ		ALESDKTFIPHLESLGKNLDGKLRVIHCDFFKLDPRSGGVIKPP
j	j	•	AMSSRGLFKNLGIEAVPWTADIPLKVVGMFPSRGEKRALWKLAY
1			DLYSCTSIYKFGRIEVNMFIGEKEFQKLMADPGNPDLYHVLSVI
		1	WQLACEIKVLHMEPWSSFDIYTRKGPLENPKRRELLDQLQQKLY
1			LIOMIPRONLFTKNLTPMNYNIFFHLLKHCFGRRSATVIDHLRS
			LTPLDARDILMQIGKQEDEKVVNMHPQDFKTLFETIERSKDCAY
}			MIPHDARDIEMQIGRQEDERVVMMRPQDFRIEFEITERSRDCAI
5550	3500	66	
5558	1509	96	RAGCTHPQVPADLGAPAEPRRPQKTCVCLLQPQPGGQRGPTTMI
j i			TGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRS
•			LLKLKMVQVVFRHGARSPLKPLPLEEQVEWNPQLLEVPPQTQFD
1	,		YTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFA
	ĺ		LGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLA
	•	•	GLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTA
1			SLQPGISEDLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPS
a contractor contractor and a	and the market in specific leases a feet place and	instrumental existing and include the second of the second	CPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
[NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPP
]		!	FAVDLTMELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCPLDMF
4 11			LNAMSVYTLSPEKYHALCSQTQVMEVGNEE
5559	150	1983	PLAATAHFAKMSRVAKYRROVSEDPDIDSLLETLSPEEMEELEK
]	·	!	ELDVVDPDGSVPVGLRQRNQTEKQSTGVYNREAMLNFCEKETKK
			LMOREMSMDESKOVETKTDAKNGEERGRDASKKALGPRRDSDLG
[]			KEPKRGGLKKSFSRDRDEAGGKSGEKPKEEKIIRGIDKGRVRAA
			VDKKEAGKDGRGEERAVATKKEEEKKGSDRNTGLSRDKDKKREE
]			MKEVAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNTDMKKEDEK
			VKRGTGNTDTKKDDEKVKKNEPLHEKEAKDDSKTKTPEKOTPSG
]			
1	1		PTKPSEGPAKVEEEAAPSIFDEPLERVKNNDPEMTEVNVNNSDC
1 1			ITNEILVRFTEALEFNTVVKLFALANTRADDHVAFAIAIMLKAN
			KTITSLNLDSNHITGKGILAIFRALLQNNTLTELRFHNQRHICG
[·	1	ļ	GKTEMEIAKLLKENTTLLKLGYHFBLAGPRMTVTNLLSRNMDKQ
} !			RQKRLQEQRQAQEAKGEKKDLLEVPKAGAVAKGSPKPSPQPSPK
	1		PSPKNSPKKGGAPAAPPPPPPPPLAPPLIMENLKNSLSPATQRKM
			GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ
5560	9	921	SSVVEFSALSVSMACLSPSQLQKFQQDGFLVLEGFLSAEECVAM
,	1		QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDK
1 1	ŀ		IRFFFEKGVFDEKGNFLVPPEKSINKIGHALHAHDPVFKSITHS
<u> </u>			FKVQTLARSLGLQMPVVVQSMYIFKQPHFGGEVSPHQDASFLYT
1 1	ſ		EPLGRVLGVWIAVEDATLENGCLWFIPGSHTSGVSRRMVRAPVG
1 1			SAPGTSFLGSEPARDNSLFVPTPVQRGALVLIHGEVVHKSKQNL
1			SDRSRQAYTFHLMEASGTTWSPENWLQPTAELPFPQLYT
	1		K
5561	2175	1775	CYFIFQFFSSPYPGLHPHOTPAPLPNPGLYPPPVSMSPGQPPPQ

المراجع المراجع المناج

				The said as well containing signal montide	
	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=	
1	ID	beginning	nucleotide location	Glutamic Acid, F=Phenylalanine, G=Glycine,	
	NO:	nucleotide	corresponding	H=Histidine, I=Isoleucine, K=Lysine,	
1		location corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,	
ì		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,	
{		amino acid	residue of	S=Serine, T=Threonine, V=Valine,	
1		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop	
ì		amino acid	sequence	Codon, /=possible nucleotide deletion,	
. (sequence	201	\=possible nucleotide insertion)	
 -		5040000		QLLAPTYFSAPGVMNFGNPSYPYAPGALPPPPPPHLYPNTQAPS	
1				QVYGGVTYYNPAQQQVQPKPSPPRRTPQPVTIKPPPPEVVSRGS	
				S	
	5562	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH	
				LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP	
		·		LASFLDFITYSYMIDNVILLITGTLHQRSIAELVPKCHPLGSFE	
				QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI	
1				IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT	
į				INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA	
				DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF	
Ļ			1385	GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLBDLKLH	
l	5563	342	1305	LOSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP	
}			1	LASFLDFITYSYMIDNVILLITGTLHQRSIABLVPKCHPLGSFE	
ì				QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI	
1		1		IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT	
)				INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA	
į.		\		DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF	
ŀ				GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF	
<u> </u>	5564	3	914	RVRRDKRAVWTARGRRRCGDSMSGGWMAQVGAWRTGALGLALLL	
				LLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSGLC	
i		Ì	1	VPLTWRCDRDLDCSDGSDEEECRIBPCTQKGQCPPPPGLPCPCT	
j			1	GVSDCSGGTDKKLRNCSRLACLAGELRCTLSDDCIPLTWRCDGH	
			'	PDCPDSSDELGCGTNEILPEGDATTMGPPVTLESVTSLRNATTM	
				GPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLV TATLLLLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP	
<u> </u>	6565	993	138	RWNSPNPARAGSISRPQRAPGSVSAVAMTAAVFFGCAFIAFGPA	
	5565	393	130	LALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIID	
		<u> </u>		NKDGPTOKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSIN	
				PGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIH	
				GDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVL	
				LTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRS	
		·		LKLCLLCQDKNFLLYNQRSR	
	5566	2043	1232	SHIQHHGRGAQAPVKMVSWMISRAVVLVFGMLYPAYYSYKAVKT	·
ngan sagaga asal kabangan na na na na na na na na na na na na n		and the same of an a	and a second second second was	KNVKEYVRWMYWIVFALYTVIETVADQTVAWFPLYYELKIAFV IWLLSPYTKGASLIYRKFLHPLLSSKEREIDDYIVQAKERGYET	, etalle im statuetti.
type gage a wind die eine and die eine gewert		The second secon	3-	MVNFGRQGLNLAATAAVTAAVKSQGAITERLRSFSMHDLTTIQG	
	i			DEPVGQRPYQPLPEAKKKSKPAPSESAGYGIPLKDGDEKTDEEA	1
	ı			EGPYSDNEMLTHKGPRRSQSMKSVKTTKGRKEVRYGSLKYKVKK	
Į		ŀ		RPQVYF	
	5567	1554	233	EFLGSGVSPDLANEDGLTALHQCCIDDFREMVQQLLEAGANINA	
			1	CDSECWTPLHAAATCGHLHLVELLIASGANLLAVNTDGNMPYDL	
		·		CDDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSRLQ	
			}	AGADLHAPLDHGATLLHVAAANGFSEAAALLLEHRASLSAKDQD	1
				GWEPLHAAAYWGQVPLVELLVAHGADLNAKSLMDETPLDVCGDE EVRAKLLELKHKHDALLRAQSRQRSLLRRRTSSAGSRGKVVRRV	1
		1	Ì	SLTQRTDLYRKQHAQEAIVWQQPPPTSPEPPEDNDDRQTGAELR	
]	PPPPEEDNPEVVRPHNGRVGGSPVRHLYSKRLDRSVSYQLSPLD	Į.
		\		STTPHTLVHDKAHHTLADLKRQRAAAKLQRPPPEGPESPETAEP	
4		1	ł	GLPGDTVTPQPDCGFRAGGDPPLLKLTAPAVEAPVERRPCCLLM	[
	5568	1731	587	AEDROPASRRGAGTTAAMAASGPGCRSWCLCPEVPSATFFTALL	
ì				SLLVSGPRLFLLQQPLAPSGLTLKSEALRNWQVYRLVTYIFVYE	
				NPISLLCGAIIIWRFAGNFERTVGTVRHCFFTVIFAIFSAIIFL	
				SFEAVSSLSKLGEVEDARGFTPVAFAMLGVTTVRSRMRRALVFG	
				MVVPSVLVPWLLLGASWLIPQTSFLSNVCGLSIGLAYGLTYCYS	
		İ		IDLSERVALKLDQTFPFSLMRRISVFKYVSGSSAERRAAQSRKL	
				NPVPGSYPTQSCHPHLSPSHPVSQTQHASGQKLASWPSCTPGHM PTLPPYQPASGLCYVQNHFGPNPTSSSVYPASAGTSLGIQPPTP	
				PTLPPYQPASGLCYVQNAFGPNPTSSSVIPASAGISLGIQFFIF VNSPGTVYSGALGTPGAAGSKESSRVPMP	}
	5569	2	835	OTPCPLAWERGSRSEDISVPGQKPPTCSSFSGMDVGPSSLPHLG	†
				***************************************	•

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	1		
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<u></u>	\=possible nucleotide insertion)
			LKLLLLLLLPLRGQANTGCYGIPGMPGLPGAPGKDGYDGLPGP
1	ĺ		KGEPGIPAIPGIRGPKGQKGEPGLPGHPGKNGPMGPPGMPGVPG
			PMGIPGEPGEEGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVL
	1		TNPOGDYDTSTGKFTCKVPGLYYFVYHASHTANLCVLLYRSGVK
	ļ	1	VVTFCGHTSKTNQVNSGGVLLRLQVGEEVWLAVNDYYDMVGIQG
			SDSVFSGFLLFPD
5570	264	946	
5570	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT
1	i	Į.	MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPQGT
	·		PYEGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL
I	İ		DVINQTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH
1	ļ		RPEBYKQKIKBYIQKYATEEALKEQEEGTGDSSSESSMSDFSED
İ	[EAQDMEL
5571	264	946	RDRRDRGGVATSTEEPARPRAPOSRGPGPVSOTGRGRERGGGDT
-3,-			MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPQGT
	}		PYEGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL
1	,		
			DVINQTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH
1			RPEBYKQKIKEYIQKYATEEALKEQEEGTGDSSSESSMSDFSED
	<u> </u>		EAQDMEL
5572	2802	2085	RTDYRTGIPGRRFRVMAAGDGDVKLGTLGSGSESSNDGGSESPG
I	<u> </u>		DAGAAAEGGGWAAAALALLTGGGEMLLNVALVALVLLGAYRLWV
1	1		RWGRRGLGAGAGAGEESPATSLPRMKKRDFSLEQLRQYDGSRNP
1			RILLAVNGKVFDVTKGSKFYGPAGPYGIFAGRDASRGLATFCLD
1	}		KDALRDEYDDLSDLNAVQMESVREWEMQFKEKYDYVGRLLKPGE
1 .			
5573	2562		EPSEYTDEEDTKDHNKQD
55/3	2562	219	VPARTPNAEDQGPEARAATATPCQSGGRERAGEAAEDGVKMAAF
	ĺ		SEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAET
ļ)		GSGKTGAFSIPVIQIVYETLKDQQEGKKGKTTIKTGASVLNKWQ
	ļ i	÷	MNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYE
			VSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD
	Į į		NYGEEFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKN
			OALFPACVLKNAELKFNFGEEEFKFPPKDGFVALSKAPDGYIVK
·	. '	,	SOHSGNAOVTOTKFLPNAPKALIVEPSRELABOTLNNIKOFKKY
I	(•		IDNPKLRELLIIGGVAARDOLSVLENGVDIVVGTPGRLDDLVST
j] .		GKLNLSOVRFLVLDEADGLLSOGYSDFINRMHNOIPOVTSDGKR
1			
1		Lau est ales or monton	LQVIVCSATLHSFDVKKLSEKIMHPPTWVDLKGEDSVPDTVHHV
1	Frank and reflect to the State of the State	प्रोक्ता । स्थान अक्षर अन्युद्धाः १८५४ । जन्म	VVPVNPKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA-
1	(IKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGGG
1			PDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA
1			RGIDIHGVPYVINVTLPDBKQNYVHRIGRVGRAERMGLAISLVA
1			TEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEE
	·	,	HLNCTISQVEPDIKVPVDEFDGKVTYGQKRAAGGGSYKGHVDIL
1			APTVQELAALEKEAQTSFLHLGYLPNQLFRTF
5574	1731	952	NEGLEVFKEOELOPEDKGAVPEDASTERSAMASLGLOLVGYILG
33/4	1/31	734	
1			LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS
1			TGITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM
}	J		RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD
1]		FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN
}	j		RSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
5575	456	766	LLWALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL
l	Ì	. = =	LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR
			SPDIGRNSPHYLMFP
5576	249	2146	RSWGAPWFWRMRLLRRRHMPLRLAMVGCAFVLFLFLLHRDVSSR
] 55/6	44.7	2146	
1			EEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA
		•	QQTLFSINQSCLPGFYTPAELKPFWERPPQDPNAPGADGKAFQK
1			SKWTPLETQEKEEGYKKHCFNAFASDRISLQRSLGPDTRPPECV
)		DQKFRRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK
.			EIILVDDASTEEHLKEKLEQYVKQLQVVRVVRQEERKGLITARL
1			LGASVAQAEVLTFLDAHCECFHGWLEPLLARIAEDKTVVVSPDI
			VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWBTLPPHEKQRR
1	1		VIIDIMITEE ARE VORGRANSKGMEDMS III FIGMRIDEE FRANKISK
			KDETYPIKSPTFAGGLFSISKSYFEHIGTYDNQMEIWGGENVEM

DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITMNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSBKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL				
NO: nucleotide	_			
corresponding				
to first amino acid residue of amino acid sequence equence sequence sequence sequence sequence sequence sequence sequence sequence sequen	NO:		_	
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid sequence S-Serime, T-Threnoine, V-Valline, S-Serime, T-Threnoine, V-Valline, W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop Coden, '-possible nucleotide deletion, S-SerwicoGogLE: IP-CVGOWIP-RTS-SPIPTPYGATS-VIARNOVA LASWNOSYEKITYRENIQAAUMAGEKS-FODISER-LQLEEGLING KNEWLING-SERIMED_PETPYGATS-VIARNOVA LASWNOSYEKITYRENIQAAUMAGEKS-FODISER-LQLEEGLING KNEWLING-SERIMED_PETPYGATS-VIARNOVA LASWNOSYEKITYRENIQAAUMAGEKS-FODISER-LQLEEGLING KNEWLING-SERIMED_PETPYGATS-VIARNOVA LASWNOSYEKITYRENIQAAUMAGEKS-FODISER-LQLEEGLING KNEWLING-SERIMED_PETPYGATS-VIARNOVA LASWNOSYEKITYRENIQAAUMAGEKS-FODISER-LQLEEGLING-SERIMED_ AMACRIS-SDEPHQUIM-FV SERIMED_NISS-SERIMED_PETPYGATS-VIARNOVA LASWNOSYEKITYRENIQAAUMAGEKS-FODISER-LQLEEGLING-SERIMED_ING-SERIME				
amino acid sequence discovered amino acid sequence control sequence contro				
mein acid sequence ### ### ### ### ### ### ### ### ### #		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence Codon, /=possible nucleotide deletion, Lpewwholsykif proking the provided	'	amino acid	residue of	
amino acid sequence Codon, /=possible nucleotide deletion, Lpewwholsykif proking the provided	İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence N=possible nucleotide insertion		amino acid	semience	
SFRWGCGGGLEI PCSVGGWYRTKS PHTPFKGTSVTARNOGY LAEWWADSYKLT FYRTLAAMANGEKS PGDTSBRIJCHEGLIEG HNTSWYLINWYPEMPUDLT PTYGAL KNIGTNOCLDUGENING GRDLIWYS GIGLOROV FEYTTORD LERM TAX ROLL-HIVSKGALG LOSCHTTKING OV FREEWELADD LIRNG GGTCLT SORK PA MAPONS PHOLINE V STANDAM PROSPOPHOLINE V TSLALDANNY PEMPUDLT HODRAL MACK OF STREEK CHILLEPULD POR PARTY HOR STANDAM CONTROL OF STREEK CHILLEPULD DOVERADORY LITH HORDAL MACK OVER STREET PER STREET PRESENT FROM THE STREET PROSPECTIVE OF THE WATER GOLLOWG CVPOSTER VILLY WELL SER STREET VERY YHELE ME SPENGS WERE PROVINCE WITH THE PARTY HORDAL MACK OVER PER LAW THE STREET PROSPECTIVE OF THE WATER GOLLOWG CVPOSTER VILLY WELL THE PROBLEM CONTROL OF THE WATER GOLLOWG CVPOSTER VILLY WELL THE PROBLEM CONTROL OF THE WATER GOLLOWG CVPOSTER VILLY WELL THE PROBLEM CONTROL OF THE WATER GENERAL THE PROBLEM CONTROL OF THE WATER SPENGS WERE PROBLEM OF THE WATER OF THE WATER PER PER SER SEAR TYM THE PER THE WAS A VESSURAS PROBLEM TO SER SEAR TYM THE PER THE WAS A VESSURAS PROBLEM TO SER SEAR TYM THE PER THE WAS A VESSURAS PROBLEM TO SER SEAR TYM THE PER THE WAS A VESSURAS PROBLEM TO SER SEAR TYM THE PER THE WAS A VESSURAS PROSPECTIVE OF THE PER LIVLY CONSAL SEAL FLOOR THE PER LIVLY CONSAL SEAL FLOOR THE PER LIVLY CONSAL SEAL FLOOR THE PER LIVLY CONSAL SEAL FLOOR THE PER LIVLY CONSAL SEAL FLOOR THE PER LIVLY CONSAL SEAL FLOOR THE PER LIVLY CONSAL SEAL FLOOR THE PER LIVLY CONSAL SEAL FLOOR THE PER LIVLY THE PER PER LIVLY CONSAL SEAL FLOOR THE PER LIVLY THE PER PER LIVLY CONSAL SEAL FLOOR THE PER LIVLY THE PER PER LIVLY THE PER PER LIVLY THE PER PER LIVLY THE PER PER LIVLY THE PER PER LIVLY THE PER PER LIVLY THE PER PER LIVLY THE PER PER LIVLY THE PER THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIVLY THE PER LIV		1	20400000	
LAEVWINDS YIKT FYRINICAMAMAGEKS PEDISERIOLREOLINE RINPSWYLINNYS PENPOLT PET PYGAL RINJATYRICLUSVENING GRPLINYSCIGLORGYPEYTTORDLARINI TANGLICHYSKOLIG GRPLINYSCIGLORGYPEYTTORDLARINI TANGLICHYSKOLIG GRPLINYSCIGLORGYPEYTTORDLARINI TANGLICHYSKOLIG GRPLINYSCIGLORGYPEYTTORDLARINI TANGLICHYSKOLIG AMAPCINSDPHOLIMLEY REGIONAL REGIONAL PROSTRICT OF THE CONTROL		sequence	 	
INPSWYLINNYPEMPVDILTFYGALTNICIDVGENNING GREINYGCIGIGORYPEYTORGIRINTAGCICHYSKRAG LGCHPTGKNSQUPERDEMBLADQLIRNSGSGTCLTSQDKKPA MAPCHSDDHOUMLY SPECHALADDRIVSPUP TIDLKWBSSMFCPLKLTLLFULLO SPECHALADDRIVSPUP TIDLKWBSSMFCPLKLTLLFULLO SPECHALADDRIVSPULLOF TIDLKWBSSMFCPLKLTLLFULLO SPECHALADDRIVSPULLOF TIDLKWBSSMFCPLKLTLLFULLO GULQGCVPQSTEVRINSVPIGREQNRYLLMSDLICKDGSILL QDVQRADGGTYICSTRIKGSSQVPKKAVVLHULBEPFKELMYRY GULQGCVPQSTEVRIVTKYRNI SPEGRARESEVTYFYHELBE SVEYSQSMGHFQNRVILVGDI FRINGSTMLQGVRESDGGNYTCS HILLDAVLKYKKTULHAPSPEPRTLUTPALARIPLLIGGGNGUNITV GIVCATILLIPVLILVKKTCGKSSVNSTULVKNYKKTNBERK REPCHPERCEGRENHTYSPIVREVE BEBPSSKEAPTATIMHEV WPSLESDENNISLEKKSGGMNYCQAF WFGDFSSFRALLEFELFBROKYTQVFKEVBYYDQRYQGAADSAPYD WFGDFSSFRALLEFELFBROKYTGAFFWHYMOPT TSVYSSVVVAMANGATANFOLMENTYSSGYHHTUTJMHKGK ERCHLALAGSRDDWTVSSSGVHTVDQVLSSVSRVLVDGGRFT STSYSSVVAMANGATANFOLMENTYGSGYHHTUTJMHKGK LSVAQLALGAGALADHAPTSFFTHATVGSGYHTUTJMHKGK LSVAQLALGAGALADHAPTSGGTHATVGSGYHHTUTJMHKGK LSVAQLALGAGALADHAPTSGGTHATVGSGYHHTUTJMHKGK CRALPALATCSRGLGGVYCRFHHCAPTRGGRHLLSRVOPODAL ERDRUKJCRVTOCHAADATAGGGCHAVCGAARGAWGGLLFR CRALPALATCSRGLGGVYCRFHHCATALAGKKTSKVHCHLDFYLLGF REGULADLLAGERGFTMATATTGSGFHHTUTJMHKGK ELLELDRRIGKEVGTGFTHERATTALAGKKTSKVHCHLDFYLLGF REGULADLAGERGFTMATATTGSGFHHTUTJMHKGK ELLELDRRIGKEVGTGFTHERATTALAGKKTSKVHCHLDFYLLGF REGULADLAGAGGGAGAGAAGAAGAAAAAAAAAAAAAAAAAA				
GEPLINYS CHILDROND LIRINGS GTCLTSOKKEA JASCHPTORNSON PICEMENLADOL LIRINGS GTCLTSOKKEA MAPONISD PHOLMLEY SENSCEGGES GYCLPWULF ILDLEVES SMECPLEKI JLLEVILLO SEGHALDEVILLY SINGEN JORGONE YEAR JONG SEGHALDEVILLY SINGEN JORGONE YEAR JONG SEGHALDEVILLY SINGEN JORGONE YEAR JONG GOLLOWIC CYDS TEVEN THE SEGRAL RESULT SEGHALDEVILLY SINGEN JORGONE YEAR JONG GOLLOWIC CYDS TEVEN THE SEGRAL RESULT SEGHALDEVILLY SINGE PROTECTIVE THE JONG GOLLOWIC CYDS TEVEN THE SEGRAL RESULT SEGNAL THE SEGNAL RESULT SEGNAL THE SEGNAL RESULT SEGNAL THE SEGNAL RESULT SEGNAL THE SEGNAL RESULT SEGNAL THE SEGNAL RESULT SEGNAL THE SEGNAL RESULT SEGNAL THE		İ		
LISCHITGKINGOVPKDERMELAQDOLIENSKSSTCLISOKKPA MAPCHSDPHOLIEV		})	1
MAPCNISDEGICHAVE TIDLKVESSMFCPIKLILEVILD SERGEACES VILVANICH STEUCH STEUCH STEUCH STEUCH STEUCH STEUCH STEUCH STEUCH STEUCH SPECIAL STEUCH STEUCH STEUCH STEUCH STEUCH STEUCH SPECIAL STEUCH STEUCH STEUCH STEUCH STEUCH STEUCH STEUCH STEUCH STEUCH STEUCH SPECIAL STEUCH		i		1 · · · · · · · · · · · · · · · · · · ·
1275 RRSCCSCGETSVEICHWUFTIDLICKUSSMFCPLKKITLICPULD SPORHAKDEYVLYYYSILSVEIGRORRYNILMODILCHOSSILL ODVORADOGYTICSTRIKGESQVFKKAVVLHVLPBEPKELMIHV SPORHAKDEYVLYYYSILSVEIGRORRYNILMODILCHOSSILL ODVORADOGYTICSTRIKGESQVFKKAVVLHVLPBEPKELMIHV GGLIQMGCVPGSTEVKHYTKVBN FSGRRAKEETVEPRITHKLRM SVEYSGSWGHCQRKVNILVGDIFRADGS INLIGGVRESDGSTYTCT IHLENNIPKKTITUHUSPBEPPKITUTPAALAPRLICHGRUDVIIV GIVCATILLLEVLILIVKKTCCRKSSVNSTVLVKNTKKTBER ERPCHPERRCGEGEHTYSFITVERUTEEBPEPKERSEATYMTHEV WPSILRSDRINSLEKKSGGOMPKTQQAF 15078 3 783 AVERMAS POAGRAPPEDERBRICKYLEEBPEPKERSEATYMTHEV WPSILRSDRINSLEKKSGGOMPKTQQAF TSVDYSSVVVAMAMARAYHPOLAREMDVRKLDSASJEVVL EKGTLDALLAGSRDPHTVSSGVHEVEWDORYQGAADSAPD WGOPSSFRALLEPELRPEDRILVLGCGKSALSVELFLGGFFSASFIVVL EKGTLDALLAGSRDPHTVSSGVHEVEWDORYQGAADSAPD WGOPSSFRALLEPELRPEDRILVLGCGKSALSVELFLGGFFSASFIVVL EKGTLDALLAGSRDPHTVSSGVHEVDRYQGAADSAPD STAAPHFRTRHYAQAYYGHSLERHDVKRLDHKHGK LSVAQLALGAQILISPPRPTSSCPLQDSDHEDFISAIQL SVAQLALGAQILISPPRPTSSCPLQDSDHEDFISAIQL SVAQLALGAGILSGVPCRHIKAGARGKRALLERWOPGONL REDBRUSLODDSDLTCKSGRIMLQVGLIYPASSGCYHLEPTLA CRAMPALATCRSGLSSVPCRHIKAGARGKRALLERWOPGONL REDBRUSLODDSDLTCKSGRIMLQVGLIYPASSGCYHLEPTLA CRAMPALATCRSGLSSVYPCRHIKAGARGKAGASKLOGATRINDIMK BLILKIARDRIGKSVCLSPTHERAITALLASQKKLSYKQLFFLLV VYRKFDDEPRFRSCLGSVYPCTHKAGARGKRALLERWOPGONL ARDRYCHERORYCHAGARGKAGASSLLIGUAGATRINDIMK BLILKIARDRIGKSVCLSPTHERAITALLASQKKLSYKQLFFLLV VYRKFDDEPRFRSCLLGSVPCTHKMATTENSSPGCYHLLEFTL CKYSSIPHAGILPPKVCADAUGTIGTVSHEFQLPVDIGGENDIMC VYRKFDDEPRFRSCLLGSVPCTHKAGARGKRALGRYFLGAT KYSSIPHAGILPPKVCADAUGTIGTVSHEFQLPVDIGTSVLTAT ASGKKLRYVDOOLLIPKKGSKERAASALIGOKTONATRINDIMC CVRMSLLAPVOOLLIPKKGSKERAASALIGOKTONATRINDIMC CVRMSLAPVOOLLIPKKGSKERAASALIGOKTONATRINDIA LIPCKSSEANMETULISGMCCAGGAASSLLIGOKYTHITAVATOY VRIKFDBFFTAGGTTAVATHVKGMSCLOGRILAGA SPDTTASVVLLEGERISTTETHLAGSKVHSVANSCLOGRILAGA SPDTTASVVLLEGERISTTETHLAGSKVHSVANSCLOGRILAGA SPDTTASVVLLEGERISTTETHLAGSKVHSVANSCLOGRILAGA SPDTTASVVLLEGERISTTETHLAGSKVHSVANSCLOGRILAGA CSPDTSSTATAVTAVATATATATATATTATATATATATATATAT		l		LGSCHFTGKNSQVPKDEEWELAQDQLIRNSGSGTCLTSQDKKPA
YSLGAIDINVSPURICHINGULFUNGUNGULFUNGU		1	j	MAPCNPSDPHQLWLFV
SPERHANDEYULTYTSINLSVPIGREGNEVHIMODILLOSSILL QUVQBADQCTYLCSILLOSSQVPKRAVULTUPREPREIMMYN GGLIOMGCVPQSTEVEHVTKVEN I FSGRRAKEBIUPRYYHKLEM SVEXSGNGHEQNEVNIVGDI FRINDGS IMLQGVRESDGGNYTCS IHLGNLYFKKTUHVSPEBERTLUTPAALEPLULIGGNQIVI IV GIVCATILLLEVULLUTKKTCGNESSVNSTULVKATKKENPEIK ERPCHFREGEGEKHIUSPI LUREV LIEBEBPSERSEATMTMHHPY WPSLESDRRINSLEKASGGGMPKTQOAF AVESMASPGAGRAPPELPERRIKOGYREVSTWDQRYQGAADSAPYD WPSLESDRRINSLEKASGGGMPKTQOAF WPSLESDRRINSLEKASGGGMPKTQOAF WPSLESDRRINSLEKASGGGMPKTQOAF WPSLESDRRINSLEKASGGGMPKTQOAF WPSLESDRRINSLEKASGGGMPKTQOAF WPSLESDRRINSLEKASGGGMPKTQOAF WFGDFSSFFALLEPELRPEDRILVLGCONSALSYLEIFLGGFNV TSVDYSSVVVAMOARYATVOQVIRENTHOVENKLDPFSASFOVUL EKGTLDALLAGERDPHTVASEGVHTVDQVLSEVSRULVPGGRFI SNTSAAPHTERTHVAQAYYGGSLENATYGSGFHHLYIMHKGGK LSVQLIALGAOLLSPPPPTSPCFLOGDSHEDFLSAIOL RESGLARGASALARHGGGLAGGVGDCGAGSRCGGFHHLYIMHKGGK LSVQLIALGAOLLSPPPPTSPCFLOGDSHEDFLSAIOL RESGLARGASALARHGGGLAGGVGDCGAGSRCGGAFHHLYIMHKGGK LSVQLIALGAOLLSPPPPTSPCFLOGDSHEDFLSAIOL REDRVISLQDRSDDLTCKSGRIMLQVGLIYPSASGCYHHLIPTV RAMEKLWRVLOGROGAGGPTYKKTKKGLEVGHTPLLOT REDRVISLGDRSONDTOKSGRIMAGNGSARGAGKSKSKOLPFLLOY VYRKFREDEPRFFCLLURGEFYNLOWTEDSEAQQTYSLVCU DAYCSLENKLGLPPVKVQADVGTIGGTVSHEFFQLLPVTIGGBGRLA ICPRGSSANMETLDISQNOHAGAGGPTIKKGIEVGHTPTLOT VXSSIFRAGFTNVCGKPTLABMCYCLQTHTLAAAISUSTED CVRWPSLLAPVQACLIPP KKGSKRQAASELIGQLTHTIAAAISUSTED CVRWPSLLAPVQACLIPP KKGSKRQAASELIGQLTHTIAAAISUSTED CVRWPSLLAPVQACLIPP KKGSKRQAASELIGQLTHTTEVATOR LUGGVELLDORTHLYTIKGLTVTTKGEINTUGCHTPTLOT VXSSIFRAGFTNVCGKPTPAAMSSFALIGSGGGGSAPPAGVTSV GSPOTTASVFLLEKORLVKRNNYRGHGDSVDQLCWHESPFDLFVT ASGORTIR HOVOTTKCIA TUTVTKGEINTIGCHTTIANGC LINLSYPELKYQGSINAPHSKYANGCGRGLASG SPDXTASVFLLEKORLVKRNNYRGHGDSVDQLCWHESPFDLFVT ASGORTIR HOVOTTKCIA TUTVTKGEINTIGKSCGGRGASG SPDXTASVFLUEKDRVKRNYRGHGBSVDQLCWHESPFDLFVT ASGORTIR HOVOTTKCIA TUTVTKGEINTIGKSCGGRGASGER DDVVTPTDAKTTRISAAGCGCIA TUTVTKGEINTIGKSCGGRGASG SPDXTASVFLUEKDRVKRNYRGHGBSVDQLCWHISHFDLFVT ASGORTIR HOVOTTKCIA TUTVTKGEINTIGKTCATAMASAGTLT LTULVTSTIELFRGTSLARAFTATGTFTKYTAMASAGTLT CSPSPYNJERVCGGGFTASAFTRYTAGTFTKYTAMASAGTLT TUTVDPNSTIELFRGTSLAR	5577	3	1275	RNSDCSCGEISVHCLPWVLFILDLKVESSMFCPLKLILLPVLLD
QDVQRADQCTYTICSIELKGESQVPKKAVUHIVLPEEPERMYTYKLEM GOLIQMGCVGGSTEVHTYKEW IPSGERAKUTATIVTÄKERETVERYYKLEM SVEYSQSWGHPQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCS IHLINLIVFKKTIVLHVENSEBERTLVTPÄALRPILVLGGNQLVIIV GIVCATILLLEVLILIVKKTGKASKSUNSTVIKKKENPEIK ERPCHFRRCEGEKHIYSPILVREVIEBEEPSEKSEATMYMHEV WPSLRSDRNNSLEKKSGGGMRYTQAF SPERLENSTVILLEVLILIVKTCKGKSSUNSTVIKKKENPEIK ERPCHFRRCEGEKHIYSPILVREVIEBEEPSEKSEATMYMHEV WPSLRSDRNSLEKKSGGVBKYNGVAF WPSSLRSDRNSLEKKSGGVBKTVGVAF TSVDYSSVVVAAMQARYANVEQLRWETHDVRKLDFPSASTDVIL EKGTLDALLAGERDPHTVSSEVSTVTDOULGSVSKVLDFGGFFIN TSVDYSSVVVAAMQARYANVEQLRWETHDVRKLDFPSASTDVIL EKGTLDALLAGERDPHTVSSEVSTVTDOULGSVSKVLDFGGFFIN SMTSAAPHFRTRHYAQAYYGWSLRHATYGSGFHEILJMHKGGK LSVAQLALAGAGILSPFPPTSPCFLQDDDHEDFLGAIQL EKGTLDALLAGGGVWDCGAGGVWDCGAGRARGGVWEGGLIFR CRALPALATCSRQLSGVYVCCFFHICAPRGRRLLLSRYFQCQNL REDRUKLSQDKSDDLTCKSGRGVWDCGARRGGVWBEGLLFR CRALPALATCSRQLSGVYVCCFFHICAPRGRRLLLSRYFQCQNL REDRUKLSQDKSDDLTCKSGRGVWDCGAGRGVAHLDGVILLPRYTY RAMKKLJRVINDEWQAIGGGVNMPSLSFABLWQATNRUMKK ELLELIRDRIGKSYLCGPTHERATTALLASGKYGLIPFILGDY RAMKKLJRVINDEWQAIGGGVNMPSLSFABLWQATNRUMK ELLELIRDRIGKSYLCGPTHERATTALLASGKYGLIPFILGDY TRYRDEPPSPFCLLEGREFYMEDWYTFDSSPEAAQOTYSLVC DAYCSLENLEGREYVLGDWCTTGGTVSHEQUTGITGHDTGGETHL ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEWGHTPYLGT KYSSIFRAQFTNVCGKPTLAGABCCCLGAVTRILAAAIBUSTED CVRWPSLLAPYQACLIPPKKASKRQAASELIGQVTHTERAYD LHGSVLLDDRTTHLTICNRIKDANKCPYPFVLIAGKRALEDPAHP EWCQNTGSKPLFUKGWUDLITTVQTV SCHWCQNTGSKPLFUKGWUDLITTVQTV SCHWCQNTGSKPLFUKGWUDLITTVQTV AGGKTTILLKORLIKDANKCHGDSVDLCUMERSPPDLFTV AGGKTTILKWRTTKCIATVNTKGENINICKSPRDPLFTT AGGCKTTILKKORLIKDANKCHGUNGSVGROSMAWCSVSS GPSRVLGWGLEFFGUSKRTRANGFSAGGROSMAWCSVS GPSRVLGWGLEFFGUSKRTRANGFSAGGROSMAWGSCGGRLAGG SPDKTASVFULLKORLIKKTRTGGENINICKSPRDPLFTINGNGC INILSYPELKPVQSINAHPSKYTGHGDSVDLAWAGTTMANSAGTLL LDVDTEILTDHTTTTUTATHTSGENINGARAGTSBADALVSCSCGTTGS TTHLPVDTGTENRTYGASAAAAAVAGGEDKGTASAAAAAAVACS CGPPDGSSTMNDVSPVQPGAAYGNFRMAATTGYPTAYDAAAAA YNPSLYTNSPSTAPFVQTAATHTRAVATGYPTAYDAYAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ŀ	1		YSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTL
QDVQRADQCTYTICSIELKGESQVPKKAVUHIVLPEEPERMYTYKLEM GOLIQMGCVGGSTEVHTYKEW IPSGERAKUTATIVTÄKERETVERYYKLEM SVEYSQSWGHPQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCS IHLINLIVFKKTIVLHVENSEBERTLVTPÄALRPILVLGGNQLVIIV GIVCATILLLEVLILIVKKTGKASKSUNSTVIKKKENPEIK ERPCHFRRCEGEKHIYSPILVREVIEBEEPSEKSEATMYMHEV WPSLRSDRNNSLEKKSGGGMRYTQAF SPERLENSTVILLEVLILIVKTCKGKSSUNSTVIKKKENPEIK ERPCHFRRCEGEKHIYSPILVREVIEBEEPSEKSEATMYMHEV WPSLRSDRNSLEKKSGGVBKYNGVAF WPSSLRSDRNSLEKKSGGVBKTVGVAF TSVDYSSVVVAAMQARYANVEQLRWETHDVRKLDFPSASTDVIL EKGTLDALLAGERDPHTVSSEVSTVTDOULGSVSKVLDFGGFFIN TSVDYSSVVVAAMQARYANVEQLRWETHDVRKLDFPSASTDVIL EKGTLDALLAGERDPHTVSSEVSTVTDOULGSVSKVLDFGGFFIN SMTSAAPHFRTRHYAQAYYGWSLRHATYGSGFHEILJMHKGGK LSVAQLALAGAGILSPFPPTSPCFLQDDDHEDFLGAIQL EKGTLDALLAGGGVWDCGAGGVWDCGAGRARGGVWEGGLIFR CRALPALATCSRQLSGVYVCCFFHICAPRGRRLLLSRYFQCQNL REDRUKLSQDKSDDLTCKSGRGVWDCGARRGGVWBEGLLFR CRALPALATCSRQLSGVYVCCFFHICAPRGRRLLLSRYFQCQNL REDRUKLSQDKSDDLTCKSGRGVWDCGAGRGVAHLDGVILLPRYTY RAMKKLJRVINDEWQAIGGGVNMPSLSFABLWQATNRUMKK ELLELIRDRIGKSYLCGPTHERATTALLASGKYGLIPFILGDY RAMKKLJRVINDEWQAIGGGVNMPSLSFABLWQATNRUMK ELLELIRDRIGKSYLCGPTHERATTALLASGKYGLIPFILGDY TRYRDEPPSPFCLLEGREFYMEDWYTFDSSPEAAQOTYSLVC DAYCSLENLEGREYVLGDWCTTGGTVSHEQUTGITGHDTGGETHL ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEWGHTPYLGT KYSSIFRAQFTNVCGKPTLAGABCCCLGAVTRILAAAIBUSTED CVRWPSLLAPYQACLIPPKKASKRQAASELIGQVTHTERAYD LHGSVLLDDRTTHLTICNRIKDANKCPYPFVLIAGKRALEDPAHP EWCQNTGSKPLFUKGWUDLITTVQTV SCHWCQNTGSKPLFUKGWUDLITTVQTV SCHWCQNTGSKPLFUKGWUDLITTVQTV AGGKTTILLKORLIKDANKCHGDSVDLCUMERSPPDLFTV AGGKTTILKWRTTKCIATVNTKGENINICKSPRDPLFTT AGGCKTTILKKORLIKDANKCHGUNGSVGROSMAWCSVSS GPSRVLGWGLEFFGUSKRTRANGFSAGGROSMAWCSVS GPSRVLGWGLEFFGUSKRTRANGFSAGGROSMAWGSCGGRLAGG SPDKTASVFULLKORLIKKTRTGGENINICKSPRDPLFTINGNGC INILSYPELKPVQSINAHPSKYTGHGDSVDLAWAGTTMANSAGTLL LDVDTEILTDHTTTTUTATHTSGENINGARAGTSBADALVSCSCGTTGS TTHLPVDTGTENRTYGASAAAAAVAGGEDKGTASAAAAAAVACS CGPPDGSSTMNDVSPVQPGAAYGNFRMAATTGYPTAYDAAAAA YNPSLYTNSPSTAPFVQTAATHTRAVATGYPTAYDAYAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		1		SPGEHAKDEYVLYYYSNLSVPIGRFONRVHLMGDILCNDGSLLL
GGLIOMGCYPGSTEVHYTKVENI PSGRRAKEBIUPRIYHKIRM SYEVSGSWHCHONVAULUGU PERNOSTHUGGWSDGWYTGS IHLGHLVFKKTTULHVSPEEPRILTPALREPLULGGWGUITU GTVCATTILLPVILLIVKKTCGKSVNSTVLVKNTKKTNBIK EKPCHPERCEGEKHITSDITUREVIEBEEPSEKSATTMTWHEY WESLRSDRNNSLEKKSGGMPKTQGAF 5578 3 783 AVESMASGGAGAPSPELEERIKGYREVSTWDQRYQGAADSAFYD WEGDFSSFRALLEPELRFEDRILVLGCONSALSYLEFIGGFRV TSVDYSSVVVAMMARYATVGURETTDVSKLOFFSASFDVUL EKGTLDALLAGERDPWTVSSSGVHTVDQVLSEVSRULYPGGFRV TSVDYSSVVVAMMARYATVGURETTDVSKLOFFSASFDVUL EKGTLDALLAGERDPWTVSSSGVHTVDQVLSEVSRULYPGGFRV STSAAPHFRTHVAQAYVGGRGVENDGGAGGGVGWDGGAGGGFHILYIMHKGGK LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDFLSAIQL ENGGLABGASALAHGGGLAGGVWDGGAGGGVGWDGGAGGGVGWGGGAGG LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDFLSAIQL REDREVISLQDKSDDLTCKSGRIMLQVGLIYPASPGCYHLDFTV RAMKKLVRVIDGWAGIGGGVWDGGAGGGVWBGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	l	}	j	
SVEYSGNMSHPONRVALIVADI FRNDESS MILGGVRESDGGRYTCS HILGNLYFKKTIVHNSPEREFTAUTPABLEVIGORQUI IV GIVCATILLLPVLILIVKCTCONKSSVNSTVLVKNTKKTNPBIK EKPCHFERCEGEKHITSPILVFRAVIEBEPSERSATTMTHEV WESLESDRNALBEKKSGGGMENTOGAF SVEYGGRADSBEKKSGGAMENTOGAF SVEYGGRADSBEKKSGGGMENTOGAF WEGGSSFRALBEERLERDRIVLGCONSALSYBLFIGGFROV TSVDYSSVVVAAMQARYANVOLRMETHUVLGCYGAADSAFYD WEGGSSFRALBEERLERDRIVLJCCONSALSYBLFIGGFROV TSVDYSSVVVAAMQARYANVOLRMETHUVLGCONSALSYBLFIGGFROV TSVDYSSVVVAAMQARYANVOLRMETHUVLGCONSALSYBLVIJGGGREY SMTSAAPHRTHHYAQAYGKSURHATVGSGFHFHLYLMHKGGK LSVAQLALGAOLLSPPRPTSPEPCLQDSDHEVSARJVJPGGREY SMTSAAPHRTHHYAQAYGKSURHATVGSGFHFHLYLMHKGGK LSVAQLALGAOLLSPPRPTSPEPCLQDSDHEVSARJVPGGREI SMTSAAPHRTHHYAQAYGKSURHATVGSGFHFHLYLMHKGGK LSVAQLALGAOLLSPPRPTSPEPCLQDSHEVSARJVPGGREI SMTSAAPHRTHHYAQAYGKSURHATVGSGFHFHLYLMHKGGK LSVAQLALGAOLLSPPRPTSPEPCLQDSHEVSARJVPGGREI SMTSAAPHRTHHYAQAYGKSURHATVGSGFHFHLYLMHKGGK LSVAQLALGAOLLSPPRPTSPECLLGDRENGAGGFHLERSRIVDGAT REDRVISLQDKSDDLTCKSGRUHAQVGJTAGSGFHLIBGRVDLMK REDRVISLQDWIJDCHAGGGGRANGAGGGFHALGARTVSLOW REDRVISLQDWIJDCHAGGGGGGGGGGAGGGGAASRCQGVMEGLLTR RAMEKLJRVINDDENQALGGGCNMMPSLSPARLMGATNRADMAK ELLLAIRDRINGKYSLGPTHUGHUTTGAUT RAMEKLJRVINDGENGALGGGCYGLGVTILLAAALBEVLSTED CVRAPSLLAPYQACLIPPKKOSKEQAASELIGGLATDHITARVQ LIGGVLLDDRTHLITIGNRIKDANKGYSPVILIAGKRALEDPAHF KYSSIFNAQFTNVCGKPTLAEMGCYSLGVTILLAAALBEVLSTED CVRAPSLLAPYQACLIPPKSGSKGAASELIGGLATDHITARVQ LIGGVLLDDRTHLITIGNRIKDANKGYSPVILIAGKRALEDPAHF KYSSIFNAGAPALIKGGVGUDUTTTUTGVT AGGAGTATATATATGCAGGAGGGGGGGAAAAAAPACS GESRYNLGMGELFRGHSKTREFLAHSAKHSVANGCGGRAAGG GESRYNLGMGELFRGHSKTREFLAHSAKHSVANGCGGRAAGG GESRYNLGMGELFRGHSKTREFLAHSAKHSVANGCGGRAAGG GESRYNLGMGELFRGHVKWANGGGGAGGGAGGAGGGAGGAGGAGGAGGAGGAGGAGGAG		1		
INLINIUPKKTIVLHVSPEEPRILIPAALRIPLUIGONUVIIV GIVCATILLIPVILIUVKYCCKINKSSUNSTVLVKNTKKTHPEIK EKPCHPERCEGEKHIYSPIIVREVIEEBEPSEKSEATYMTMHPU WPSLRSDRNISIELEKSGGMPKTQQAP 15578 3 763 AVESMAS PGAGRAPPELPERNGYREVEYMDQRYQGAADSAPYD WFGDFSSFRALLEPELRPERNIGVREVEYMDQRYQGAADSAPYD WFGDFSSFRALLEPELRPERNIGVREVEYMDQRYQGAADSAPYD WFGDFSSFRALLEPELRPERNIGVREVEYMDQRYQGAADSAPYD WFGDFSSFRALLEPELRPERNIGVREVEYMDQRYQGAADSAPYD WFGDFSSFRALLEPELRPERNIGVREVEYMDQRYQGAADSAPYD WFGDFSSFRALLEPELRPERNIGVREVEYMDQRYQGAADSAPYD WFGDFSSFRALLEPELRPERNIGVREVEYMDQRYQGAADSAPYD WFGDFSSFRALLEPELRPERNIGVREVEYMDGRYAGGAASTROWLDFSSFDVVIL BKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSSFDVVIL BKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSSFDVVIL BKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSSFDVILLPTWYVI SKTAAPHPRTTHYAGGAACACACACACACACACACACACACACACACACACA				
GIVCATILLIPULLIVKATCORKSSYNSTVUVKNYKKTNEPELK EKYPCHPERCEGKHYSPY LIVERVIEGEBEPSEKSEATYMTMHPV WPSIRSDRNNSLEKKSGGMPKTQQAF 3 783 AVESMASPCAGRAPPELPERNIGYREVEYMDQRYQGAADSAPD WPGOPSSFRALLEPELLEPERNIGYREVEYMDQRYQGAADSAPD BKGTLDALLAGERDWYVSSSEVHYDQUSSEVSKYLPGGFPN TSVDYSSVVVAMAQARYAHVPQLRRETMDVRKLDFSASTDVUL BKGTLDALLAGERDWYVSSSEGVHYDQVJSEVSSVLJVPGGRFI SMTSAAPHFRTRHYAQAYYGWSLRHATYGSGFHFHLYJMHKGGK LSVAQLALGAQILSPPPPTSPCFLQDSDHEDFLSAIQL SMSGLARGSALARRIGGGLAGGVGNDCGAGSRCGGVMEGLLTR CRALPALATCSRQLSGVYDCFFHHCAPRRGRELLISMFYCPQNL REBWLSLQDKSDDLTCKSGRIMLQVGI 17PASPGCYHLLIPTYV RAMEKLVRVIDQEMQAIGGGKVNMPSLSPAELWQATNRNDIMKK BELLRLRDRHGKSYCLGPTHERAITALLASQKKLSYKQLPFLLYQ VYRKFRDEPRPRFGLLIRGREFYMKQMTPISSPAELWQATNRNDIMKK BELLRLRDRHGKSYCLGPTHERAITALLASQKKLSYKQLPFLLYQ VYRKFRDEPRPRFGLLIRGREFYMKQMTPISSPERAQQTYSLVC DAYGSLENKLGLPFVKVQADVGT IGGTVSHETQLEVJIGEDRIA ICPRCSSSAMMSTLDLSQMCDACQGCVINTERIABATEVJSTED CVRWPSLLARYQACLIPFKKGSKEQAAGATURGLAFVYLGE CVRWPSLLARYQACLIPFKKGSKEQAAGATURGLAFVYLGE CVRWPSLLARYQACLIPFKKGSKEQAAGATURGLAFVYLGE CVRWPSLLARYQACLIPFKKGSKEQAAGATURGAWBWGCORGRIAGG GPSRVILGMGEFFRGHSKTEFLAHSKARLIGQAFDRSMAPGSVSS GPSRVILGMGEFFRGHSKTEFLAHSKARLIGQAFDRSMAPGGSVS GPSRVILGMGEFFRGHSKTEFLAHSKARLIGQAFDRSMAPGGSVS GPSRVILGMGEFFRGHSKTEFLAHSKARLIGQAFDRSMAPGGSVS GPSRVILGMGEFFRGHSKTEFLAHSKARLIGGAFDRSMAPGGSVS GPSRVILGMGEFFRGHSKTEFLAHSKARLIGGAFDRSMAPGGSVG GPSRVILGMGEFFRGHSKTEFLAHSKARLIGGAFDRSMAPGGSFR GPSRVILGMGEFFRGHSKTEFLAHSKARLIGGAFDRSMAPGGSFR GPSRVILGMGEFFRGHSKTEFLAHSKARLIGGAFDRSMAPGGSFR AGGDTKLFGUFWTSGSSTAFFRKARLIGGAFDRSMAPGCSTGS GFSRVILGMGEFFRGHSKATLLDTGESVAAVASGEDKGIAASAAAAVFACS CSPDPQSSTMNEVYSPVQFRAPYRTGSFTHGSMADALTYAGT THILDYDTGTBRRTTQASSAAFRYTAGTPYKUPPTGSNTAPPY SPSMPYGTAMYPISSPVQPQNLYAQGAYTYQPVVAAQPHVIHK TTVQPNSTPSAPETPFHSAYATLLMKQAMPONSSSCGTEG TFHLEVOTGTBRRTTYQASSAAFRYTAGTPYKUPPTGNATAPAAAAAAVFACS SPSMPYGTAMYPISSPAPPAGQAFPASTALLMKQAMPAGTTAMSAGTLL TTPQHTAIGAHPVSMPTTPAQGTPARSYTYGPTVAMPAGATPTTMST SPSMPYGTAMYPISSPAPPAGAPAGRAFTAGFPKUPPTGYNTAPAAAAAAAAAAAPFACSS SALDHDBSSTOVAQFRABLCKLHVNRAACTFTMGLF EKALDSSKALGLIDSSSLAPRKARAINELGRHKSAYCSSKG SLALHDBSST				
ERPCHFERCEGENHITSPIIVEEVIEEEEPSEKSEATYMTMHPV WPSILESPINSILEKKSGEGMPTQOAD 5578 3 783 AVESMAS PAGRAPPELPERNCGYREVEYWDQRYQAADSAPYD WFGDPSSFRALLEEELRPEBRILUTGGSNALISYBIJGGFPNV TSVDYSSYVVAMQARATAPPQLREEMDVRKLDPSASTDVVI EKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSSKIVPGGRPI SMTSAAPHRTHHYAQATYVGSLENATTYGGSPHFHLYIMIKGGK LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDPLSAIQL 5579 3 1540 RNSGLARGASALARHGGGLAGGVGMCGACASCQGVMEGLLTR CRALPALATCSRQLSGVYPCRFHHCAPRGRELLLSRVFQPQNL REDRYLSLQDKSDDLTCKSGRIMLQVGLIYPASPGCTYLLDPTYV RAMEKLIVRYLDGEMQAIGGKVMMPSLSPAEMQATNRWDLMK ELLRIRDRHGKSYCLGFTHERAITALLASGKKLSYKQLFFLLVQ VTRKFRDERPRFGLLKGGKVMMPSLSPAEMQATNRWDLMK ELLRIRDRHGKSYCLGFTHERAITALLASGKKLSYKQLFFLLVQ VTRKFRDERPRFGLLKGGKVMMPSLSPAEMQATNRWDLMK ELLRIRDRHGKSYCLGFTHERAITALLASGKKLSYKQLFFLLVQ VTRKFRDERPRFFGLLKGGKVMMPSLSPAEMQATNRWDLMK ELLRIRDRHGKSYCLGFTHERAITALLASGKKLSYKQLFFLLVQ VTRKFRDERPRFFGLLKGFFYMKOMTAPSLEPALMQATNRWDLMS ELLRIRDRHGKSYCLGFTHERAITALLASGKKLSYKQLFFLLVQ VTRKFRDERPRFFGLLKGDKFFYMKOMTAPSLEPALMQATNRWDLMS ELLRIRDRHGKSYCLGFTHERAITALLASGKKLSYKQLFFLLVQ VTRKFRDERPRFFGLLKGDANKGPYSLFVLLAGATNRWDLMS LICPRCSFSAMMETLDLSQMCPACAGGPLTKTKGIEVGHTFYLGT KYSSIFNAGFTHVCSKFTLLAGGVGLGGYTRILAAALEVSTED CVRMPSLLAPYQACLIFPKKGSKRGASEEIGGLHHTEAVPQ LHIGSVLLDDSTHTLTGGWATTALLASGKKLSYKAGLGFTSLGAR EWCONTGSWAFLIKDGVMDLLTFVQTV ABGANTIT MOWRITKGCARGYSAPAQKGRRSSGGMRAAAAPGGTAPA WRLLQCCEBEAGEGMAVPAAMGPSALGGSGGGSGAMAWGSVSS GPSRYVLGMQELFRGHSKTRTKGENDTOLTGRPDDFDLFVT ASGNTTIT MDVRITKCLATVATIKGENINICGSPGGLAGAGAAAVAFCS SPDKTASVFLLEKDRLVKENNYRGHGBVDVQLCWHENNPDLFVT ASGNTTIT MDVRITKCLATVATIKGENINICGSPGGLAGAGAAAVAFCS SPDKTASVFLLEKDRLVKENNYRGHGBVPQLGWHENNPDLFVT ASGNTTIT MDVRITKCLATVATIKGENINICGSPGGLAGAGAAAVAFCS SPDKTASVFLLEKDRLVKENNYRGHGBVPQLGWPGSAPAGAAAVFCS CSPDPQSSTMNPVYSPVQDGAPYGRPKMMAYTGSTPAYPAAAAR VMSHSTYTNSPSYAPAGFFHASAYATLIMKGAMPONSSCGTEG THILPVDTGERNTYOASSAAPRAYAGGTPKVMPTAYAPAAAA VMSHSTYNSPSYAPAGPHASAAAAAVFCS SCATTALHDSTATAAAAAAAVFTAGGTPKVMPTAYAPAAAAA THOVATMGLAGAGAAAAAVFTAGGTPKVMPTAYAPAAAAAAAAVFCS SPSMPYGTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA				
### S578 3 783 AVESMASPGAGRAPPELPERNCGYREVEYWDQRYQGAADSAPYD ### WFODPSSFRALEPBLRPERNLUTGCOMSALSYELFIGGFINV TSVYSSVVVAMQARYAHVPOLTMERTMOYRKLDFSASFDVVL BEGTLDALLAGENDRIVTSSEGWHTDOVLSEVSRVLVPGGRFI SMTSAAPHFRTRHYAQAYYGMSTRHATYGSGFHELINHKIGGK LEVNQLALGAQILSPPEPTSPEPLODSHHEDFISATQL 5579 3 1540 RISGLARGALSARHGGGLAGGVGWDCGACASRCQVMEGLLTR CRALPALATCSRQLSGVYPCGFHHCAPRIGRELLSRVFQPOML REDRIVLSLOPKSDDLTCKSQRLHLQVGLIYPASPGCTHLLPTV RAMEKLWRVIDGEMQAIGGOKVMPSLSFAELWAATKRWDLMKK BLLARLARDRKGEVGLOPHFHEATTALLASGKKLSYKQLFFLLVY VRKFRDEFRERFGLLRGREFYMKDMYTFDSSPEAAQOTYSLVC DAYCSLFNKLGFKVGLFFVKVQADVGTIGGTVSEFQLPVDIGEDRLA ICPRCSFSAMMELDLSJOMNCPACQSFLTKTKGIEVGHTFYLGT KYSSIFNAQFTNVCKPFLARMGCYGLGVTKTGIEVGHTFYLGT KYSSIFNAQFTNVCKPFLARMGCYGLGVTKGIEVGHTFYLGT KYSSIFNAQFTNVCKPFLARMGCYGLGVTKGIEVGHTFYLGT KYSSIFNAQFTNVCKPFLARMGCYGLGVTKGIEVGHTFYLGT KYSSIFNAQFTNVCKPFLARMGCYGLGVTKGIEVGHTFTLGT KYSSIFNAQFTNVCKPFLARMGCYGLGVTKGIEVGHTFTLGT KYSSIFNAQFTNVCKPFLARMGCYGLGVTKGIEVGHTFTLGT KYSSIFNAQFTNVCKPFLARMGCYGLGVTKGIEVGHTFTLGT KYSSIFNAQFTNVCKPFLARMGCYGLGVTKGIEVGHTFTLGT KYSSIFNAQFTNVCKFFLARMGCYGLGVTKGIEVGHTFTLGT KYSSIFNAQFTNVCKKPTLARMGCYGLGVTKGIEVGHTFTLADAG CYRMPSLLAPAQACI PPKKGSKEPABLIGQLVGHTTEAVPQ LIGGEVLAPAGACI FRYNCKSTRAFLAHASALGUCHTTTAAV QUENCTSKLAPVQACI PPKKGSKEPABLIGQLVGHTTEAVPQ LIGGEVLAPAGACI FRYNCKTRAGAAAGAFACAGA GESKTATLANGKALGDAH GARAAGA GESKTATLANGKALGDAH GARAAGA GA				1
S578 3 763 AVESMAS PCAGRAPPEL PERNICTYREVEYWDORYQGAADSAPYD WFGDFSFRALLEPELR PEDRILULGCORALISYEL FLGGFINV TSVDYSSVVVAMQARYAHVPOLURSTMUVRCLDFPSASEDVVL BEGTLDALLAGERD WTVSSEGVHTVDOVLSSVSVIV.PGGRPT SMTSAAPHFTRIRHYAGY YVGWSLRHATYGSGFHFLIKHMIKGGK LSVAQLALGAQILSPPRPPTPSPCFLQDSDHEDFLSATQL	1			
WEGDPSSFRALLEPBLRPEDRILVLGCGNSALSVELFLGGFPNV TSVDYSSVVVAAMQARYAHVPQLRWETMOVRKLDFPSASFDVVIL EKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSRVLVPGGRFI SMTSAAPHFRITRHYAQAYYGMSHATYGSGFHHLIVLMIKGGK LSVAQLALGAQILSPPPSTPSTCPLQDSHEDFISAIQL 5579 3 1540 RISGLAGGASALARIGGGLAGGVGWDCGACASRCGGVWEGLITR CRALPALATCSRQLGGYVPCRFHHCAPRGRELLLSRVFQPQML REDRVLSLQDKSDDLTCKSGRLMLQVGLYPASRGCHLLBRVFQPQML REDRVLSLQDKSDDLTCKSGRLMLQVGLYPASRGCHLLPTVTV RAMEKLWRVIDGEMQALGGGVXMPSLSPABLIMGATRKWDLMGK ELLRIRDRHCKSFYLGFPHERATTALIASGKKLSYKQLFPLLYQ VYRKFRDEFREPRGLLRGREFYMKDMYTPDSSPAQQYTSLVC DAYCSLFWKLGLFPVKVQADDWGTIGGTVSHEFQLFVUIGEDRIA ICPRCSFSANMETLDLSQMNCPACQSPLTKTKGIEVGHTFYLGT KYSSIFNAQFTNVCKKPTLAEMGCYGLGYTRILAATEVLSTETE CVRWPSLLAPYQACLI PPKKGSKEQAASELIGQLYDHITEAVPQ LIGGVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF EWWCNNTSWAFLIKGGMDLITPVGAASELIGQLYDHITEAVPQ LIGGVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF EWWCNNTSWAFLIKGKGMDLITPVGASGGFRSSGRMAAAAPGLATA FRELQCCELEBAGELEMAVPARAMGFSALGGGFDSMAPACVSVS GFSRVVLGMGELFRGHSKTREFLAHSAKVHSVAMSCGGRLASG SPDKTASVFLLEKDRLVKENNYRGHGDSVOQLCHPENPDLFVT AGGMTRI HÖVVSTTGK TATNYTRGHOSVOGLEPENPDLFVT AGGMTRI HÖVVSTTGK TATNYTRGHOSVOGLEPENPDLFVT AGGMTRI HÖVVSTTGK TATNYTRGHOSVOGLEPENPDLFVT AGGMTRI HÖVVSTTGK TATNYTRGHOSVOGLEPENPDLFVT AGGMTRI HÖVVSTTGK TATNYTRGHOSVOGLEPENPDLFVT AGGMTRI HÖVVSTTGK TATNYTRGHOSVOGLEPENPDLFVT AGGMTRI HÖVVSTTGK TATNYTRGHOSVOGLEPENDLFVT BEGTVLLGGGSPSTEFTVAMHEKRP LLAFACODKOGKTDSSR EGGTVLLFGLJAPD LLDVDELVCVRCPSRLDHPVRTLSFSHDGKMLASASEDHFIDIA EVETDBLIMBVQCESSFTFTVAMHEKRP LLAFACODKOGKTDSSR THLEVDTGTERNTYQASSAAFRYTAGTFYKVPTQAVTAPAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TTHLEVDTGTERNTYQASSAAFRYTAGTFYKVPTQFVTAAPAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWTYMPTAPATAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWTYMPTAPATAPA YNPSLYPTNSPSYAPEFQFLHAGAGAYTTQFVTAAPQFVTAH TTVQVPNSIPSATYPAQATAPATQCAYTTQFVTAAPQTPVTAHPATAPATTAPATAPATAPATAPATAPATAPATAPATA				
TSVDYSSVVTAMOARYAHIPOLIRMETMDVRXLDFPSASFIDVUL EKGTLDALLAGERDWTVSSEGVHTUDQVJSEVSRVILVPGGRFI SMTSRAPHFRTRHYAQAYYGMSLRHATYGSGFHFILLIMHKIGK LSVAQLALGAQILSPPRPTTSPCFLQOSDHEDFISATQL FRISGLAGGASALARIGGGLAGGVGWAGGAFGRGYMEGILTR CRALPALATCSRQLSGYVPCRFHHCAPRRGRRLLLSRVFQPQML REDRVLSLQDKSDDITCKSRGRIMLQVGLIYPASPCYHLLPHTV RAMELLWRVIDQBMQAIGGGKVMPSSLSPAELMQATRMNUMGK BLLRIRDRHGKEYCLGPTHERATTALIASGKKLSYKQLPFLLVQ VTRKRPDEPRPRGILLGRGEF YMKDMYTDSSPEAQQTYSLVC DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEPQLPVDIGEDRIA ICPRCSSSAMMETLDLSQMNCPACQSFLIKKTKGIEVGHTFYLDY VTRKRPDEPRPRGILLAGREF YMKDMYTDSSPEAQQTYSLVC DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEPQLPVDIGEDRIA ICPRCSSSAMMETLDLSQMNCPACQSFLIKKTKGIEVGHTFYLGT VXSSIFNAQFTNVCKYDLAMGCYGLGVTRILABALEVLSTED CVRWPSLLAPFYQACLIPPKKSSKSQAASELIGQLYDHITEAVPQ LHIGGVLLDDFTHLTIGNIKLGANNFQFPFVILAGKRALEDPAHF EVWCQNTGEVAFLTKGGVMDLLTFVQTV ADAGTRCTPGFVVPGGAGYSAFAQRGRRSSGRMRAAAPGLTAP WELQQCCEEBAGELGMAVPAAXMGFSPLGQSGPGSMAPWGSVSS GPSRVTASVFLLEEDRIJKLENAKVHSVAWSCDGTRLASG SPDKTASVFLLEEDRIJKENAKVHSVAWSCDGTRLASG SPDKTASVFLLEEDRIJKENAKVHSVAWSCDGTRLASG SPDKTASVFLLEEDRIJKENAKVHSVAWSCDGTRLASG SPDKTASVFLLEEDRIJKENAKVHSVAWSCDGTRLASG SPDKTASVFLLEEDRIJKENAKVHSVAWSCDGTRLASG SPDKTASVFLLEEDRIJKENAKVHSVAWSCDGTRLASG SPDKTASVFLLEEDRIJKENAKVHSVAWSCDGTRLASG SPDKTASVFLLEEDRIJKENAKVHSVAWSCDGTRLASG SPDKTASVFLLEEDRIJKENAKVHSVAWSCDGTRLASG SPDKTASVFLLEEDRIJKENAKVHSVAWSCDGTRLASG SPDKTASVFLLEEDRIJKENDENGENTATTAGRADALVS LUDVDELUCVRCPSRLDMFVTLSFSHDCKMLASASEDHFIDTA BUTTGDLAKTHSKAREQFFTVAMHPKRPLLAFACDDKGKXDSSR EAGTVKLFGLPNDS SSSRT SGSSTNRPYSTSPVQPGAPVGNRNMAYTGYPTAYPAAAPA VNPSLYPTNSSSVAPEFOPLISAVATLLMKQAWPONSSSCGTEG TFHLPYDTGTENRTYQAGSAAPRTYKYPPTUSTYPAPAAPA VNPSLYPTNSSSVAPEFOPLISAVATLLMKQAWPONSSSCGTEG TFHLPYDTGTENRTYQAGSAAPRTYKYPPTUSTYPAPAAPA VNPSLYPTNSSSVAPEFOPLISAVATLLMKQAWPONSSSCGTEG TFHLPYDTGTENRTYQAGSAPTYRQPVVAPATHAPACTYFTNGLY SSSRMPYGTAMYPRAGGTBYAKPRPCHLETSFLLSKG THADNNVITSLYLAVHLSGAAPACDGTTRMASAGTLL TTOGTATATGAHPYMBYTTAGGTTSVAYPPTH TTVQPNSIESALYPADAPTRAGGTBYAKPRPCHLETSFLLSKG LENDBESVYOLOGGLAQKLIGLWKARPPCDELTSFLLSKG SLALPHBEBSVYOLOGGLAQKLIGLWKARPPCDELTSFL	5578	3	783	AVESMASPGAGRAPPELPERNCGYREVEYWDQRYQGAADSAPYD
BRGTLDALLAGERDPHTVSSEGVHTVDOVLSEVSRULVPGGRF1 SMTSAAPHERRRYAGAYYGWSLRHATYGSGFHFHLYLMHKGK LSVAQLALGAQILSPPRPTTSPCTLQDSDHEDFLSAIQL 5579 3 1540 RNSGLAGGASALARHGGGLAGGVGMDCGACASRCOGVMBGLUTR CRALPALATCSRQLSGVVPCRPHAPRGRKILLSRVPQPOML REDRIVLSLQNKSDDLTCKSQRIMLQVGLIYPASPGCYHLLPYTV RAMEKLVRVIDQEMQAIGGGKVNMPSLSPABLMQATNRWDLMGK BLIKLRDRHGEVGLGPTHEBAILAGSKKISFKQLPFLLVQ VYTKKFRDEPRRFSGLLGGREFYMKDMYTPDSSPEAAQQTYSLVC DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRIA ICPRCSFSAMMETLDLSQNNCPACQGPLTKTKGIEVGHTFYLGT KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILABAIEVLSTED CYMPSPLAPYQAGLIPPKKGGAGVAPAGASELIGQLYDHITFAVPQ LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHP EWWQNTSBVAFLTKDGVWDLLTPVQTY LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHP EWWQNTSBVAFLTKDGVWDLLTPVQTY ARGORTIFINGVFTLGGAGVAPAAMGPSALGSGFOSMAPMCSVSS GPSRYVLGMQELFRGHSKTEFJAHSAKVHSVAWSCGGRLASG SPDKTASVFLLEKDRLVKENNINGENDSUCGCHANSPDLFVT ASGDRTIFIHDVRTTKCIATVKGENDIUCMSPDGGTIAVGNK DDVVTPIDAKTHRSKAEGPKFVENEISMNDNINMFLITGNGC INILSYPELKPVQSINAHPSNCICKFDPMGKYFATGSADALVS LMDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETDDKLMEVQCSSPTPTVAMPRRPLLAFACDKGKYDSKS EAGTVKLFGLDNDS 5581 54 947 GGGSGFRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFILABAYATLLMKQAWPONSSSCGTEG TFHLEVDTGTENRTYOASSAAFYTAGGTPYKWPTTOSNTAPPPY SPSPWPYGTAMYPIRSAYPOQNLVAQGAYYTOPVYAAQPHVIHH TTVQPNSIPSAIPSAVPARAFTNGVAMGMVAGTTMAMSAGTIL TTPGHTAIGAHPVSMPTYRAQGTPAYSVYPPHW FYDYDTTSMRTYTQASSAAFYTAGGTPYKWPTOSNTAPPY SPSPWPYGTAMYPIRSAYPOQNLVAQGAYYTOPVYAAQPHVIHH TTVQPNSIPSAIPPANSTAPRANGAMGMVAGTTMAMSAGTIL TTPGHTAIGAHPVSMPTYRAQGTPAYSVYPPHW FYDYDTTSMRTYQDSAAFARGRRAPARGKRKADI EKGLOFIOGSTEPLKQEEYARFLKVALNUGLFREDVYNG LEGGLGFROGLGLGKCLGLVANLANGRAVAGTTLL TTPGHTAIGAHPVSMPTYRAQGTPAYSVYPPHW FYDYDTSMPTYRAQGTPAYSTVPDHW FYDYDTSMPTYRAQGTPAYSTVPDHW FYDYDTSMPTYRAQGTPAYSTVPDHW FYDYDTLAPBLSVYTQCGELAQKLGRVANLANGRVAGTTLLDTRIDLYG LKALEDSSKALGLDSSSIRALFRKARALNEGRKKAEGSRC SLALPHDSSVYQLOGELAQKLGLYNLANGRVAGTTLLDSSL SLALPHDSSVYQLOGELAQKLGRVANLANGRVAGTTLLDSSL SLALPHDSSVYQLOGELAQKLGRVANLANGRVAGTTLLDSSL TAGWADGGTSNGLGSGUPSGLPG		•		WFGDFSSFRALLEPELRPEDRILVLGCGNSALSYELFLGGFPNV
SMTSAAPHERTRHYAQAYYGMSLARHATYGSGFHEHLYLMHKGGK LSVAQLALGQILSPPRPPTSPCFLQDSDHEDFLSAIQL 5579 3 1540 RRSGLARGASALARHGGGLAGGVGMCGACASRCQGVMEGLUTR CRALPALATCSRQLSGYVPCRFHHCAPRRGRELLLSRVFQPQNL REDRVLSLQDKSDLTCKSQRIMLQVGLIYPASPGCYHLLPYTV RAMEKLWRVIDQEMQAIGGGVNWPSLSPAELMQATNRWDLMSK ELLRIRDRHGGEYCLGPTHERAITALIASQKKLSYKQLPFLJYQ VTKKPRDPRPRFGLLERGREFYMWTYTDSSPEAAQQTYSLVC DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA ICPRCSFSAMMETLDLSQNNCPACQGPLTKKGIEVGHTFLGA VYSSIFNAQFTNVCGKPTLARMGCYGLGVTHILAAALEVLSTED CVRWPSLLAPYQACLIPPKKGSKEQAASELIQQLYDHITAAVPQ LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIJAGKRALEDPAHP EWCONTGEVAPITKGOVDLLTPYQTV 450 ADAGTRCITGFVVVSGAGYSAPAQRGRRSSGRMRAAAPGLTAP WRLLQCCELRAGELGMAVPAAMGPSALIQGSGPGSMAPMCSVSS GPSRTVLGMGELFRGHSKTRETLAISAKVHSVAWSCDGRLASG SPDKTASVFLLEKDRLVKENNYRGHGDSVDJCWHPSNPDLFVT AGGDKTIRIBVDRTTKCLATVYTKKGHINICKSPGGTIAVGNK DDVVTFIDAKTHRSKABEQFKFEVNEISWNNDNMFFLTMGNGC INILSYPELKPVQSINAHPSNCICIKFPSHGKMLASASEDHFIDIA EWETGDKLMEWQCSSPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMMPVYSDVQPGAPYGNFKMMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFOFLHSAYATLLMKQAWPONSSCGTEG TTHLEVDTGTENRTYQASSAATYTAGGTPYKVPTOSNTAPPPY SPSPMPYGTAMYPIRSAYPQQNLYAQGAYTYQFVYAAQPHVIHH TTVVQDNSIPSAITAPAVAAPSTURGHYKWAMMAGTLTMMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 ITTNNNNVITPLVTAYHLSGSAQARGERSPARRMERQKKKADI EKGLOFIOSTDIKKGESYBAFLKKLVQNIFABGNDLFREDYYQ ALVQYMEGLNVADYAASQUVALPRELLCKLHVMRAACYPTMGLY EKALBDSSKALGLDSSSIRALFRKRALNIGGRKEAPYECSSRC SLALPHDSSVQILOGELAQKLIGKVRKAYKRPQELETTSILSISG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPINDLF PHVLDLLAPLDSSRTLPSTDSDDDFDDDVPGSPALLPSTPINDLF PHVLDLLAPLDSSRTLPSTDSDDDFDDDVPGSPALLPSTPINDLF PHVLDLLAPLDSSRTLPSTDSDDDFDDDVPGSPALLPSTPINDLF PHVLDLLAPLDSSRTLPSTDSDDDFDDDVPGSPALLPSTSSDLPD PHVLDLLAPLDSSRTLPSTDSDDDFDDDVPGSPALLPSTSSDLPD PHVLDLLAPLDSSRTLPSTDSDDDFDDDVPGSPALLPSTSSDLPD PHVLDLLAPLDSSRTLPSTDSDDDFDDDVPGSPALLPSTSSDLPS PHVLDLLAPLDSSRTLPSTDSDDDFDDDVPGSPALLPSTSSDLPS PHVLDLLAPLDSSRTLPSTDSDDDFDDDVPGSPALLPSTSDLSDFD	ì	İ	1	TSVDYSSVVVAAMQARYAHVPQLRWETMDVRKLDFPSASFDVVL
LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDFLSAIQL 5579 3 1540 RNSGLARGASALARHGGGLAGGVØDCGACAGRCQGVMEGLTR CRALPALATCSRQLSGVVPCRFHHCAPRGORRLLLSRVPQPQNL REDRVLSLQDKSDDLTCKSQRLMLQVGLIYPASPGCYHLLPTYV RAMEKLVRVIDQEMQAIGGQKVMPSLSPAELWQATNRNDLMKK BLLRLRRNRHGKYCLGFTHERATTALIASQKKLSYKQLPFLLYQ VYTKYRDBPRPRFGLLRGREFYMKDMYTDSSPEAAQQYTSLVC DAYCSLFRKLGLIPPKVQADDVGTIGGTVSHEFQLPVDIGEDRIA ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT KYSSITMAQFTNLOWGRTLAGMCYGLGVTRILAAAIEVLSTED CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYPHITEAVPQ LIGGVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHP EWCQONTGEVAFLTKDGVMDLTPVQTV 5580 1681 450 ADAGTRCTFGFVVPSGAGYSAPAQRGRRSSGRMRAAAPGLTAP WRLLQCCELEAGELGMAVPAAAMGFSALGGGFGSMAPMCSVSS GPSRYVLMQBLFKGHSKTBFLAHSAKVHSVWSCDGRRLASG GPSRYVLMQBLFKGHSKTBFLAHSAKVHSVWSCDGRRLASG SPDKTASVFLLEKDRLVKENNYRCHGDSVDQLCWHPSNPDLFVT ASGDKTIRIMDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK DDVVTFIDAKTHRSKAERGFFEVNEISMNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFPWNGKYPATGSADALVS LMDVDELVCVRCPFSRLDMPVSTSFBIDGKMLASASEDHFIDIA EVETTDKLWEVQCSSPTFTVAWHPKRPLLAFACDDKDKGKYDSSR EAGTVLLRGLENDS EXGTVLLRGLENDS THELPVDTGTERRTTQASSAAFRYTAGTPYKVPPTOSNTAPPPY SPSPMFYGTAMYPIRSAAFQCHAYATLHMKQAWPQNSSSCGTEG TFHLPVDTTSRRTTQASSAAFRYTAGTPYKVPTOSNTAPPPY SPSPMFYGTAMYPIRSAYPQCMAYTQCYTAMPANAGGTLL TTPQRTAIGAHPVSMPYTRAQGTPAYSYVPPHW TTVQVPNSIPSAITPAQGTTAYSYVPPHW TTVQVPNSIPSAITPAQGTTAYSYVPPHW EKGLGPIGSTEPLKQEEVRAFLKLVONLFPREGNDLFREENDYKQ ALVQYMEGLNVADYAAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESTRALFREARLBEGRIKKARTGSRC SLALPDBSSTYLGGELAQKLGRVTRAYKRPQELETFFSLLSNG TAAGVADQGTSNGLGSIDDISTDCVVPGGSPALLPSTPTMPLF PHVLDLLAPLDLSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGGSVPSSELPQLIPVFPGGTPLLPPLVVGGSTPVSSPLLP				BKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSRVLVPGGRFI
LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDFLSAIQL 5579 3 1540 RNSGLARGASALARHGGGLAGGVØDCGACAGRCQGVMEGLTR CRALPALATCSRQLSGVVPCRFHHCAPRGORRLLLSRVPQPQNL REDRVLSLQDKSDDLTCKSQRLMLQVGLIYPASPGCYHLLPTYV RAMEKLVRVIDQEMQAIGGQKVMPSLSPAELWQATNRNDLMKK BLLRLRRNRHGKYCLGFTHERATTALIASQKKLSYKQLPFLLYQ VYTKYRDBPRPRFGLLRGREFYMKDMYTDSSPEAAQQYTSLVC DAYCSLFRKLGLIPPKVQADDVGTIGGTVSHEFQLPVDIGEDRIA ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT KYSSITMAQFTNLOWGRTLAGMCYGLGVTRILAAAIEVLSTED CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYPHITEAVPQ LIGGVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHP EWCQONTGEVAFLTKDGVMDLTPVQTV 5580 1681 450 ADAGTRCTFGFVVPSGAGYSAPAQRGRRSSGRMRAAAPGLTAP WRLLQCCELEAGELGMAVPAAAMGFSALGGGFGSMAPMCSVSS GPSRYVLMQBLFKGHSKTBFLAHSAKVHSVWSCDGRRLASG GPSRYVLMQBLFKGHSKTBFLAHSAKVHSVWSCDGRRLASG SPDKTASVFLLEKDRLVKENNYRCHGDSVDQLCWHPSNPDLFVT ASGDKTIRIMDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK DDVVTFIDAKTHRSKAERGFFEVNEISMNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFPWNGKYPATGSADALVS LMDVDELVCVRCPFSRLDMPVSTSFBIDGKMLASASEDHFIDIA EVETTDKLWEVQCSSPTFTVAWHPKRPLLAFACDDKDKGKYDSSR EAGTVLLRGLENDS EXGTVLLRGLENDS THELPVDTGTERRTTQASSAAFRYTAGTPYKVPPTOSNTAPPPY SPSPMFYGTAMYPIRSAAFQCHAYATLHMKQAWPQNSSSCGTEG TFHLPVDTTSRRTTQASSAAFRYTAGTPYKVPTOSNTAPPPY SPSPMFYGTAMYPIRSAYPQCMAYTQCYTAMPANAGGTLL TTPQRTAIGAHPVSMPYTRAQGTPAYSYVPPHW TTVQVPNSIPSAITPAQGTTAYSYVPPHW TTVQVPNSIPSAITPAQGTTAYSYVPPHW EKGLGPIGSTEPLKQEEVRAFLKLVONLFPREGNDLFREENDYKQ ALVQYMEGLNVADYAAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESTRALFREARLBEGRIKKARTGSRC SLALPDBSSTYLGGELAQKLGRVTRAYKRPQELETFFSLLSNG TAAGVADQGTSNGLGSIDDISTDCVVPGGSPALLPSTPTMPLF PHVLDLLAPLDLSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGGSVPSSELPQLIPVFPGGTPLLPPLVVGGSTPVSSPLLP	ŀ			
1540 RNSGLARGASALARHGGLAGGVGWDCGACASRCQGVMEGLLTR CRALPALATCSRQLSGVVPCRFHHCAPRIGRILLISPTVPQRONL REDRIVISLQDUSDLTCKSGRIMLQVGLIYPASPGCYHLLPTV RAMEKLVRVIDQEMQA.IGGQKVMMPSLSPAELMQATNRWDLMGK ELLRLRDRHGKEYLGPTHERAITALIASQKKLSYKQLPFLLYQ VTRKFRDEPRFRFCLLKGREFYMKDMTFDSSPEAAQQTYSLVC DAYCSLFRKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRIA ICPRCSFSANMETLDLSQMNCQGDLTRKKGLEVGHTFYLGT CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ LIGGULLDDRTHLITIGRRLADDAKPGYPFVILAGKRALEDPAHF EVWCQNTGBVAFLTKDGVMDLLTPVQTV 5580 1681 450 ADAGTRCITGFVVPSGAGYSAPAQGGRESGGRMAAAAPGLTAP EVWCQNTGBVAFLTKDGVMDLLTPVQTV ASGDKTIASVFLLEKGRLVKENNYRGHSGGRGSGRMAPAGCSVSS GPSRYVLMQELFRGHSKTRFFLAHSAKVISVXWSCDGRLASG SFDKTASVFLLEKGRLVKENNYRGHDINTCWSPDGQTIAVGNK DDVVTFIDAKTHRSKABEQFKFEVNBISMNDNMFFLTINGNC LINILSYPELKPVQSINAHPSNCICIKFDPWGKYFATGSADALUS LMDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCSSPTFTVAWHBKRPLLAFACDDKDGKYDSSR EAGTVALFGLBMDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAVFACS CSPDPQSSTMMEVYSPVQPGAPYGNFKNMAYTGYPTAYPAAAPA VYPSSLYPTINS SYAPEFOFLIAATAILLMKOMPONSSCGTET THLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAAPPPY SPSPMPYGTAMYPIRSAYPQQNLYAQGAYTQDVYAAQPHVIHH TTVVQPNSIPSAITVPAVAARPTRIGVAMGWVAGTTMMMSAGTLL TTPQHTAIGAHDVSMPTRAGGTDAYSYVPPHW 5582 5775 2739 ITINNNNVIITPLVIAYHLSGSAQARGERSPARERLMERQKKRADI EKGLGFIQSTLPLKQEEVERAFLLKLVQNLFPAGKONLFREKDYNQ ALVQYMGGLIVAUADYAASDQVALPPELLCKLHVNRAACYFTMGLY EKALEDBSKALGLISSESIRALFRKRARALNELGRHKEAYECSSRC SLALPHDSSVTQLGGELAQKLGRVNRAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETCCVUPRGGPALLDFSLLSNG TAAGVADQGTSNGLGSIDDIETCCVUPRGGPALDFSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSLL VQQGLSGGSGVFSELPQLITVPFPGGTPLLDPLVVGGSIPVSPSLPP	j			· · · · · · · · · · · · · · · · · · ·
CRALPALATCSRQLSGYVPCRFHHCAPRRGRRLLLSRYFQPQNL REDRVLSLQDKSDDLTCKSGRIALGVGLIYPASPGCYHLLPYTV RAMEKLIVRVIDGEMQAIGGGVKNMPSLSPAELMQATNRNDLMGK BLLRLRDRHGKEYCLGPTHERAITALIASQKKLSYKQLPFLLYQ VTRKREBERRFFELLKGREFYMKDMYTFDSSPEAAQOTYSLVC DAYCSLFRKLGLIPPKVQADLVGTIGGTVSHEFGLPVDLIGEDRIA ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILAAAIEVLSTED CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYPHITEAVPQ LHGEVLLDDRTHLTIGRRLKDAKKFGYPFVIIAGKRALEDPAHF EWCQNTGBVAFLTKDGVMDLLTPVQTV 5580 1681 450 ADAGTTCIPGFVVPSGAGYSAPAQRGRRSSGRMRAAAPGLTAP WRLLQCCSLEAGELGMAVPAAAMGPSALGOSGPGSMAPMCSVSS SPDKTASVVLEMGELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG GPSRYVLGMCLEKRDLYKGTHSTNTWGENINICWSPDGGTIAVGNK DDVVTFIDAKTHRSKABEQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKEVQSINAHPSKICIKFDPMGKYTATGSADALVS LWDVDELVCVRCFSRLDDPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCBSPTFTVAWHPKRPLLAFACDDKDGKYDSSR RAGTVKLBGLENDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPETGFLHSAYATLLMKQAMPQMSSSCGTEG TFHLPVDTGTERRTVQASAAFRYTAGTPVKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQQAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAVAAPRTNGVAMGMVAGTTMMMSAGTLL TTPGHTAIGAHPVSMPTYRAQGTPAYSYVPPHW TTVVQPNSIPSAIYPAVAAPRTNGVAMGMVAGTTMMMSAGTLL TTPGHTAIGAHPVSMPTYRAGGTPAYSYVPPHW TTVVQPNSIPSAIYPAVAAPRTNGVAMGMVAGTTMMMSAGTLL TTPGHTAIGAHPVSMPTYRAGGTPAYSYVPPHW EKALEDSEKALGLDSSITALFRKARALNELGRIKERYECSSKC SLALPHDESVTQLGGELARLLGLVGNKKAYKRPGELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCVVDPRGSPALLPSTPTMPLF EKALEDSEKALGLDSSITALFRKARALNELGRIKERYECSSKC SLALPHDESVTQLGGELARLGLGRVRKAYKRPGELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCVVDPRGSPALLPSTPTMPLF PHVLDLLAPLDLSRTDSLDDFSDGDVMPGEDDTLLDSLSL VQGGLSGSGVPSELPQLIPVPPGGSTPLDPPVVGGSIPVSSPLPP		ļ	1540	
REDRVLSLQDKSDDLTCKSQRIMLQVGL1YPASPGCYHLLPYTV RAMEKLVRVIQDEMAJGGQKVMADAGGGYATRWDLMGK BLLRIRDRRIGKSYCLGPTHERAITALIASQKKLSYKQLPFLLYQ VTKKFRDBPRPRFGLRGREFYMKDMYTPDSSPEAAQQTYSLUC DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA ICPRCSFSANMETLDLSQMNCPACQSPLKKTKGISVGHTFYLGT KYSSIFNAQFTNVCSKPTLAEMGCYGLGYTRILAAAIEVLSTED CVRWPSLLAPYQACLIPPKKSGKEQAASELIGQLYDHITEAVPQ LHGEVLLDDRTHLITIGNRLKDANKFGYPFVIIAGKRALEDPAHF EWWCONTGEVAFLITKDGYMDLLTPVQTV 5580 1681 450 ADAGTRCIPGFVVPSGAGYSAPAQGGRRSSGRMRAAAPGLTAP WRLLQCCELERAGELSMAVPAAMMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG SPDKTASVBLLEKDRLVKENNYKGHGDSVDQLCWHENPIDLFVT ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK DDVVTPIDAKTHRSKABEGFKFEVWEISMNNDNNMFFLINGNGC LINILSYPELKPQSINAMPSNCICIKFPDMGKYFATGSADALVS LMDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLMEVQCSSPTFTVAWHPKRPLLAFACDKDKGKYDSSR EAGTVALFGLPNDS 5581 54 947 GGGSGFRAPSATLLDTGSSVANASGEDKGIAASAAAAVFACS CSPDPQSSTMNEVYSPVQPGAPYGMFKMNAYTGYPTAYPAAPA YNFSLYPTNSPSYSPOPFGPLHSAYATLLMKQAWPONSSSCGTEG TFHLPVDTGTENRTVQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQDNLYAQGAYYTQPVYAAQPHVIHH TTVQPNSIPSAIYPAVAAPRTNGVAMMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 1TTNNNNVIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQESYRAFLLKLVQNLFAEGNDLFREDYKQ ALVQYMGGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGIY, ALVQYMGGLNVADYAASDQVALPRELLCKLHVRAACYFTMGIY, ALVQYMGGLNVADYAASDQVALPRELLCKLHVRAACYFTMGIY, CKALEDSEKALGLDSSSIRALFKKRALINELGRHKEAYECSSRC SLALEDSESVTOLGGELAQKLGLRVKAYKRPQEBETFSILLSING TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTTPMPLF PHVLDLLAPLDSSRTLPSTGSTDDFSDGDVFGFBELDTLLDSISLL VQGGLSGSGVPSSLPQLIFVFPGGTFLLPPVVGGSIPVSSPLPP	5579	, 3	1540	
RAMEKLVRVIDQEMQAIGGQKVNMPSLSPAELWQATNRNDLMGK ELLRLRDRRGKSYCLGPTHERAILASQKKLSYKQLPFLLYKY VTRYRDBEPRFGLLRGEFYMKDMYTPDSSPEAQQTYSLVC DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA ICPRCSFSANMETLDLSQMNCPACQSPLTKTKIGLEVGHTYLISTED KYSSIFNAQFTVVCKSPTLAEMGCYGLGYTRILABAIEVLSTED CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ LHGEVLLDDRTHLITIGNRLKDANKFGYPFVIIAGRAEDPAHF EWWCONTGEVAFLITKDGYMDLITPVQTV 5580 1681 450 ADAGTRCIPGFVVPSGAGYSAPAQRGRRSSGRMRAAAPGLTAP WWRLLQCCELEAGELGMAVPARAMGPSALGQSGFGSMAFWCSVSS GPSRTVLGMQELFGGHSKTFLAHSAKVHSVAWSCDGRRLASG SPDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIRIWDVRTTKCIATVMTKGENINICKSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEGFKFEVWEISMNDNMFFITINGNOC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LMDVDELVCVRCFSRLDWVRTLSFHDGKMLASASEDHFIDIA EVETGBKLWEVQCESFTFVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAANVFACS CSPDPQSSTMNPVYSPVQPGAPYGRFKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTERRTVQASSAARTYLTAGTFYKVPPTQSNTAPPFY SPSPNPYQTAMYPIRSAYDQOKLYAQGAVYTOPVYAAQPAVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW EKGLOFIQSTLPLKQEEYBAFLLKKLVQNLFAEGNDLFREKDYKQ ALVQYMGGLNVADYAASDQVALPRELLCKLHVARAACYFTMGLY EKGLOFIQSTLPLKQESYBACHLERKPKRALKEGSSRC SLALPHDESVTQLGQELAQKLGLRVKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTFTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGFBELDTLLDSLSL VQGGLSGSGVPSELPQLIPVPGGTPLLPPVVGGSIPVSSPLPP		1	Ì	
BLIRLRDRHGKEYCLGPTHERAITALIASQKKLSYKQLPFLLYQ VTRKFRDBPRPREGLLRGREFYMKDMTTPDSSPEAQQTYSIVC DAYCSLFNKLGLPFVKNDMTTPDSSPEAQQTYSIVC DAYCSLFNKLGLPFVKNDMTTPDSSPEAQQTYSIVC DAYCSLFNKLGLPFVKNGLGPFVKDDTGEDRLA ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILABAIEVLSTED CVRWPSLLAPAYQACLIPPYKGSKEQAASELJGQLVDHITEAVPQ LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF EWCONTGEWAFLIKDGVMDLLTPVQTV 5580 1681 450 ADAGTRCIPGFVVPSGAGYSAPAQRGRRSSGRMRAAAPGLTAP WRLLQCCELEAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRLASG SPDKTASVFLLEKDRIVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK DDVVTFIDAKTHRSKAEQFKFEVNEISWNDNNFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTPTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFCLPNDS 5581 54 947 GGGSGPRAPSATLLIDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKMAYTGYPTAYPAAAPA YNPSLVPTNSPSYAPEFQFLHSAYATLLMKQAWPONSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPBY SSSPNPYQTAMYPIRSAYPQONLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSATYPAVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW SSSPNPYQTAMYPIRSAYPQONLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSATYPAVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMGGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKGLEDFSVTQLGGELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTTMPLF PHVLDLLAPLDSSRTLPSTGLDDFSDGDVSGPELDTLLDSLSL VQGGLGSGVPSSLPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	}			
VTRKFRDEPRPGLLRGREFYMKDMYTFDSSPEAAQQTYSLVC DAYCSLFNRLGLPFVKVQADVGTTIGGTVSHEFQLPVDLGEBRIA ICPRCSFSAMMETLDLSOMMCPACQGPLTKTKKGIEVGHTFYLGT KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILAAAIEVLSTED CVRWPSLLAPYQACLIPPKGSKRQAASELIGQLYDHITEAVPQ LHGEVLLDDRTHLTIGNRLKOANKFGYPFVIIAGKRALEDPAHF EVWCQNTGEVAFLTKDGVMDLLTPVQTV 5580 1681 450 ADAGTRCIPGFVVVSGAGYSAPAAQGGRRSSGRMRAAAAPGLTAP WRLLQCCELEAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS GPSRYULGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG SPDKTASVFILLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPPOGYTAVGNK DDVVTFIDAKTHRSKAREQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICKFPPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEHFIDIA EVHTGDKLMEVQCESPTFTVAWHKRFLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMATTGYPTAYPAAAPA YNPSLVPTNSPSYAPEFQFLHSAYATLLMKCAWPONSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SSPSNPYQTAMYPIRSAYPQONLYAQGAYYTQPVVAAQPHVIHH TTVVQPNSIPSAIYPASVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSVVPPHW TTVVQPNSIPSAIYPAVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSVVPPHW EKGLQPIQSTLPLKQEEYEAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMGGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKGLEPIGSTLPLKQEEYEAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMGGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKGLEPIGSVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCVVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDJDFSDGDVFGBEBLTLLDSLSL VQGGLGSGVPSSLPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP			1	1
DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA ICPRCSFSAMMETLDLSQMNCPACQGPLITKTKGIEVGHTFYLGF KYSSIFNADPTNVCSKTLAMEGYCJGUTRILAAAIEVLSTED CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIJAGKRALEDPAHF EVWCQNTGBVAFLTKDGWMCLLTPVQTV 5580 1681 450 ADAGTRCIPGFVVPSGAGYSAPAQRGRRSSGRMAAAAPGLTAP WKLLQCCEERAGEGMAVPAAMMGPSALGGSGPSMAPWCSVSS GPSRYTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEQFKEVWEISMNDNNMFFLINGNGC INLISYPELKPVQSINAHPSNCICIKFDPMSKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGNKLWEVQCSSPTTTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGFRAPSATLLDTGESVAAVASGEDKGIAASAAAAVFACS CSPDPQSSTMNPV3PVQPGAPYGNFKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYOASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAVAAPRTNGVAMGWVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 ITTNNNVITPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFTQSTLPLKQEEVRAFLIKLUQNLFABGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKKALEDSEKALGLDSESTRALPRKAPALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHYLDLLAPLDSSRTLPSTDSLDDFSGDDVFGSPALDFSTPTMPLF PHYLDLLAPLDSSRTLPSTDSLDDFSGDDVFGSPALDFSTPTMPLF PHYLDLLAPLDSSRTLPSTDSLDDFSGDDVFGSPALDFSTPTMPLF PHYLDLLAPLDSSRTLPSTDSLDDFSGDDVFGSPALDFSTPMBLF PHYLDLLAPLDSSRTLPSTDSLDDFSGDDVFGSPALDFSTPMBLF PHYLDLLAPLDSSRTLPSTDSLDDFSGDDVFGSPALDFSTPMBLF PHYLDLLAPLDSSRTLPSTDSLDDFSGDDVFGSPALDFSTPMBLF PHYLDLLAPLDSSRTLPSTDSLDDFSGDDVFGSPALDFSTPMBLF PHYLDLLAPLDSSRTLPSTDSLDDFSGDDVFGSPALDFSTPMBLF PHYLDLLAPLDSSRTLPSTDSLDDFSGDDVFGSBGDTTLLDSLSL VQGGLGGSGVPSELPQLIFVFPGGTPLLPPVVGGSIPVSSPLPP	Ì	}	į.	
ICPRCSFSAMMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT XYSSIENAGTTNVGKETLAEMGCYGLGYTRILAAAIEVLSTED CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ LHGEVLLDDETHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF EWCQNTGEVAFLTKGGWMDLLTPVQTV 5580 1681 450 ADAGTRCIPGFVVPSGAGYSAPAGRGRRSSGRMRAAAAPGLTAP WRLLQCCELERGEELGMAYPAARMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG SPDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPERPDLFVT ASGDKTIRIWDVRTTKCLATVNTKGENINICWSPDGQTIAVGNK DDVYTFIDARTHRSKAERQFKFEVHEISWNNDNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCSSPTVVWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAVFACS CSPDPQSSTINNPYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNFSLYPTNSPSYAPEFOFLHSAYATLLMKQAWPCNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQMLYAQGAYYTQPVYAAQPHVIHH TTVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTTRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEVEAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRIKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVKKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPMPLF PHYLDLLAPLDSSRTLPSTDSLDDFSDGDVFGFBLDTLLDSLSL VQGGLSGSVPSELPQLIFVFPGGTPLLPPVVGGSIPVSSPLPP	1	ŀ		VTRKFRDEPRPRFGLLRGREFYMKDMYTFDSSPEAAQQTYSLVC
KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILAAAIEVLSTED CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ LHGEVLLDDRTHLTIGNRLKDANKFGYPPVIIAGKRALEDPAHF EWCQNTGBVAFLTKDGVMDLLTPVQTV 5580 1681 450 ADAGTRCIPGFVVPSGAGYSAPAGGRRSSGRMRAAAPGLTAP WRLLQCCELEAGELGMAVPAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRLASG SPDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIRIMDVRTTKCIATVNTKGBINICWSPDGGTIAVGNK DDVVTPIDAKTHRSKAEEQFKFEVNEISWNNDNMFFLITNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFVVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMMFVYSPVQPGAPYGNPKMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTVQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQONLXQGAYYTQPVYAAQPHVIHH TTVQQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKERAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHULDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSISL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	l	}		DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA
CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ LHGEVLLDDETHLTTGRELKDANKFGYPFVIIAGKRALEDPAHF EVWCQNTGEVAFLTKDGVMDLLTPVQTV 5580 1681 450 ADAGTRCIFGFVVPSGAGYSAPAQRGRESSGRMRAARAPGLTAP WRLLQCCELEAGELGMAVPAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQBLFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG SPDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIRIWDVRTTKCIATVNTKGENINICMSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLENDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMMPVYSPVQDGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYFTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQONLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNVIIPLVIAYHLSGSAQARGERSPAERLMERGKKKADI EKGLQFTQSTLPLKQBESYBAFLLKLVQNLFAEBMDLFREKDYK ALVQYMEGLNVADYAASDQVALPPSLLCKLHVNRAACYFTMGLY EKALEDBEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQBLAQKIGLEVRKAYKRPQBLETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHULDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	j			ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT
CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ LHGEVLLDDETHLTTGRELKDANKFGYPFVIIAGKRALEDPAHF EVWCQNTGEVAFLTKDGVMDLLTPVQTV 5580 1681 450 ADAGTRCIFGFVVPSGAGYSAPAQRGRESSGRMRAARAPGLTAP WRLLQCCELEAGELGMAVPAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQBLFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG SPDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIRIWDVRTTKCIATVNTKGENINICMSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLENDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMMPVYSPVQDGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYFTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQONLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNVIIPLVIAYHLSGSAQARGERSPAERLMERGKKKADI EKGLQFTQSTLPLKQBESYBAFLLKLVQNLFAEBMDLFREKDYK ALVQYMEGLNVADYAASDQVALPPSLLCKLHVNRAACYFTMGLY EKALEDBEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQBLAQKIGLEVRKAYKRPQBLETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHULDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	į.			KYSSIFNAOFTNVCGKPTLAEMGCYGLGVTRILAAAIEVLSTED
LHGEVLLDDRTHLTIGNRLKDANKPGYPFVIIAGKRALEDPAHF EWWCQNTGBVAFLTKGGVWDLLTPVQTV 5580 1681 450 ADAGTRCIPGFVVPSGAGYSAPAQRGRSSGRWRAAAAPGLTAP WRLDGCELEAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG SPDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTTRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGRGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGIKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNFSLYPTNSPSYAPETQHSASAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQONLYAQGAYYTOPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 ITTNNNNVIIPLVIAYHLGGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGGELAQKLGLRVRKAYKRPQELETTSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP			·	1 · · · · · · · · · · · · · · · · · · ·
EVWCQNTGEVAFLTKDGVMDLLTPVQTV 5580 1681 450 ADAGTRCI PGFVVPSGAGYSAPAQRGRSSGRMRAAAAPGLTAP WRLLQCCELEAGGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG SFDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIRIWDVRTTKCLATVNTKGENINICWSPDGGTLAVGNK DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNFVYSPVQPGAPYGNFKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTERRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 ITMNNNVIIPLVIAYHLIGGSAQARGERSPAERLMERQKKKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGGELAQKLGLRVRKAYKRPQELETTSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDGLSLS VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP		(
ADAGTRCIPGFVVPSGAGYSAPAQRGRRSSGRMRAAAAPGLTAP	1	1		
WRILQCCELEAGEIGMAVPAAMGPSALGQSGPGSMAPWCSVSS GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG SPDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIR IMDVRTIKCIATVNTKGENINICWSPDGOTIAVGNK DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRILSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQONLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSNPTYRAQGTPAYSTVPPHW 5582 5775 2739 IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGGELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHYLDLLAPLDSSRTLPSTDSLDDFSDGDVFGSPALDFSTPTMPLF PHYLDLLAPLDSSRTLPSTDSLDDFSDGDVFGSPALDFSTPTMPLF PHYLDLLAPLDSSRTLPSTDSLDDFSDGDVFGSPALDTLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP			150	
GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG SPDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIR IMDVRTTKCIATVNTKGENINI CWSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLVAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSALYPAPVAAPARTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITMNNNVITPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESTRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSILLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTYDMPLF PHYLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPBLDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	5580	1681	1	
SPDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTMGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAVATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIBSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCTVDPRGSPALLPSTPINPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP		The comment of the state of	Andrew James Library Service	
ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 ITTNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVKKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP		1		GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG
DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCBSPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	1	1	1	
INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQONLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	}	l		ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK
LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW EKGLQFIQSTLPLKQESYBAFLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKGLEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	1	1		DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC
EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYEAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP		1	{	INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS
EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYEAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	}	1]	LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA
EAGTVKLFGLPNDS 5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYEAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	1	1		
5581 54 947 GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYK ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	1			
CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGINVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	FERS	 	DA 7	
YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITMNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMGGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	2281	34] 34/	
TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	1	1		~ · · · · · · · · · · · · · · · ·
SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELBTFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	1	1	}	
TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITMNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP			1	
TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW 5582 5775 2739 IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	1	1	1	SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH
5582 5775 2739 IITMNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	,			TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL
5582 5775 2739 IITMNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP				
EKGLQFIQSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	5582	5775	2739	IITNNNNVIIPLVIAYHLSGSAOARGERSPAERLMEROKRKADI
ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP		1	1	
EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP				
SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	1		(
TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP	1	1	1	
PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP			1	
VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP			1	T TAAGVADOGUSNGIGS IDD DETOCYVDPRGSPALLPSTPTMPLF
			1	
acressmoderkt.aacut.nat.nooccort.not.nis.pvcerri.nat.				PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL
ASTOLIVING VIDALIDE TO LIBER				PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP

SEQ Predicted nucleotide location corresponding to first amino acid sequent containing signal peptid (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, E=Phenylalamine, G=Glycine, H=Histidine, I=Isoleucine, K=Iysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, C=Glutamine, R=Arginine, S=Serine, T=Threonine, N=Asparagine, P=Proline, C=Glutamine, R=Arginine, S=Serine, T=Threonine, N=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, N=possible nucleotide
No: nucleotide location corresponding to first amino acid amino acid residue of amino acid sequence se
Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence Peroline, Q=Glutamine, R=Arginine, Residue of amino acid sequence S=Serine, T=Threonine, V=Valine, Codon, /=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide insertion DSFGSTRGSLDKPDSFMEETINGDHPPSGACKPAPSPEPCMP
L=Leucine, M=Methionine, N=Asparagine, p=Proline, Q=Glutamine, R=Arginine, residue of amino acid sequence S=Serine, T=Threonine, V=Valine, w=Trytophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
to first amino acid residue of amino acid residue of amino acid sequence P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, amino acid sequence P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, V=Serine, T=Threonine, V=Valine, V=Serine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Serine, V=Threonine, V=Valine, V=Valine, V=Valine, V=Valine, V=Serine, V=Threonine, V=Vali
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DSFGSTRGSLDKPDSFMEETNSQDHRPFSGAQKPAPSPEPCMPI TALLIKNPLANTHEFKQACQLCYPKTGPRAGDYTYREGLEHKCI RDILLGRLRSSEDQTWKRIRPRPTKTSFVGSYYLCKDMINKQDC KYGDNCTFAYHQBEIDVWTEERKGTLNRDLLFDPLGGVKRGSLI IAKLLKEHQGIFTFLCEICTDSKPRIISKGTKDSFSVCSNLAAI HSFYNNKCLVHIVRSTSLKYSKIROFQBHFOFDVCRHEVRYGGI REDSCHFAHSFIELKVWLLQQYSGNTHEDIVQESKKYWQQMEAI AGKASSSMGAPRTHGBSTFDLQMKFVCGQCWRNGQVVGPDKDLI YCSAKARHCWTKERRVLLVWSKAKRKWVSVPPLPSIRNFPQQYT LCHAQNGRKQCQYGNGSFAHSPEERDMWTFMKENKILDMQQTT DMWLKKHNPGKPGGGTPISSREGEKQIQMPTDYADIMMGYHCWI CGKNSNSKKQWQQHIQSEKKKEKYFTSDSDASGMAFRFPMGEFS LCDRLOKGKACPDGDKCRAGQEELNEWLDRREVLKQKLAKAA KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE SSGCRGCRFGRSDRPRPPFPRRHKWKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYT QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERGKNV- HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI CKGRGMHIHQGIGFGWVQQICTVCIECKGGGERINFRDRCESG SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQDSEALCGFKKTIKTLDNRI SGCCRGGFGFGSDRPRPPPRPRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYT PERHWISLEKLPQLEALLPPRQKVRITDDMQVELKEFCPNEON WRQHREAYEEDDGPQAGVOCOTA SGCCRGGRFGSDRPRPPPPRPRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYT QGGEQAIKEGGSSPSPSSPPRDFFFFGGGGRMARERGKNV- HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYT QGGEQAIKEGGSSPSPSSPSPRRPPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYT QGGEQAIKEGGSSPSPSSPSPRRPPPPRPRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYT QGGEQAIKEGGSSPSPSSPSPRRPPPFRGRGGGRGRNARERGKKNV- HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI CKGRGMHIHQQIGPGMVQQICTVCIECKGGGGRINFKDRDCESG SGAKVIREKKIIEVHVEKGMKDQQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHBLIMKMKIQSSEALCGFKKTIKKTLDNRI IVLDQKDHSVFQRRGHBLIMKMKIQSSEALCGFKKTIKKTLDNRI
residue of amino acid sequence W-Tryptophan, Y-Tyrosine, X-Unknown, *=stop Codon, /=possible nucleotide deletion,
amino acid sequence Codon, /=possible nucleotide deletion,
=possible nucleotide insertion
DSFGSTRGSLDKPDSFMEETINSQDHRPPSGAQKPAPSPEPCMPI TALLIKNPLAATHEFKQACQLCYPKTGPRAGPYTYREGLEHKCI RDILLGRIRSSEDQTMKRIRPRPYKTSFVGSYYLCKDMINKQDG KYGDNCTFAYHQEEIDVWTEERKGTLNRDLLFDPLGGVKRGSLT IAKLLKEHQGIFTFLCEICFDSKPRIISKGTKDSPSVCSNLAAI HSFYNNKCLVHIVRSTSLKYSKIRQFQBHFQFDVCRHEVRYGCI REDSCHPAHSFIELKVWLLQQYSGMTHEDIVQESKKYWQQMEAR AGKASSMGAPRTHGPSTPDLQMKFVCGQCWRNGQVVEPDKDLF YCSAKARHCWTKERRVLLVMSKAKKKWVSVRPLPSIRNFPQQYI LCHHAQNGRKCQYVGNCSFAHSPEERDWHTPMKENKILDMQQTY DMWLKKHNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWI CGKNSNSKKQWQQHIQSEKHKEKYFTSDSDASGWAPRFPMGEPF LCDRLQKGKACPDGDKCRCAHGQEELNBWLDRREVLKQKLAKAF KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE 5583 3 1265 SSGCRQGRPGRSDRPPPPPRHKWVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDKKRDVYI QGGEQAIKEGGSGSPSFSSPMDIPMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI CKGRGMHHIQQIGPGMVQQITVCIBCKGQGERINFRDRCESC SGAKVIREKKIIEVHVEKGMKDGGKILFHGEGDQEPELBFGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDECMPIYKAPLEKGILIIQFLVIR PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRCHREAYEEDEDGPQAGVQCQTA 5584 3 1265 SSGCRQGRPGRSDRPPPPPRRHKWVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYZ QGGEQAIKEGGSGSPSSSSPMDITPMFFGGGGRMARERRGKNV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHQQIGPGMVQQIOTVCIECKGGGERINFRKDRCESC GGGEQAIKEGGSGSPSSSSSPMDITPMFFGGGGRMARERRGKNV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHQQIGPGMVQQIOTVCIECKGGGERINFRDRCESC CKGRGMHIHQQIGPGMVQQIOTVCIECKGGGERINFRDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELBFGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI CKGRGMIHHQQIGPGMVQQIOTVCIECKGGGERINFRDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEDQEPELBFGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI IVUDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI IVUDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI IVUDQKDHSVFQRRGHDDLIMKMKIQLSEALCGFKKTIKTLDNRI
TALLIKNPLAATHEFKQACQLCYPKTGPRAGDYTYREGLEHKCI RDILLGRLRSSEDQTWKRIRPRPTKTSFVGSYYLCKDMINKQD KYGDNCTFAYHQBEIDVWTBERKGTLNRDLLFPPLGGVKRGSIT. IAKLLKEHQGIFTPLCEICFDSKPRIISKGTKDSPSVCSNLAAI HSFYNNKCLVHIVRSTSLKYSKIROFQBHFQFPVCRHEVRYGCI REDSCHPARSFIELKWWLLQQYSGMTHEDIVQESKKYWQQMEAH AGKASSSMGAPRTHGPSTFDLQMKFVCGQCWRNGQVVEPDKDLI YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYI LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMQQTY DMMLKKHNPGKPGEGTPISSREGEKQICMPTDYADIMMGYHCMI CGKNSNSKKQMQQHIQSEKHKEKVFTSDBASGMAPRFPMGEFF LCDRLQKGKACPPDGNKCRCAHGQBELNEWLDREVVLKQKLAKAR KOMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE 5583 3 1265 SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYJ QGGEQALKEGGGSESPSSPMDIPMFFGGGGRMAPERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI CKGRGMHHIQQIGPGMVQQICTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKOHSVPQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQPLVIE PEKHULSLEKLPQLEALLPPRQKVRITDDMQVELKEFCPNEQN WRCHREAYEEDEDGPQAGVQCQTA 5584 3 1265 SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYJ QGGGQALKGGGSGSPSFSSPMDIPMFFGGGGRMARERRGKNV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGGGERINPKRDKPCESC GGGCQALKEGGGSSPSFSSPMDIPMFFGGGGRMARERRGKNV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGGGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEBGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI CKGRGMHIHIQQIGPGMVQQIQTVCIECKGGGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEBGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
RDILLGRLRSSEQTWKRIRPRPTKTSFVGSYYLCKDMINKQDC KYGDNCTFAYHQBEIDWTBERKGTLNRDLLFDPLGGVKRGSIY IAKLLKEHGGIFTPLCBICFDSKPRIISKGTKDSF9VCSNIAAN HSFYNNKCLVHIVRSTSLKYSKIRQFQBHFQFDVCHBVRYGCI REDSCHFAHSFIELKVWLLQQYSGMTHEDIVQESKKYWQQMEAN AGKASSSMGAPRTHGPSTFDLQMKFVCGQCWRNGQVVEPDKDLK YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYI LCHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMQQTY DMMLKKHNPGKPGGTPISSREGEKQIQMPTDYADIMMGYHCWI CGKNSNKKQWQQHIQSEKHKKVKTSDSDASGWAFRFPMGEFF LCDRLQKGKACPDGDKCRCAHGQEELNEWLDRREVLKQKLAKAR KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYI QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI CKGRGMHHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDDEPELBPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIE PEKHWLSIEKLFQLEALLPPRQKVRITDDMDQVELKEFCPNEQM WRQHREAYEEDEDGPQAGVQCQTA 1265 SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYL QGGEQAIKEGGSSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGKKGSVEKCPI CKGRGMHHIQQIGPGMVQQIQTVCIECKGQGGRINFKDRCNYC GGGQAIKEGGSSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGKKGSVEKCPI CKGRGMHHIQQIGPMVQQIQTVCIECKGQGGRINFKDRCSSC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELBPGDVI IVLDQKDHSVFQRGHDLIMKMKIQLSSEALCGFKKTIKTLDNRI
KYGDNCTFAYHQEEIDVWTEBRKGTLNRDLLFDPLGGVKRGSLN IAKLLKBHQGIFTFLCBICFDSKPRIISKGTKDSBSVCSNLAAI HSFYNNKCLVHIVRSTSLKYSKIRQFQBHFQFDVCRHEVRYGCI REDSCHFAHSFIELKWWLLQQYSGMTHEDIVQESKKYWQQMEAH AGKASSSMGAPRTHGPSTFDLQMKFVCGQCWRNGQVVEPDKDLH YCSAKARHCWTKERRVLLLWSKAKRKWVSVRPLPSIRNFPQQYT DMMLKKHNPGKPCGGTPISSREGEKQIQMPTDYADIMMGYHCWI CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFF LCDRLQKGKKACPDGDKCRCAHGQEELNEWLDRREVLKQKLMKAP KDMLLCPRDDDFGKYNFILQEBGDLAGATPEAPAAAATATTGE SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYI QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI CKGRGMHHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESG SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PBEHMLSLEKLPQLEALLPPRQKVRITDDMQVELKEFCPNEQM WRQHREAYEEDEDGPQAGVQQQTA SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYT QGGEQAIKEGGSGSPSFSSMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL GGGQAIKEGGSGSPSPSSMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGGGRRINPKDRCESG SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELBPGDVI IVLDQKDHSVFQRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI IVLDQKDHSVFQRGHDLIMKMKIQLSCAGGRRINPKDRCESG SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELBPGDVI IVLDQKDHSVFQRGHDLIMKMKIQLSCACKGFKKTIKTLDNRI
IAKLIKEHQGIFTFLCEICFDSKPRIISKGTKDSPSVCSNLAAI HSFYNNKCLVHIVRSTSLKYSKIRGFQEHFQFDVCRHEVRYGCI REDSCHFAHSFIELKWLLQQYSGMTHEDIVQESKKYWQQMEAF AGKASSSMAAPRTHGPSTFDLQMKFVCGQCWRNGQVVEPDKDLI YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYI LCHAQNGGKCQYVGNCSFAHSPSEERDMWTFMKSNKILDMQQTY DMWLKKHDPGKPGGFTPISSREGEKQIQMPTDYADIMMGYHCWI CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFF LCDRLQKGKACPDGDKCRCAHGQEELNEWLDRREVLKQKLAKAF KDMLLCPRDDDFGKYNFLLQEDGDLAGATPBAPAAATATTGE SGGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEF LKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYL QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQICTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA 1265 SSGCCQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKFSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHHHIQQIGPGWVQQIQTVCIECKGQGERINPKDRCESC CKGRGMHHIQQIGPGWVQQIQTVCIECKGGGRKGSVEKCPL CKGRGMHHHIQQIGPGWVQQIQTVCIECKGGGGRKGSVEKCPL CKGRGMHHIQQIGPGWVQQIQTVCIECKGGGGRKGSVEKCPL CKGRGMHHIQQIGPGWVQQIQTVCIECKGGGGRKGSVEKCPL CKGRGMHHIQQIGPGWVQQIQTVCIECKGGGGRKGSVEKCPL CKGRGMHHIQQIGPGWVQQIQTVCIECKGGGGRKINFKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELBPGDVI IVLDQKDHSVFQRRGHDLIMKWKIQLSEALCGFKKTIKTLDNRI IVLDQKDHSVFQRRGHDLIMKWKIQLSEALCGFKKTIKTLDNRI IVLDQKDHSVFQRRGHDLIMKWKIQLSEALCGFKKTIKTLDNRI IVLDQKDHSVFQRRGHDLIMKWKIQLSEALCGFKKTIKTLDNRI IVLDQKDHSVFQRRGHDLIMKWKIQLSEALCGFKKTIKTLDNRI IVLDQKDHSVFQRRGHDLIMKWKIQLSEALCGFKKTIKTLDNRI IVLDQKDHSVFQRRGHDLIMKWKIQLSEALCGFKKTIKTLDNRI
HSFYNNKCLVHIVRSTSLKYSKIRQFQBHFQFDVCRHEVRYGCI REDSCHFAHSFIELKWLLQQYSGMTHEDIVQESKKYWQQMEAH AGKASSSMGAPRTHGPSTFDLQMKFVCGQCWRNGQVVEPDKDLK YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYI LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMQQTY DMWLKKHNPGKPGGTPISSRBGEKQTQMPTDYADIMMGYHCMI CGKNSNSKKQWQHLQSEKHKEKVFTSDSDASGWAFRFPMGBFF LCDRLQKGKACPPDGDKCRCAHGQEELMEWLDRREVLKQKLAKAR KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYI QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGYGGKKGSVEKCPI CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGGRINPKDRCSC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVTTSKAGRVIKHGDLRCVRDEGMPTYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEZDEDGCPQAGVQCQTA SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYT QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGGRINPKDRCSSC CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGGRKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGGRNARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGGRINPKDRCSSC CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGGRNARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGGRINPKDRCSSC CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGGRNARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGGRNARERGGNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGFKCTKTLDNRI
REDSCHFAHSFIELKVWLLQQYSGMTHEDIVQESKKYWQQMEAF AGKASSSMGAPRTHGPSTFDLQMKFVCGQCWRNGQVVEPDKDLI YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYI LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMQQTY DMWLKKHNPGKPGBGTPISSREGEKQIQMPTDYADIMMGYHCNI CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFF LCDRLQKGKACPDGDKCRCAHGQEELNEWLDRREVLKQKLAKAF KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE LCDRLQKGKACPDGDFKYNFLLQEDGDLAGATPEAPAAAATATTGE SSGCRQGRPGRSDRPPRPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYI QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI CKGRGMHIHQQIGPMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKLLFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PBKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYBEDEDGPQAGVQCQTA SGGCQGFPGSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVW HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC CKGRGMHIHQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC CKGRGMHIHQQIGPGMVQQIQTVCIECKGQGGRKGSVEKCPL CKGRGMHIHQQIGPGMVQQIGTVCIECKGQGERINPKDRCESC CKGRGMHIHQQIGPGMVQQIGTVCIECKGQGERINPKDRCESC CKGRGMHIHQQIGPGMVQQIGTVCIECKGQGERINPKDRCESC CKGRGMHIHQQIGPGMVQQIGTVCIECKGQGERINPKDRCESC CKGRGMHIHQQIGPGMVQQIGTVCIECKGQGERINPKDRCESC CKGRGMHIHQQIGPGMVQQIGTVGIECKGQGERINPKDRCESC CKGRGMHIHQQIGPGMVQQIGTVGIECKGQGERINPKDRCESC CKGRGMHIHQQIGPGMVQQIGTVGIECKGQGERINPKDRCESC CKGRGMHIHQQIGPGMVQQIGTVGIECKGQGERINPKDRCESC CKGRGMHIGGGGGAACCGFKKTIKTLDNRI
AGKASSMGAPRTHGPSTFDLQMKFVCGQCWRNGQVVEPDKDLK YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYT LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMQQTT DMWLKKHNPGKPGGGTPISSREGEKQIQMPTDYADIMMGYHCWI CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFF LCDRLQKGKACPDGDKCRCAHGQEELNEWLDRREVLKQKLAKAR KDMLLCPRDDDFGKYNFLLQEDGDLAGATTEAPAAAATATTGE SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYKKLALKYHPDKNPDDEGEKFKLISQAYEVLSDPKKRDVYI QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERIMFKDRCESG SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYBEDEDGPQAGVQCQTA SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVW HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHHIQQIGPGMVQQIQTVCIECKGQGERINFKDRCESG CKGRGMHHIQQIGPGMVQQIQTVCIECKGQGERINFKDRCCSG SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELBPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYI LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMQQTY DMWLKKHNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCMI CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFR LCDRLQKGKACPPGDKCRCAHGQEELNBWLDRREVLKQKLAKAR KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE 5583 3 1265 SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYI QGGEQAIKEGGSGPSFSSPMDIFDMFFGGGGRMARERGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESG SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESG SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI CKGRGMHIHIQQIGPGMVQQIQTVCIECKGGGGRKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGGGGRINPKDRCESG SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMQQTY DMWLKKHNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWI CGKNSNKKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFF LCDRLQKGKACPDGDKCRCAHGQEELNEWLDRREVLKQKLAKAF KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAATATTGE SGGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYI QGGEQAIKEGGSGSFSFSSPMDIFDMFFGGGGMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHHIQQIGFGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA SGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC CKGRGMHHIQQIGPGMVQQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELBPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
DMWLKKHNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWI CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFF LCDRLQKGKACPPDDKCRCAHGQEELNEWLDRREVIKQKLAKAFA KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFFLISQAYEVLSDPKKRDVYL QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI CKGRGMHIHIQQIGFGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKJQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PBKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEON WRQHREAYEEDEDGPQAGVQCQTA SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSSPMDIFDMFFGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGFGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFF LCDRLQKGKACPDGDKCRCAHGQEELNEWLDRREVLKQKLAKAR KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE 5583 3 1265 SSGCRQGRPGRSDRPPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYL QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGGRINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGBVIKHGDLRCVRDEGMPIYKAPLEKGILIIQPLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA 5584 3 1265 SSGCRQGRPGRSDRPPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKVVD CKGRGMHIHIQQIGPGNVQQIQTVCIECKGQGERINPKDRCESC CKGRGMHHIQQIGPGNVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEFGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
LCDRLQKGKACPDGDKCRCAHGQEELNEWLDRREVLKQKLAKAF KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE 5583 3 1265 SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYL QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQPLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHHIQQIGPGMVQQIOTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE 5583 3 1265 SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQPLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
5583 3 1265 SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQQTTA 5584 3 1265 SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYT QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA WRQHREAYEEDEDGPQAGVQCQTA SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVVY QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGNVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPI CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYBEDEDGPQAGVQCQTA SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVVY QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGNVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVVY QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGNVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA 5584 3 1265 SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA 5584 3 1265 SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELBPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIK PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA 5584 3 1265 SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA 5584 3 1265 SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKPKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELBPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
WRQHREAYEEDEDGPQAGVQCQTA 5584 3 1265 SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
5584 3 1265 SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELBPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELBPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELBPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELBPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
I STEERN OF STRUCTURE TO THE PROPERTY OF THE P
LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLBKGILIIQFLVIF
PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN
WRQHREAYEEDEDGPQAGVQCQTA 5585 2619 915 LPAGTPESSLHEALDOCMTALDLFLTNOFSEALSYLKPRTKESM
The proof of the
YHSLTYATILEMQAMMTFDPQDILLAGNMMKRAQMLCQRHRRKS SVTDSFSSLVNRPTLGQPTEEEIHAEVCYAKCLLQRAALTFLQD
ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS
GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEBAEKLLKPYLNR VDWGAIEF FAGDIEWLYGNIDAA TEDERGORA GOWYYGHUM
YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM
CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK
AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS
ISANEKKIKYDHYLIPNALLELALLIMEQDRNEEAIKLLESAKQ
NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL 5586 2619 915 LPAGTPESSLHEALDOCMTALDLFLTNOFSEALSYLKPRTKESM
Distribution of the contract o
YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS
SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD
ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS
GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR
YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM
CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK
AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS
ISANEKKIKYDHYLIPNALLELALLMEQDRNEEAIKLLESAKQ
NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
5587 1768 148 SSAVPDGAVGRPVAVAVGGPPHSCRCRPCCLMAAIGVHLGCTSA

			The state of the s
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
[corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
\	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	ľ	sequence	\=possible nucleotide insertion)
	sequence		CVAVYKDGRAGVVANDAGDRVTPAVVAYSENEEIVGLAAKQSRI
		li .	RNISNTVMKVKQILGRSSSDPQAQKYIAESKCLVIEKNGKLRYE
J	ł	·	RNISNIVMKVKQILGRSSSDPQAQKITAESKCDVIBANGKDKIE
j		1	IDTGEETKFVNPEDVARLIFSKMKETAHSVLGSDANDVVITVPF
1		l	DFGEKQKNALGEAARAAGFNVLRLIHEPSAALLAYGIGQDSPTG
	Ì	1	KSNILVFKLGGTSLSLSVMEVNSGIYRVLSTNTDDNIGGAHFTE
1	}	ł	TLAQYLASEFQRSFKHDVRGNARAMMKLTNSAEVAKHSLSTLGS
İ		1	ANCFLDSLYEGQDFDCNVSRARFELLCSPLFNKCIEAIRGLLDQ
		{	NGFTADDINKVVLCGGSSRIPKLQQLIKDLFPAVELLNSIPPDE
1]	VIPIGAAIEAGILIGKENLLVEDSLMIECSARDILVKGVDESGA
	(1	SRFTVLFPSGTPLPARRQHTLQAPGSISSVCLELYESDGKNSAK
i	1	j	BETKFAQVVLQDLDKKENGLRDILAVLTMKRDGSLHVTCTDQET
1	I	1	GKCEAISIEIAS
	<u></u>		
5588	3	589	TPPPPEQAMVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGK
1	1	Ī	LVSLEKYRGSVSLVVNVASECGFTDQHYRALQQLQRDLGPHHFN
1		1	VLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
1			AHPAFKYLAQTSGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEEV
1]	RPQITALVRKLILLKREDL
5589	1884	553	LRQAWHEGGIGQTDKERGAAALPGEEGDPTRGRSLGRASWESGS
} 3303	100.	}	PRRPRSPFSSFLPRPICLSLEARPCSIEDRRNWSLIGRPGAPAS
1	İ		GLNRSSGLWLGPDRCRPRSRCSCRVMENPSPAAALGKALCALLL
1		l	ATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPLF
		Į	RPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALM
1		1	KEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLVSF
1	ı	Į.	KETEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRAASLIVSF
ì		1	VVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGF
-			TFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARV
		İ	TLLRLRQSPRAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLW
]	ļ	SSWGLCGGHCGRLGTKSRTRYVRVQPANNGSPCPELEEEAECVP
	1	1	DNCV
5590	72	896	LCSSGALRLLPAMVAWRSAFLVCLAFSLATLVQRGSGDFDDFNL
3330	1		EDAVKETSSVKQPWDHTTTTTTNRPGTTRAPAKPPGSGLDLADA
		1	LDDQDDGRRKPGIGGRERWNHVTTTTKRPVTTRAPANTLGNDFD
1	1 .	· ·	LADALDDRNDRDDGRRKPIAGGGGFSDKDLEDIVGGGEYKPDKG
1	1		KGDGRYGSNDDPGSGMVAEPGTIAGVASALAMALIGAVSSYISY
]	1 .	1	QQKKFCFSIQQGLNADYVKGENLEAVVCEEPQVKYSTLHTQSAE
1			
<u>L</u> .	l		PPPPPEPARI
5591	68	1494-	AGSSRRAAAERLLVSAGCRSLAGRASGVLLLPAELLPGEEEAMA
Ì	1	1	LRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPRTALG
1			DIGNKVSEQLQAKMPMKKEAKPSATGKVIDKKLPKPLEKVPMLV
1		1	PVPVSEPVPEPEPEPEPEPVKEEKLSPEPILVDTASPSPMETSG
1	1		CAPAEEDLCQAFSDVILAVNDVDAEDGADPNLCSEYVKDIYAYL
I			ROLEEEQAVRPKYLLGREVTGNMRAILIDWLVQVQMKFRLLQET
ł	1		MYMTVSIIDRFMQNNCVPKKMLQLVGVTAMFIASKYEEMYPPEI
1	1		GDFAFVTDNTYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRAS
1	1		KIGEVDVEQHTLAKYLMELTMLDYDMVHFPPSQIAAGAFCLALK
i			ILDNGEWTPTLQHYLSYTEESLLPVMQHLAKNAAMVNQGLTKHM
ł			
		<u> </u>	TVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV
5592	242	924	YGESKOWNQKOLLSALVLTTVNCLPTPIMAKSAEVKLAIFGRAG
1)	1	VGKSALVVRFLTKRFIWEYDPTLESTYRHQATIDDEVVSMEILD
1			TAGQEDTIQREGHMRWGEGFVLVYDITDRGSFEEVLPLKNILDE
1			IKKPKNVTLILVGNKADLDHSRQVSTEEGEKLATELACAFYECS
			ACTGEGNITEIFYELCREVRRRRMVQGKTRRRSSTTHVKQAINK
1			MLTKISS
		1112	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
5593	3	1113	SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
1			DOGIVADDOCQUANTGEERGEEDFEERBUF VOIDI TROTENTEET OCTO
1			DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR
1	}		BLDLYDNQIKKIENLEALTELBILDISFNLLRNIEGVDKLTRLK
]			KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE
1	1		SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
1	1		ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQ
	1	į	EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV
. 1	1	1	

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
1 .	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			MLALPSVRQIDATFVRF
5594	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
	ì	į.	SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
	ŀ	1	DVDLNHYRIGKIEGFEVLKKVKTLCLRONLIKCIENLEELOSLR
1	į.	Ĭ	ELDLYDNOIKKIENLEALTELEILDISFNLLRNIEGVDKLTRLK
1	J.	ļ	KLFLVNNKISKIENLSNLHQLOMLELGSNRIRAIENIDTLTNLE
	!		SLFLGKNKITKLONLDALTNLTVLSMOSNRLTKIEGLONLVNLR
1	ì		ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELO
1	1		EFWMNDNLLESWSDLDELKGARSLETVYLERNPLOKDPOYRRKV
1	1		MLALPSVROIDATFVRF
5595	 	1476	I
2225	3	14/0	ARWNGRWVQVPAWPGPGCGTNASGERORQLPRAWRPVGRTLGSE
1	i		PIALAWSPPLYLFPIPLPSWAVSQPTPTLGTMFADLDYDIEEDK
1	(LGIPTVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVFDNTP
1			AALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKGEVTIHY
			NKLQADPKQGMSLDIVLKKVKHRLVENMSSGTADALGLSRAILC
1			NDGLVKRLEELERTAELYKGMTEHTKNLLRAFYELSQTHRAFGD
1	ì	}	VFSVIGVREPQPAASEAFVKFADAHRSIEKFGIRLLKTIKPMLT
			DLNTYLNKAIPDTRLTIKKYLDVKFEYLSYCLKVKEMDDEEYSC
1			IALGEPLYRVSTGNYEYRLILRCRQEARARFSQMRKDVLEKMEL
1	J		LDQKHVQDIVFQLQRLVSTMSKYYNDCYAVLRDADVFPIEVDLA
1	Į.		HTTLAYGLNQEEFTDGEEEEEEEDTAAGEPSRDTRGAAGPLDKG
1	1		GSWCDS
5596	698	219	GAVLAPSSLPAAELAAQGESQSLEDLSNTSRPTSEVYKISFIFP
İ	ŀ		NGDKYDGDCTRTSSGIYERNGIGIHTTPNGIVYTGSWKDDKMNG
	ĺ		FGRLEHFSGAVYEGQFKDNMFHGLGTYTFPNGAKYTGNFNENRV
İ	}		KGEGEYTHIQGTRMDVVTFHFTSCSQT
5597	3	731	ISCKMAADGOSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP
1			VFVIVGFVTLIIFKRELHTISFLGGLALNEGVNWLIKNVIOEPR
		,	PCGGPHTAVGTKYGMPSSHSOFMWFFSVYSFLFLYLRMHQTNNA
ł			RFLDLLWRHVLSLGLLAVAFLVSYSRVYLLYHTWSQVLYGGIAG
1			GLMAIAWFIFTQEVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW
	:		FEYTVTRAEARNRORKLGTKLO
5598	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
3330	1 320	. 2410	VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
1	į į		DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSOLELLSGG
ŀ			EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
	,	,, ,	I KCALCSPHSOSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
			GHIPGFLOTTADEFCFYYARKDGGLCFPDFPRKOVRGPASNYLD
	:		· · · · · · · · · · · · · · · · · · ·
			QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
!			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
İ			SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
			NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
1	į		ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
1			TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS
1			SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
1			YGSYVFGDRNGNFLTLQQSPVTKQWQBKPLCLGTSGSCRGYFSG
			HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
L			CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5599	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
]			VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
]			DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG
(EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
1			IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
1			GHIPGFLOTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
1		'	QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
1			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
1			SLAFHPNYKKNGKLYVSYTTNOERWAIGPHDHILRVVEYTVSRK
1 1			NPHOVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
)	j		ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
1 [TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS
1 1			

1 650			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide		H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
\	to first		
ļ .	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
!	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
1	1		YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG
			HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
	1		CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5600	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE
			EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
	ļ		SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
			FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
	ļ.		AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
1			TFYHPTINVPPRHALKWIRPQTSB
5601	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE
1			EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
[SNAEMSELSVAOKPEKLLERCKYWPACKNGDECAYHHPISPCKA
1			FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
			AVAPPAPPSSSOLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
			TFYHPTINVPPRHALKWIRPOTSE
5602	246	766	YHTSCTVWRTAKEALENTEVPVGCLMVYNNEVVGKGRNEVNQTK
5602	246	/66	NATRHAEMVAIDQVLDWCRQSGKSPSEVFEHTVLYVTVEPCIMC
ı			1 · ·
1		1	AAALRLMKIPLVVYGCQNERFGGCGSVLNIASADLPNTGRPFQC
			IPGYRAEEAVEMLKTFYKQENPNAPKSKVRKKECQQILNMF
5603	1	565	FRGRTPISGGERGCAQYPIPATPARSGENRTMPGAGDGGKAPAR
1			WLGTGLLGLFLLPVTLSLEVSVGKATDIYAVNGTEILLPCTFSS
1			CFGFEDLHFRWTYNSSDAFKILIEGTVKNEKSDPKVTLKDDDRI
.]	l		TLVGSTKEKRNNISIVLRDLEFSDTGKYTCHVKNPKENNLQHHA
	1		TIFLQVVDRRMQ
5604	1	1506	EDIFPAQLLKLQRHERVWQQEPPVRDHRSWGGSGAGGVAGREWT
İ			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG
1	ļ		GGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ
			RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR
ŧ.	:		DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV
		, i	VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI
1	•		
			SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE
			•
			SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG
			SLSNNSGKNVELKFYDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL
			SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL
			SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV
ECOE	26	1021	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSFSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHTTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHTTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHTTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHTTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG
5605	35	1821	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL
			SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL
			SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA
			SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA IEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA
			SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA IEECQYQFRNRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG
			SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA IEECQYQFRNRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC
			SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHTTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVINTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGFGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA IEECQYQFRNRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRVG
			SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHTTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA IEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRVG SSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGR
			SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHTTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVINTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGFGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA IEECQYQFRNRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRVG

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	Amino acto segment containing signal peptide
NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W Martanhan W Marra '
	1		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	1	\=possible nucleotide insertion)
5607	521	141	PPVCNPAEAMPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRV
	ì	1	QQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAP
!	1	Ì	FDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK
5608	 		
5608	2	983	WFQSPLRQADPGPPRHTLFMDFVAGAIGGVCGDAVGYPLDTVKV
	i .		RIQTEPKYTGIWHCVRDTYHRBRVWGFYRGLLLPVCTVSLVSSE
	1	i e	VFGTYRHCLAHICRLRFGNPDAKPTKADITLSGCASGLVRVFLT
l .	1		SPTEVAKVRLQTQTQAQKQQRRLSASGPLAVPPMCPVPPACPBP
	1)	
1			KYRGPLHCLATVAREEGLCGLYKGSSALVLRDGHSFATYFLSYA
1		ł	VLCEWLSPAGHSRPDVPGVLVAGGCAGVLAWAVATPMDVIKSRL
			QADGQGQRRYRGLLHCMVTIVRBEGPRVLFKGLVLNCCRAFPVN
1			MVVFVAYEAVLRLARGLLT
5609	1628	304	AKGVWVLPSPPPRPGRGALVSGSGLRRGRSGTSWRPRRMNHKSK
1			KRIREAKRSARPELKDSLDWTRHNYYESFSLSPAAVADNVERAD
1			
1	1		ALQLSVEEFVERYERPYKPVVLLNAQEGWSAQEKWTLERLKRKY
1	 		RNQKFKCGEDNDGYSVKMKMKYYIEYMESTRDDSPLYIFDSSYG
1 .			EHPKRRKLLEDYKVPKFFTDDLFQYAGEKRRPPYRWFVMGPPRS
1			GTGIHIDPLGTSAWNALVQGHKRWCLFPTSTPRELIKVTRDEGG
1			NQQDEAITWFNVIYPRTQLPTWPPEFKPLEILOKPGETVFVPGG
1			
ļ			WWHVVLNLDTTIAITQNFASSTNFPVVWHKTVRGRPKLSRKWYR
1			ILKQEHPELAVLADSVDLQESTGIASDSSSDSSSSSSSSSSDSD
			SECESGSEGDGTVHRRKKRRTCSMVGNGDTTSQDDCVSKERSSS
			l R
5610	54	1196	LERTPASADMAWTKYQLFLAGLMLVTGSINTLSAKWADNFMAEG
		2230	
			CGGSKEHSFQHPFLQAVGMFLGEFSCLAAFYLLRCRAAGQSDSS
			VDPQQPFNPLLFLPPALCDMTGTSLMYVALNMTSASSFQMLRGA
1			VIIFTGLFSVAFLGRRLVLSQWLGILATIAGLVVVGLADLLSKH
,	·		DSQHKLSEVITGDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLRA
į	ľ		VGTEGLFGFVILSLLLVPMYYIPAGSFSGNPRGTLEDALDAFCQ
1			VGQQPLIAVALLGNISSIAFFNFAGISVTKELSATTRMVLDSLR
1		•	TVVIWALSLALGWEAFHALQILGFLILLIGTALYNGLHRPLLGR
			LSRGRPLAEESEQERLLGGTRTPINDAS
5611	. 2	577	FVLPNRLGIPGSTFRGPGACASSSSLAASAKPGAGGSPALAMSG
	:		ELSNRFQGGKAFGLLKARQERRLABINREFLCDQKYSDEENLPE
		•	KLTAFKEKYMBFDLNNEGEIDLMSLKRMMEKLGVPKTHLEMKKM
1.			
1 .	*		ISEVTGGVSDTISYRDFVNMNLGKRSAVLKLVMMFEGKANESSP
لـــــا			KPVGPPPERDIASLP
5612	. 1	721	ASRDGYMDATIAPHRIPPEMPQYGEBNHIFELMQAMWLCKHLNS
			SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA
1			EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL
1	1		
			IERNLGKRIDPQTGEIYHTTFDWPPBSEIQNRLMVPEDISELET
1	Ì		AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS
<u> </u>			NHRTNAPFTPRVLLLGPVGS
5613	115	1279	RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD
1 1	i	į	KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST
1 .	ļ	ĺ	AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF
1			
i			FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH
] [l		GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH
	[AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI
	İ		ASAIMMONFGLMIADPICSILIAILIVVSVIPLLRESVGILMOR
; I	.		TPPLLENSLPQCYQRVQQLQGVYSLOEOHFWTLCSDVYVGTLKL
i !		ļ	
 			IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM
5614	3	1268	LLSRNEHACPLQAGLGLTQRKPKAIRGREGRATNQGQGETQNER
j ſ			APWGARQRLGVMAELQQLQEFEIPTGREALRGNHSALLRVADYC
<u> </u>			EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD
			LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG
		j	· · · · · · · · · · · · · · · · · · ·
	ľ	[QKVIAPENLPPLTPYCRRPLNFGCLDDIGHGIKDLSTQLSRTGT
1 1		ŀ	LSRKSIKAPATPASATLGRPPRIPEPVHLPVVPDGRLSAASSAS
		1	SLASAGSAEGVGGAPTPKGQAAPPAPPLPSSLDPPPPPAAVEVF
	1	i	QRPPTLEELSPPPPDEELPLPLDLPPPPPPLDGDELGLPPPPPGF
		ļ	GPDEPSWVPASYLBKVVTLYPYTSQKDNELSFSEGTVICVTRRY
L			TATE OF THE PROPERTY OF THE PR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	_	Codon, /=possible nucleotide deletion,
		sequence	\=possible nucleotide insertion)
	sequence		SDGWCEGVSSEGTGFFPGNYVEPSC
		1558	ALGRRRPGDPREMEAAATPAAAGAARREELDMDVMRPLINEQNF
5615	9	1550	DGTSDEEHEQELLPVQKHYQLDDQEGISFVQTLMHLLKGNIGTG
1			LLGLPLAIKNAGIVLGPISLVFIGIISVHCMHILVRCSHFLCLR
ļ			FKKSTLGYSDTVSFAMEVSPWSCLQKQAAWGRSVVDFFLVITQL
Į		İ	GFCSVYIVFLAENVKQVHEGFLESKVFISNSTNSSNPCERRSVD
1			LRIYMLCFLPFIILLVFIRELKNLFVLSFLANVSMAVSLVIIYQ
1			YVVRNMPDPHNLPIVAGWKKYPLFFGTAVFAFEGIGVVLPLENQ
ļ			MKESKRFPQALNIGMGIVTTLYVTLATLGYMCFHDBIKGSITLN
Į			LPODVWLYQSVKILYSFGIFVTYSIQFYVPAEIIIPGITSKFHT
l			KWKOICEFGIRSFLVSITCAGAILIPRLDIVISFVGAVSSSTLA
			LILPPLVEILTFSKEHYNIWMVLKNISIAFTGVVGFLLGTYITV
			EEIIYPTPKVVAGTPQSPFLNLNSTCLTSGLK
5616	1	719	DDFVRCGPQSAAMGASARLLRAVIMGAPGSGKGTVSSRITTHFE
3010			LKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDDVMTRLAL
1	1		HELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
1		1	IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDD
!			KPETVIKRLKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYV
l			YAFLQTKVPQRSQKASVTP
5617	176	765	PWRGRGSRPRGAGAMAEEQVNRSAGLAPDCEASATAETTVSSVG
1			TCEAAGKSPEPKDYDSTCVFCRIAGRQDPGTELLHCENEDLICF
1			KDIKPAATHHYLVVPKKHIGNCRTLRKDQVELVENMVTVGKTIL
1	i		ERNNFTDFTNVRMGFHMPPFCSISHLHLHVLAPVDQLGFLSKLV
1			YRVNSYWFITADHLIEKLRT
5618	3	1692	YLNYINLKSENKLSGKEDLWEKLQYLWKSTLNLPEDLLRVPDES
			LFLNSGGDSLKSIRLLSEIEKLVGTSVPGLLEIILSSSILEIYN
İ			HILQTVVPDEDVTFRKSCATKRKLSNINQEEASGTSLHQKAIMT
			FTCHNEINAFVVLSRGSQILSLNSTRFLTKLGHCSSACPSDSVS
		'	QTNIQNLKGLNSPVLIGKSKDPSCVAKVSEEGKPAIGTQKMELH
1 .		Ì	· VRWRSDTGKCVDASPLVVIPTFDKSSTTVYIGSHSHRMKAVDFY
1			SGKVKWEQILGDRIESSACVSKCGNFIVVGCYNGLVYVLKSNSG
ļ		, ·	EKYMMFTTEDAVKSSATMDPTTGLIYIGSHDQHAYALDIYRKKC
			VWKSKCGGTVFSSPCLNLIPHHLYFATLGGLLLAVNPATGNVIW
}			KHSCGKPLFSSPQCCSQYICIGCVDGNLLCFTHFGEQVWQFSTS
			GPIFSSPCTSPSEQKIFFGSHDCFIYCCNMKGHLQWKFETTSRV
			YATPFAFHNYNGSNEMLLAAASTDGKVWILESQSGQLQSVYELP GEVFSSPVVLESMLIIGCRDNYVYCLDLLGGNQK
		 	
5619	2160	1477	DSPVLPTSGNVISTAQPAQPWSAVEAALRSLGSPPGAGRGCPCP AQSLHSHQLAAWDPLKPSLRSYPPHLLQHPQLRSLTASSGHLGR
			RSCPQPRPLEELLRAGSSTRPQPLTSSCCGMSCMYSFLGHCSVL
		}	LWGTKGRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVGWQPPLGP
1			TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPSPWAA
1			ECSPPATP
F 600	930	182	PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAIEAIKLGST
5620	330	102	AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGCAMSG
			LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLALQFG
			EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQCDAR
			AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEEKLNA
	1		TNIELATVQPGQNFHMFTKEELEEVIKDI
5621	3	819	VVEFVEYTATDANVKNESLSSVQQLGIKMTVRYGKFLSLLKDGA
3021			ENDLTWVLKHCERFLKQQQTSIKSSLLCLQGNYAGHDWFVSSLF
	1	!	MIMLGDKEKTFQFLHQFSRLLTSAFLWLPRLHISSYLPNDTVES
1			GIHPVYFCSTHYIEMLLKAELPLVFSAFHMSGFAPSQICLQWIT
		1	QCFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLQQDILQ
	,	}	HTQTQDLQVFLKEEALHGFRVSDYFEYMEILEQNYRTVLLRDMR
1			NIRLOST
5622	1122	456	AASTKDAVSRKRSHSASEKSGTGTSISKRLNMNPQIRNPMKAMY
			PGTFYFQFKNLWEANDRNETWLCFTVEGIKRRSVVSWKTGVFRN
			OVDSETHCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDCA
			GEVAEFLARHSNVNLTIFTARLYYFQYPCYQEGLRSLSQEGVAV

SEO	Predicted	Predicted end	Amino agid gogment containing almay
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
.1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	'	\=possible nucleotide insertion)
			BIMDYEDFKYCWENFVYNDNEPFKPWKGLKTNFRLLKRRLRESL
			Q
5623	3	954	FLPFFIRAPKISRNGQWLFTFTTPFPFANKALPGWEGIVPACFW
ļ			RKKILTPSTGTMELLQVTILFLLPSICSSNSTGVLEAANNSLVV
			TTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNELLKMSLMST
			ATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAVSTLQS
			SKPKTETQSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPENT
			SQSQVIGTEGGKNASTSATSRSYSSIILPVVIALIVITLSVFVL
			VGLYRMCWKADPGTPENGNDQPQSDKESVKLLTVKTISHESGEH
			SAQGKTKN
5624	159	898	PGVAAAAGALPQYHGPAPALVSCRRELSLSAGSLQLERKRRDFT
İ			SSGSRKLYFDTHALVCLLEDNGFATQQAEIIVSALVKILEANMD
1			IVYKDMVTKMQQEITFQQVMSQIANVKKDMIILEKSEFSALRAE
}			NEKIKLELHQLKQQVMDEVIKVRTDTKLDFNLEKSRVKELYSLN
			EKKLLELRTEIVALHAQQDRALTQTDRKIETEVAGLKTMLESHK
5625	ī	1180	LDNIKYLAGSIFTCLTVALGFYRLWI TIPSSAAAQRAGPPAGALEALSPGGARAHAERRGEMRATPLAAP
	-	1100	AGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPP
			TAPDRATAVATASRLGPYVLLEPEEGGRAYQALHCPTGTEYTCR
1			VYPVQEALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTH
1			GDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVLRDLKL
			CRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPE
			ILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEPVLLFGKI
			RRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRO
i			DPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG
5626	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI
			TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
1			ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
			EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN
			LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
			SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE
	•		IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ
			SIPIFNETGRFSFTLPYPVKIKVRFSPFLQIYLIMIFLGLYINF RHLYKQRRRYGOKKKKIH
5627	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI
			TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
1 1			ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
			EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN
			LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
			SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE
			IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ
			SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF
F. C. C.			RHLYKQRRRRYGQKKKKIH
5628	75	1455	VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP
	1		SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG
	l		GGWFGEGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR
	}		IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVBI
1			DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD
[]	ł		LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV
	İ		DLNRVLEEMRCQYETLVENNRRDAEDWLDTQSEELNQQVVSSSE
]	1		QLQSCQABIIELRRTVNALEIELQAQHSMRDALESTLAETEARY SSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVLLDVRARLEC
	l	ļ	EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA
	İ		ARTNCSARPICVPCPGGRF
5629	2287	938	GRPRSSSDNRNFLRERAGLSSAAVOTRIGNSAASRRSPAARPPV
 	·		PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVVSAVAWAMA
			NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP
			QEVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR
			DEEVKSFRVLQAHGCAPQLYCTFNNGLCYEFIQGEALDPKHVCN
			PAIFRLIARQLAKIHAIHAHNGWIPKSNLWLKMGKYFSLIPTGF
	-		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
			P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	P=Proline, Q=Glucamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	(· · · · · · · · · · · · · · · · · · ·	bequeine	\=possible nucleotide insertion)
	sequence		ADEDINKRFLSDIPSSQILQEEMTWMKEILSNLGSPVVLCHNDL
	1	1	
	1		LCKNIIYNEKQGDVQFIDYEYSGYNYLAYDIGNHFNEFAGVSDV
		1	DYSLYPDRELQSQWLRAYLEAYKEFKGFGTEVTEKEVEILFIQV
			NOFALASHFFWGLWALIQAKYSTIEFDFLGYAIVRFNQYFKMKP
		İ	EVTALKVPE
	L	<u> </u>	
5630	1194	278	GFWAIAQTCAHHLPPGSPWLVPASPWRLPEMSSFGYRTLTVALF
		1	TLICCPGSDEKVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVG
	İ	1	GLETSLDKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESM
	1		NSNVSVYQPPRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLT
	1		NSKVSVIQEEKQVIDIDQI ISHINONSHIRMENGMADDEDQUDNEGC
1		ł	LFLFRGNETLHYETFGKAAPAPQBATATFNSTADREDGHRNFSC
l	1		LAVLDLMSRGGNIFHKHSAPKMLEIYEPVSDSQMVIIVTVVSVL
	1		LSLFVTSVLLCFIFGQHLRQQRMGTYGVRAAWRRLPQAFRP
5631	1053	290	SRVDDFVRPEPSRAEPSRSGRRPARRAATMSVFGKLFGAGGGK
2027	1023	1 290	AGKGGPTPQEAIQRLRDTEEMLSKKQEFLEKKIEQELTAAKKHG
l			WOUNDE TEAT ANY MANUAL PRINCIPLE OF THE PROPERTY OF THE PROPER
l			TKNKRAALQALKRKKRYEKQLAQIDGTLSTIEFQREALENANTN
1	l .	1	TEVLKNMGYAAKAMKAAHDNMDIDKVDELMQDIADQQELAEEIS
ļ	1		TAISKPVGFGEEFDEDELMAELEELEQEELDKNLLEISGPETVP
ì		Į.	LPNVPSIALPSKPAKKKEEEDDDMKELENWAGSM
		<u> </u>	VVLGWSPPRRLWWGSLGAAQRPAVPVSGLARSLHVETRRPHRRA
5632	3	952	AAPRASAKETAMAGSPONAČKAAA ASQUANSPUARI KALIIKKA
Ì			SVRVARGRLGVWAQPQPLLPRPVGSRREMQPPGPPPAYAPTNGD
	1	1	FTFVSSADAEDLSGSIASPDVKLNLGGDFIKESTATTFLRQRGY
	İ	•	GWLLEVEDDDPEDNKPLLEELDIDLKDIYYKIRCVLMPMPSLGF
	1	1	NRQVVRDNPDFWGPLAVVLFFSMISLYGQFRVVSWIITIWIFGS
ł			
l			LTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVIAPVLLVVGSFE
1	I	1	VVSTLIKLFGVFWAAYSAASLLVGEEFKTKKPLLIYPIFLLYIY
		1	FLSLYTGV
5633	771	460	QGCSKTMSVGRPFYRSSEFMEQLLSSHLHQVPFFCCFTVVCLCN
3633	1 ""	100	CLFENSVSKLYMLCFNFFMSIFFYSLSITKLNLIYLWGLSYQSL
j.	1	1	
1	ŀ		LLLLSGHRPWGSSMV
5634	1446	855	PRATGRIRSRAAASRPRAGAGASGAEPRSGRERSRLSGRRAPAM
			ARNTLSSRFRRVDIDEFDENKFVDEQBEAAAAAAEPGPDPSEVD
			GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAQGVVLKVLTNFK
l '	·		SSEIEQAVQSLDRNGVDLLMKYIYKGFEKPTENSSAVLLQWHEK
		•	
			ALAVGGLGSIIRVLTARKTV
5635	. 3	943	DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL
1	, ,		RSLFHPFPVTRSGAPRAVLVGSSWPAKMVAPAVKVARGWSGLAL
1			GVRRAVLOLPGLTOVRWSRYSPEFKDPLIDKEYYRKPVEELTEE
ţ		1	EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNMMMIGGNKV
1	[EVIANDRIVIANT NO LEGISTA A COLUMN A LOCAL TRANSPORTE CONTA
1	1	1	LARSLMIQTLEAVKRKQFEKYHAASAEEQATIERNPYTIFHQAL
i	[KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD
1			KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA
		1	HYRWW
	 	1 2242	LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG
5636	2253	1143	DEDITOURS ABOUT DISCORDED AND LAND AND LAND AND LAND AND LAND LA
1	1		LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI
1	1		ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK
1	1	l	YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD
1	1	1	ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR
1	Į.	1	PRINCIPAL MELINOMETI MA NOSI S CMBERLI MOGNESINDI
1			CERLEEQLNDLTELHQNEILNLKQELASMEEKIAYQSYERARDI
1		1	QEALEACQTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI
1	İ	I	LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK
1	1	1	HWDALFSYVERFFSSPR
 		 	MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHLH
5637	948	2532	MSFCGARANAKMMAA INGGISAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
1		1	HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAMLNPG
ì	1	İ	QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHP
1		· l	QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL
		1	AND ADDRESS AND ADDRESS AND A DATE OF DATE OF TAXABLE AND A SAME OF A SAME O
1			VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEBIYVVTE
1]	1	LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD
1			IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA
	1		PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQQLDL
1	l .	1	ITDLLGTPSLEAMRTACEGAKAHILRGPHKQPSLPVLYTLSSQA
1			

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Bequence	\=possible nucleotide insertion)
	boquence		THEAVHLLCRMLVFDPYKRISAKDALAHPYLDEGRLRYHTCMCK
			CCFSTSTGRVYTSDFEPVTNPKFDDTFEKNLSSVROVKEIIHOF
		l	ILEQQKGNRVPLCINPQSAAFKSFISSTVAQPSEMPPSPLVWE
5638	125	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG
			RIOMRTRRTLRGHLAKIYAMHWGTDSRLLVSASODGKLIIWDSY
			TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
			EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
	·	· ·	GOOTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
			CROTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL
			MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA
			GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5639	125	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG
			RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY
			TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
			EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
		· ·	GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
			CRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL
			MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA
į			GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5640	280	1092	QQGNKKTMLSHNTMMKQRKQQATAIMKEVHGNDVDGMDLGKKVS
			IPRDIMLEELSHLSNRGARLFKMRQRRSDKYTFENFQYQSRAQI
	,		NHSIAMQNGKVDGSNLEGGSQQAPLTPPNTPDPRSPPNPDNIAP
			GYSGPLKEIPPEKFNTTAVPKYYQSPWEQAISNDPELLBALYPK
			LFKPEGKAELPDYRSFNRVATPFGGFEKASRMVKFKVPDFELLL
			LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDTT
			VPESEDL
5641	27	332	CRHNCNGDVKLLSNQMDKLFAFHLFTFHGLLHFLDGSIQKLIQA
			EIILSDNSSILVLENNFLFKVKSKQFIHLIAKKFYISITIVSAS
			NGESFVLSMIVTG
5642	199	1247	ITPCRMDFLVLFLFYLASVLMGLVLICVCSKTHSLKGLARGGAQ
			IFSCIIPECLQRAMHGLLHYLFHTRNHTFIVLHLVLQGMVYTEY
		÷.	TWEVFGYCQELELSLHYLLLPYLLLGVNLFFFTLTCGTNPGIIT
			KANELLFLHVYEFDEVMFPKNVRCSTCDLRKPARSKHCSVCNWC
			VHRFDHHCVWVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTF
	;		LVHLVVMSDLYQETYIDDLGHLHVMDTVFLIQYLFLTFPRIVFM
			LGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQRCPL
			VAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQB
5643	1	847	PSGGVRDVETRGPGSRAARGPRVVMHRRGVGAGAIAKKKLAEAK
			YKERGTVLAEDQLAQMSKQLDMFKTNLEEFASKHKQEIRKNPEF
ĺ			RVQFQDMCATIGVDPLASGKGFWSEMLGVGDFYYELGVQIIEVC
			LALKHRNGGLITLEELHQQVLKGRGKFAQDVSQDDLIRAIKKLK
			ALGTGFGIIPVGGTYLIQSVPAELNMDHTVVLQLAEKNGYVTVS
			EIKASLKWETERARQVLEHLLKEGLAWLDLQAPGEAHYWLPALF
5644	L	1122	TDLYSQEITAEEAREALP
5644	83	1138	PRRMGSWVQLITSVGVQQNHPGWTVAGQFQEKKRFTEEVIEYFQ
			KKVSPVHLKILLTSDEAWKRFVRVAELPREEADALYEALKNLTP
			YVAIEDKDMQQKEQQFREWFLKEFPQIRWKIQESIERLRVIANE
			IEKVHRGCVIANVVSGSTGILSVIGVMLAPFTAGLSLSITAAGV
			GLGIASATAGIASSIVENTYTRSAELTASRLTATSTDQLEALRD
			ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW
			RYVPINVVETLRTRGAPTRIVRKVARNLGKATSGVLVVLDVVNL
5645	62.2	700	VQDSLDLHKGEKSESAELLRQWAQELEENLNELTHIHQSLKAG
7047	537	799	VQSVRDLKRLSPTDPPGDSGNRDVTREDPVTGPLNSASSQVPTL
1			YLCLQNSLLGHSSVEDARATMELYQISQRIRARRGLPRLAVSD
	394-		· AWAY COR COLL LOOME TO COLL OUR WATER A A TO DOT VILCE TO A DO
5646	3745	3328	AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP
	3745	3328	AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFEELEYILGF
	3745	3328	AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFEELEYILGF LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL
5646			AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFEELEYILGF LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ
	3745	800	AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFEELEYILGF LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL

SSQ Predicted Predicted en Incleotide Incleotid			·	
Not	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
location corresponding to first amino acid main	ľ		į.	
to first amino acid amino acid amino acid amino acid sequence Secrine, T-Threonine, Vevaline,	NO:	1		
to first amino acid amino acid amino acid amino acid amino acid sequence source amino acid amino acid amino acid amino acid sequence source amino acid sequence acid sequence amino acid sequence amino acid sequence acid	1			
smino acid xeridue of amino acid sequence codon, /=possible nucleotide deletion,				
maino acid sequence amino acid sequence sequ			1	
amino acid sequence Codon, /=possible nucleotide deletion, -possible nucleotide insertion ORVINDIPTIPTEMMATKEREREPTPTQLOGILALETALGOCOUN ROEWARITKOLDPVYDERGALRENISERMSQRAPKE STERTERERE STERTERE STERTERERE STERTERERE STERTERE STERTERE STERTERE STERTERE STERTERE STERTERE STERTERE STERTERE STERTERE STERTERERE STERTERE STERTERE STERTERE STERTERE STERTERERE STERTERERE STERTERERE STERTERERE STERTERERE STERTERE STERTERERE STERTERE STERTERE STERTERE STERTERE STERTERERE STERTERERE STERTERERE STERTERERE STERTERERE STERTERERE STERTERERE STERTERERE STERTERE STERTERERE STERTERERE STERTERERE STERTERERE STERTERE STERTERE STERTERE STERTERERE STERTERERE STERTERERE STERTERERE STERTERERE STERTERERE STERTERE STERTERERE STERTERERE STERTERERE STERTERERE STERTERE STERTERE STERTERE STERTERE STERTERE	Ì			1
Sequence Sequence	1	1		
GRVLPLPT FTPARMMATKEER ENDTPT GLOSELLALETALGOGCU ROEWARLT TKOLOPVUS KIPALARESIS ERSMOGRAGE 5648 7 1518 VISELCORREALEKE GARN PPTCSENT CSGLOGAGNITORISLIM APOGLOSS RMADIAL GLIMANCT PCLSHONIL KEPALTIPEK STIKETERKET KAREBIJARULEV HIPTHEWOALOPGOAVPAGA HVEINILGTGRERAKU VORKERNIL KIRKELD INTETTY GOLKS ALAK FREGARMES SKERKARGAEV KRIEPE I BELKKOPDEINVU I ETMOTIOWIN ILKNOWN SSSLEEK KARAGAEV KRIEPE I BELKKOPDEINVU LISTGGLOVU NICLUS TERLUKEVAAPULGAARS SIPKVOVEAL GUGULET LUOSKOTEV LAW VEVYTLALDILVTEKMPARESEALT QUMS PSKLOOVTROLUL POLKAKUKUV LALADILVTEKMPARESEALT QUMS PSKLOOVTROLUL POLKAKUKUV LALADILVTEKMPARESEALT QUMS PSKLOOVTROLUL POLKAKUKUV LALADILVTEKMPARESEALT QUMS PSKLOOVTROLUL POLKAKUKUV LALADILVTEKMPARESEALT QUMS PSKLOOVTROLUL POLKAKUKUV LALADILVTEKMPARESEALT QUMS PSKLOOVTROLUL POLKAKUKUV LALADILVTEKMPARESEALT QUMS PSKLOOVTROLUL POLKAKUKUV LALADILVTEKMPARESEALT QUMS PSKLOOVTROLUL POLKAKUKUV LALADILVTEKMPARESEALT QUMS PSKLOOVTROLUL POLKAKUKU LALADILASI QUS STYRLITSARADOLDR KOLKAKUS I PSILIT DELLASAN PSILIT KOTESPIS SISEN TURLEKUH PALAGOGEST KALLOOVENS SISSI SISSIBILIKKALR KOLKAKOSI PSILIT DELLASAN PSILIK KOTESPIS SISEN TURLEKUH PALAGOGESTALLOOVENS SISSISSISSISSISISISISISISISISISISISIS		1	sequence	
S648 7 1518 VIGIELGRIERAIEWERDENTGSGLOGGENTWISTIM APQSLESSRMAPLGHLIGILMAACFTECLSHONLKERALTINDEK STEETERKETKARGENDENTGSGLOGGENOAVPAGS HYRINLOTGEREAKLOVENKERNIKGERLDINTSTYTTSOLUS ALAKPEGGARMESSEKUARGAGEVELPETERKETKARGERUS INTETTTSOLUS ALAKPEGGARMESSEKUARGAGEVELPETERKEKOPLONLKERPALTINDEK ALAKPEGGARMESSEKUARGAGEVELPETERKEKOPLONLKERPALTINDEK LISTMOLINVILINKENISSSSLERKARALETULETYVKOMONAGO LLSPGGLOVINLENGKTEPLIVERSTAPLOLAPSISSMEVOVELI BOGGLOKULVILATEOPLIANKKEVLEPALCSLARHEPYVAGONAGO LLSPGGLOVINLENGKTEPLIVERSTAPLOLAPSISSMEVOVELI BOGGLOKULVILATEOPLIANKKEVLEPALCSLARHEPYVAGONAGO LLSPGGLOVINLENGKTEPLIVERSTAPLOLAPSISSMEVOVELI BOGGLOKULVILATEOPLIANKKEVLEPALCSLARHEPYVAGONAGO BOGTFOELLSYNSLILEUR 5649 1172 3006 MIGROLDBINESTRITGERKESTERREELSTAVIJOSHEALIN KOLKKROSIPPSILTOLLSLASSEPISGRISTPKLITSRAAQDLOR MOVPTLIPBILMERITRITGERKESTERREHISTRATTGERKEALIN KOLKKROSIPPSILTOLLSLASSEPISGRISTPKLITSRAAQDLOR MOVPTLIPBILMERITRITGERKESTERREHISTAVIGSBERGALIN LEILMIALGOMISLISTERSTOLLSLASSEPISGRISTPKLITSRAAQDLOR WORMANIVAACGARVINSGATISSATIKGETSPRINGER VERLIGTGABEVERKEKKRILLGLERGGATGIVILITOSEPSINGER VERLIGTGABEVERKEKKRILLGLERGGATGIVILITOSEPSINGER VERLIGTGABEVERKEKKRILLGLERGGATGIVILITOSEPSINGER VERLIGTGABEVERKEKKRILLGLERGGATGIVILTOSEPSINGER VERLIGTGABEVERKEKKRILLGLERGGATGIVILTOSEPSINGER VERLIGTGABEVERKEKKRILLGLERGGATGIVILTOSEPSINGER VERLIGTGABEVERKEKKRILLGLERGGATGIVILTOSEPSINGER VERLIGTGABEVERKEKKRILLGLERGGATGIVILTOSEPSINGER LEKKREESGHEIKDOLIVATINDOVUHIVOSI GLEDYAGNIHESGV HOALLJOHDHITIKALITALLILIGIPTOTAAQVUHREETENILLIGA GRVSTITICHTOPPERKEKTIPERAISTIKGTESSPSINGER LEKKRESGABEKTATULGEKKSSTELLARBIETENVISGSSERALIN KOLKKRESSIPSTATICHTORAQVUHREETENILLIGHAGATGIVILTOSEPSINGER LEKKRESGABEKTATULGUKKSSTELLARBIETENVISGSSERALIN KOLKKRESSIPSTATICHTORAQVUHREETENILLIGHAGATGIVILTOSEPSINGER TURLEKKRIGHLANGERANGARSTOLUS STANGARSTOLUS VARLIDORINGERTARTICHTIKATURGEKSSTELLARBIETENVISGSSERALIN KOLKKRESSIPSTATICHTURGEKSSTELLARBIETENVISGSSERALIN KOLKKRESSIPSTATICHTURGEKSSTELLARBIETENVISGSSERALIN LIKHLALGGARVATATULALLIGITENGARSTOLUS STANGARSTOLUS LEKKRESSIPSTANGARSTOLUS STANG		sequence		
1518 VISILORHIRAREVGAEMPPTCSRNICSGLOQAGNTMSLIM APQELPSSRMAPLIGHLIANGTPCLSHONLARPHAITMEK STIGHTERRETTAREELDARULEVPHPTHROALOPGOAVPAGE HYPEINLOGGRERAKUCYPEKPENLARGKERLDINTYTSOPLKS ALAMPREGARMESSKERKARQAEVKELPER ERLEKOPPELINVI LETMONIAVELINKNISSSSLEEKARADAEVKELPER ERLEKOPPELINVI LETMONIAVELINKNISSSSLEEKARADAEVKELPER ERLEKOPPELINVI LETMONIAVELINKNISSSSLEEKARADAEVKELPER ERLEKOPPELINVI LOGIQUVETIVIQEKRISSSSLEEKARADAEVKELPER ERLEKOPPELINVI COMPANIAVELINKNISSSSLEEKARADAEVKELPER ERLEKOPPELINVI COMPANIAVELINKNISSSSLEEKARADAEVKELPER ERLEKOPPELINVI COMPANIAVELINKNISSSSLEEKARADAEVKELPER ERLEKOPPELINVI COMPANIAVELINKNISSSSLEEKARADAEVKELPER ERLEKOPPELINKNISSSSLEEKARADAEVKELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER COMPANIAVELPER	1			1
APOGLPSSKMAPIGMILGILIMAACTFECISHONLKEPALTUSE SSTKETEREFEK KREERLDABVLEVHFTHEMOLOPGOAVPAGS HVEINLOTGERRAKLOYEDFERMILKEKKLDINTNYTYSOLDE ALAKFKEGABBESKENENGAGARVELIPEPT EERLKOPDEINVU 1ETOMOLWYLLINEPMSSSSLEEKLAALPOLEVYHQMONAQO LISREGLQVVINGINSTEPLIVERVAAPVILAAPPIKOPEDINVU 1ETOMOLWYLLINEPMSSSSLEEKLAALPOLEVYHQMONAQO LISREGLQVINGINSTEPLIVERVAAPVILAAPPIKOVELI BEGGALQKILVILATEDPLTAKKKVI.FALCSLIKRIPEYAQRUS LIGUVILRIVUGENTEPVILINGINTEPLIVERVAAPVILAAPPIKOVELI BEGGALQKILVILATEDPLTAKKKVI.FALCSLIKRIPEYAQRUS LIGUVILRIVUGENTEPVILINGINTERVIVILIJOULTEPHAREENLIT QEMBPBRLOQVROVIHLIPOLIJOEGHORTEVILIJOEGHOREEV LOTUVILITTCRORKOPPOLGHETASLAAPYOVLASLELQOGE DEGYTQELIGSI VISLIKERI LOTIVATITCRORKOPPOLGHETASLAAPYOVLASLELQOGE DEGYTQELIGSI VISLIKERI KULRIVATIONA ON MICHAELOOGHORTIVILIJOEGHORAER WOVATILFOLIKRINGI VISLIKARRA KULRISTITUSIAGAB PPLISGRSTELITISRAAQOLDR MCVMTILFOLIKRINGI VISLIKARRA KULRISTITUSIAGAB PPLISGRSTELITISRAAQOLDR MCVMTILFOLIKRINGI VISLIKARRA KULRISTITUSIAGAB PPLISGRSTELITISRAAQOLDR MCVMTILFOLIKRINGI VISLIKARRA KULRISTISTITUSIAGAB PPLISGRSTELITISRAAQOLDR VERALGOLDRIKAKRIALIGEN VISLIKARRA KULRISTISTITUSIAGAB PPLISGRSTELITISRAAQOLDR VERALGOLDRIKAKRIALIGEN VISLIKARRA KULRISTISTISTISTISTISTISTISTISTISTISTISTISTI				
SSTKETTRETKÆTEKLDERUPHFTHEMALOJEOGRAPHOLOGICAJOPOGALNES HVEINLOTGERERALOJENDERFINIKÄKKILDINTTYTTSODLKS ALAKFKEGAEMESSKENKARQAEVERLEPRETEELKKOPPELNITY I ETTMOLIWELLIKEPRISSESSLEEKTAALPOLEVELKKOPPELNITY I ETTMOLIWELLIKEPRISSESSLEEKTAALPOLEVELKKOPPELNITY I ELSPGALGVUVINGINSTEPIJVEVAARVIJGAAFSSNEKVOWONADO LLISPGALGVUVINGINSTEPIJVEVAARVIJGAAFSSNEKVOWONADO LLISPGALGVUVINGINSTEPIJVEVAARVIJGAAFSSNEKVOWONADO LLISPGALGVUVINGINSTEPIJVEVAARVIJGAAFSSNEKVOWONADO LLISPGALGVUVINGINSTEPIJVEVAARVIJGAAFSSNEKVOWONADO LLISPGALGVUVINGINSTEPIJVEVAARVIJGAAFSSNEKVOWONADO LLISPGALGVUVINGINSTEPIJVEVAARVIJGAAFSSNEKVOWONADO LLISPGALGVUVINGINSTEPIJVEVAARVIJGAAFSSNEKVOWONADO LUINGULTUVAARVIJAALOVATILAJOHAVATILAJOHAVATILAJOHAVATILAJOHAVATILAJOHAVATILAJOHAVATILAJOHAVATILAJOHAVATILAJOHAVATILAJOHASLAJOHAVATILAJOHASLAJOHAVATILAJOH	5648	7	1518	VLSELCGRHEALREVGAEWPPPTCSPNICSGLQQAGNTDWSLTM
HYRINGTORREAKGYENDFRINLIKGIKLIDITINTYTYSGOLD ALAKFREGABERSKENDRAQAGVRUFRPPI DELKKOPDELNIV IETIMOLIWYLILIKEPISSSSKERLAALFOLEYYYHQKONDOL LISPGGLQVLRIVILATEQPLTAKKKYLFALCSLLRHPPYAQROPLK GGGLQKLLVILATEQPLTAKKKYLFALCSLLRHPPYAQROPLK LOGIGVLRTLVQGKOTEVANEVYTLLIDIVTEMFAGRERALFOL GEMPEKLQOYROVHLJEGLINKGONCENTVHLLABERIDAREKY LOTTIGVLLTTCRORYRODPOLGRTLASLADEYQVLASLELQOGE DEGYTQELLGSVNSLLKELR MOLOGILDAINEETRIJOSERESTELRABEI ETRYTSGSMEALD KOLKKRGSI PTSITULSLABAGPPLASSRAYTIKGTSFPSSSY TURLEKKIGHPALSGEGKSALEDGSNPSSSNSSSOSISLKKARK KOLKKRGSI PTSITULSLABAGPPLASSRAYTIKGTSFPSSSY TURLEKKIGHPALSGEGKSALEDGSNPSSSNSSSOSISLKKARK KOLKKRGSI PTSITULSLABAGPPLASSRAYTIKGTSFPSSSY TURLEKKIGHPALSGEGKSALEDGSNPSSSNSSSOSISLKKARK KOLKKRGSI PTSITULSLABAGPPLASSRAYTIKGTSFPSSY TURLEKKIGHPALSGEGKSALEDGARKKONFQLEDARKKONFQLENGENGTSNALIR KOLKKRGSI PTSITULSLABAGPPLASSRAYTIKATSTSSPANDLD VPAKLGTOABENDRIKKKRIGULEDARKKONFQLEDARSONFOTYVSNL ELMYMPRAYVAACRANVISGALINGALKATIVLLTDSEPSAPETETLTSK TURSEGSBAQTLAYGUNMBRITGNBUPSLOLPQTSSYPMSCUL DAPMLDHLIKKOLRVILKUNDSTSSAPETSCONWVYHERTETLTSTS TURSEGSBAQTLAYGUNMBRITGNBUPSLOLPQTSSYPMSCUL DAPMLDHLIKKOLRVILKUNDSTRETSLOYGUNGLASARSTLPA GFRYSTLGTLQPPPAPPKKIMPERTSLOYGUNGLASARSTLPA GFRYSTLGTLQPPPAPPKKIMPERTSLOYGUNGLASARSTLPA GFRYSTLGTLQPPPAPPKKIMPERTSLOYGUNGLASARSTLPA GFRYSTLGTLQPPPAPPKKIMPERTSLOYGUNGLASARSTLPA GFRYSTLGTLQPPAPPKKIMPERTSLAYGUNGLASARSTLPA KOLKKRESGRADITAALANSARAY KOLKSI GRALFOKKERGGLI OLSARGANGPAQNOOPTYVSI LEUWOMPANYVAACRANVISGALINGKABALSDFTE GREGTISNALIR LEUWOMPANYVAACRANVISGALINGKABALSDFTE GREGTISNALIR LEUWOMPANYVAACRANVISGALINGKABALSDFTE GREGTISNALIR LEUWOMPANYVAACRANVISGALINGKABALSDFTE GREGTISNALIR LEUWOMPANYVAACRANVISGALINGKABALSDFTE GREGTISNALIR LEUWOMPANYVAACRANVISGALINGKABALSDFTE GREGTISNALIR LEUWOMPANYVAACRANVISGALINGKABALSDFTE GREGTISNALIR LEUWOMPANYVAACRANVISGALINGKABALSDFTE GREGTISNALIR LEUWOMPANYVAACRANVISGALINGKABALSDFTE GREGTISNALIR LEUWOMPANYAACRANVISGALINGKABALSDFTE GREGTISNALIR LEUWOMPANYAACRANVISGALINGKABALSDFTE GREGTISNALIR LEUWOMPANYAACRANVISGALINGKABALSDFTE	1	}		APQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEK
ALAKFEGABMESSKEDKARAQAEVYRLIPPT IEELKKUPDELNIK I IETMOLIWELIKPTSSSSSEEKTAALFOLEEKYVHOMONAOD LLSFGGLQWLINTFNSSSSSEEKTAALFOLEEKYVHOMONAOD LLSFGGLQWLINTINTSSSSEEKTAALFOLEEVYVHOMONAOD LLSFGGLQWLINTINTSSSSEEKTAALFOLEVYVHOMONAOD LLSFGGLQWLINTINGEKTEVLAVVALIJAAFSSKPKVQVERI LGGLQVLRTLIQGEKTEVLAVVALIJAATSSKPKVQVERI LGGLQVLRTLIQGEKTEVLAVVALIJATUTEMFAGERAELIT QEMSPEKLQOYROVHLJEGLBOGOKEITVHLIALBERIDAREK LGGUNGET LGGUNGET LGGUN		į.]	SSTKETERKETKAEEELDAEVLEVFHPTHEWQALQPGQAVPAGS
IETEMOLIWYELINKYMSSSSLERIAALPOLETYYHOMONDO LISFEGIQVYUNGINSTEPIUNEYAPAURJAASPSNEKYOVEAI BGGALOKILVILATEOPITAKKKVI,FALCSLIRHFEYAOROKA LGGIOVAERTUORKOTEPIUNEVYTULIVOLVYEMWA REBEABLIT QEMSPEKLQQYRQVHLIPOLMEQONCEITVHLIALPEHDAREKV LGGIOVAERTUORKSTEVILANYVTULIVOLVYEMWA REBEABLIT QEMSPEKLQQYRQVHLIPOLMEQONCEITVHLIALPEHDAREKV LQTIGVILITICKRORYRQDPOLGRITASIAGABYQVIASIELIQOE BEGYTOELIGSVINSLIKELR KOLKROSI PYSITUDISLASASPPISGRSTPELTSSSAAODLDR MOVHTLPSDLRHERKLISPVSREENREDKATI KCETSPPSSPS TURLEKKIHPALGEGEKSALEDOSSNPSSNISSOSDISHKAARR KOISSIGELFOKKERGELIQUSROGATSHVILITDSEPSMEEN VERKIGTOAERDERIKKKRIGULEGOSSNPSSNISSOSDISHKAARR KOISSIGELFOKKERGELIQUSROGATSHVILITDSEPSMEEN VERKIGTOAERDERIKKKRIGULEGABRKKMIPAGNOEPTVUSMI ELMVGMPAMYVAACRANVEGGAIMBALSDTEIQREIGISINALIR LELKIALOPMUSTIPSSAPPTSTSSONWVITHETETISTSK TISSEGSMAQITAYGINMIEWIGNEUPSIGLIPDYRGSHLETISTK TISSEGSMAQITAYGINMIEWIGNEUPSIGLIPDYRGSHLETISTK TISSEGSMAQITAYGINMIEWIGNEUPSIGLIPDYRGSHLETISTK TISSEGSHAQITAYGINMIEWIGNEUPSIGLIPDYRGSHLETISTK TISSEGSHAQITAYGINMIEWIGNEUPSIGLIPDYRGSHLEND LEKKREESGHEIKOVLVYHTDOVVEWVOSIGLIPDYRGSHLEND LEKKREESGHEIKOVLVYHTDOVVEWVOSIGLIPDYRGSHLEND LEKKREESGHEIKOVLYTHOOVVEWVOSIGLIPDYRGSHLEND TORKLODODIVYFRASISWERTPREHITGRISMALSAFED AGRICULTATURA GERVISTATURA GERVERTPREHITGRISMALASAFETLA GERVSTLGTLOPPPAPKKIMPEARISHIINGGEMESTERITRESIERSHILLIGITERITSSAAODHILAIA KOLKRISSIGRIFORKERKERGHILOSAFPSSNISSODISHKAARR KOIKSSIGRIFORKERGHILOSAFPSSNISSODISHKAARR KOIKSSIGRIFORKERGHILOSAFPSSNISSODISHKAARR KOIKSSIGRIFORKERGHILOSAFPARSHINISHA LELWOMPANYVAACRANVESGAIRMAALSTETERAPEHTERVISSOMERIMINISHA LELWOMPANYVAACRANVESGAIRMAALSTETERAPEHTERVISSOMERIMINISHA LELWOMPANYVAACRANVESGAIRMAALSTETERAPEHTERVISSOMERIMINISHA LELKALAIQOMUSLISPSAPPTSRTSSGNWVIHERMETICETSPSSR TURLEKLGIPPAGABARATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	[1		HVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTNTYTSQDLKS
LLSPEGLOVUNGLINSTEPLIKEYARAPKIGARESSNEKVQVEAI BEGGLOKELLV LARGEQUEAKKKVLPACLGLINFPYAQROPKIL LOGIQVIRTLYOEKGTEVLAVRVUTLLYDLVTEKMEABERBELT. QEMSPEKLQOYROVHLIPGLMEQGMCEITVHLLALPEHDAREKV LQTIGVILITTCRDRYROPGLGRTLASIGARYQVILSELIQDES DEGTYGELIGSVINSLIKELR MORECLDATINEETEMINGERKESTELRAEEIETRVTSGSMEAINL KOLRKRGSIPTSLITDLSLASASPPLSGRSTFKLTSRSAAQDLDR MOWNTLPSDLEKHRRKLLSPYSERERMEDKATIKCETSPPSSPR THEKKIGHPALSGEBKSALEDQGSNPSSNSSOBSHKAKAR KGIKSSIGHIGKKEKKERULGLRARKGMPFAQMDGTTVVSML ELWIGNDARVALGTOAKSGAMSALEDGSNPSSNSSOBSHKAKAR KGIKSSIGHIGKKEKKERULGLRARKGMPFAQMDGTTVVSML ELWIGNDARVALGRANKSGAMSALSDTGGISNALMEL LELIALAIQEMVSLTSPSAPPTSRTSSGNWVTHEEMETLSTSK TDSEBGSMAQTLAVGDMIEMICREMILPSLLIPYGYRSYMBCLV DARHLDHLTKKDLRVHLRWDSPHRTSLQYGINCLKKRINTDRKE LEKRRESGHEIKDVLWWTNDQVHRWOSIGLEDYAGNLHESGV HAALLALDENDHTHLALILGIPTONTGARCHESFINILLAG TDRKLDDGDDKVFRRAPSWRRFRPEHHGRGGMLSASATLPA GFRVSTLGTICJPPAPPKKINPERSHHTLYRCHEFFINILLAG TDRKLDDGDDKVFRRAPSWRRFRPEHHGRGGMLSASATLPA GFRVSTLGTICJPPAPPKKINPERSHHTLYRCHESFINILAG TRILEKLGHPAHDHTLALILGIPTONTGARCHESFINILAG WOWMILPSDLRKHRKILSPVSRESKREBKATIKCETSPSSPS THLEKKGHPALSGEBKISALEDQGSNPSSNOSDLHKKARK KGIKSSIGHLFKKEKGRIJGLSROATGHVLLTDSEFSWGEM VPAKLGTOABEKREKKKLDEPVSRESKREBKATIKCETSPSSPSR TLEEKLGHPALSGEBKISALEDQGSNPSSNOSDLHKKARK KGIKSSIGHLFKKEKGRIJGLSROATGHVLLTDSEFSWGEM VPAKLGTOABEKREKKLLEPVSRESKREBKATIKCETSPSSPSR TLEEKLGHPALSGEBKISALEDGOSNPSSNOSDLHKKARK KGIKSSIGHLFKKEKGRIJGLSROATGHVLLTDSEFSWGEM VPAKLGTOABEKREKKLEDGONPSTSROSDSHKKARK KGIKSSIGHEKKEKKERIJGLSROATGHVLLTDSEFSWGEM VPAKLGTOABEKREKKLEDGONPSTSROSHAKHARK KGIKSSIGHEKKEKKERIJGLSROATGHVLLTDSEFSWGEM VPAKLGTOABEKREKKERIJGLSROATGHVLLTDSEFSWGEM ELKWGMPANYVAACRANVKGAMSALSDTEIQRFGIGISNALHR LLKLRIAGGMVSTALEDGONPSTSROSHAKHARK KGIKSSIGHEKKERIJGLGARGERSPSPFTFTSSGROMBEN GROOTGFMSCCLAQGWGARFLAKRANDARDARDONSHVKARK ELKWGMPANYVAACRANVKGATHANDARDEFTUKTOHMSPRE LEKKRESGHER KOVLWINDQVVHVONG LELQOYRSYFMECU DARHLDHLTKKDLEVHIKHUSPFTPARGGGGMLSASAETLA GFRYSTLGTLQPFPAPKKIMPEAHHNILYGHMLSAFRD ARGEGROFTER SARRAKGARSPRAPAPLEFTGARSPSPTFTGSTL ARGEGROFTER SARRAKGARSPRAPAPAPPEHPAPAGSABASGO				ALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVV
BGGALQKLLVILATEQPLTAKKKVLFALCSLLKHIFFYAQGQFLK LGGQVLRTIVQEKGTEVLAGVVVTLILDLVERABERBEALT QEMSPEKLQQYROVHLIPGLMEQGMCEITVHLIALPEHDAREKV LQTIGVILITCERDRYRQDPQLGRTLASLQARYQVLASLELQDGE BGGYFQELLGSVNSLIKERE 5649 1172 3006 MQGRQLDAINERIEMIQEEKESTELRAEEIETKVYSGSMEARNI KOLKRRGS IPTSILDISLASASPPLSGRSTF KLTSRSAAQDLDR MOVMTLEGDLARHERKILSPVSREEMREDKATIKCETSPPSSPR TIRLEKLIFFIBALSGERKSALEDQGSNPSSKOSSLHKGARR KGIKSSIGRLFGKKERGRILGLERDGARMENSOSSLHKGARR KGIKSSIGRLFGKKERGRILGLERDGARMENSOSSLHKGARR KGIKSSIGRLFGKKERGRILGLERDARKHERVALDTDSEFSMOREM VERKLGTOABRAVESGANVASGANSALSDTEIQREIGISNALHR LEHVLAIAQEMVSLTSPSAPPISRTSGSWAVTHEEMETLETSTK TISSEGSWAQTLAYGDMINEBVIGNEBVLGSLOPYRSYFMELUV DARMLDHLIKKDLEVHLKNVDSFFRTSLGVVOTHEEMETLETSTK TISSEGSWAQTLAYGDMINEBVIGNEBVLGSLOPYRSYFMELUV DARMLDHLIKKDLEVHLKNVDSFFRTSLGVVOTHEEMETLETSTK TISSEGSWAQTLAYGDMINEBVIGNEBVLGSLOPYRSYFMELUV DARMLDHLIKKDLEVHLKNVDSFFRTSLGVVOTHGERGISNALHR LEKREESGHEI KOVLWINDQVVHVVQS ICHQRKIKESGV HAALLALDENPDHATLALLIQIPTQNTQARQVMEREFFINLLALG GFRVSTLGTLQPPAPPKKIMPERHSHVILYGHMLSAFRD MGCOLDAINEET IMMTGERKESTELDAREIETHYGGSMEALMI KQLRKRGS IPTSLTDLSLASASPPLSGRSTPKLTSRSAQDLDR MCVMTLDSDLARHRRALLSFVSREERREDKATIKCTSPSSFR TLREKLGHPALSQESGKSALDQCSNPSSNSODSLHKGARR KGIKSSIGRLFGKREKGRILQLSRACKATIKCTSPSSFR TLREKLGHPALSQESGKSALDQCSNPSSNSODSLHKGARR KGIKSSIGRLFGKREKGRILQLSBARKGMPAQMIGGTVVSNL ELMVGMPAMYVAACRANVSGALMSALSDTEIQREIG SINALIR LELKIRLAG GEMVSLTSPSAPPTSSTSSGVWVTHEEMETLETSTK TDSEGSWAQTLAYGDMNIEMIGNEBUPSLOLDQVKSYFMECUV DARMLDHLYKKOLEVHLKMVDSPFRTSLGVCHKERLINDAINE LEKKRESGHEIKDVLWWINDQVVHWQSIGLADAYGRUHERLINDAINE LEKKRESGHEIKDVLWWINDQVVHWQSIGLADAYGRUHERSPAPPT WPALKAPTJAHDAYGARAAGAPPAPPAPPARPAPPAPPAPPAPPAPPAPPAPPAPPAPPA	1		1	IETDMQIMVRLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQD
LIGILQVIRTLYQEKGTEVLAVRVYTLLYDLVTEKMEARERAELT QEMSPERLOGYROVHILPOREGORGET TYLALPEIDAREKY LOTLGVILTTCRPRYQDPQIGRTLASIQAEYQVLASLELQDGE DEGTYGELIGSVNSLIKELR 5649 1172 3006 MORCIDATIREETEMTQEEKESTELRAEEIETRVTSGSMEAINI KOLKKRGS I PTSLTDLSLASASPPLSGRSTFKLTSGSAAQDLDR MOWNTLSSIGHERHRKILSPVSERENREDKATIKGTSPPSSPR TIRLEKIGHPALSQEEKSALEDQGSNPSSSNSSOSISHKABRR KGIKSSIGHERKEKKENDLOGSRDESSNSSOSISHKABRR KGIKSSIGHERKEKKENDLOGSRDESSNSSOSISHKABRR KGIKSSIGHERKEKKENDLOGSRDESSNSSOSISHKABRR KGIKSSIGHERKEKKENDLOGSRDESSNSSOSISHKABRR KGIKSSIGHERKEKKENDLOGSRDESSNSSOSISHKABRR KGIKKSIGHERANVKSGALMSALSDTEIGREIGISKALER LEKKIALDEMVSLTSSBAPTSHTSSGSWVWTHEEMETLETSK* TDSEGSWAQTLAYGOMNEBHIGNEBLEJLOPGYKSYPHECLV DARHDBHITKKOLEVLIKMVDSPHRTSLQYDHKSYPHECLV DARHDBHITKKOLEVLIKMVDSPHRTSLQYDHKSYPHECLV DARHDBHITKKOLEVLIKMVDSPHRTSLQYDHKSYPHECLV DARHDBHITKALDLID PTONTOARCHESPINLIGH LEKKRESGHEINDVLWMTNOQVHHVQSIGLBDVAGNLHESGV HAALLALDENPHHTLALLID LIPTONTOARCHESPINLIGH TORKLODGDDXVFRRAPSWRRFPEREHRGGGMLSASATLDA GFRVSTLGTLQPPAPPKKIMPEAHSHYLYGHHLSAPRD 5650 1172 3006 MIQECLDATINEEIMTQEEKSSTELRAEEIETRVTSGSMEAINI KOLKKRGSIGHIFAKKEKGRILDEDARRKAMPFAQMOOPTVUSNIL ELMVGMPANVAACRANVSGGAINSALSDTSIGLEGTSNALIR KKISSIGHIFAKKEKGRILDERARKGMPFAQMOOPTVUSNIL ELMVGMPANVAACRANVSGGAINSALSDTSIGLEGTISNALIR LIKLELATQEMVSLTSPSAPPTSRTSSGKVWUTHERMETLETSTK TDSEGSWAQTLAYGOMNEBIGNERHINGAPR VARLGTQAEKOMADELSGLOOPKSSTYPEGLV DARMDBHLIKKOLEVLIKMVDSPRTSLGYGIMCLEKINNDRIEE LEKREESGHEIKDVLWWINDQVHHVQSIGLEDVAGNILHESGV HAALLALDENDSPRTSLGYDIMCLERINDYDRE LEKREESGHEIKDVLWWINDQVHHVQSIGLEDVAGNILHESGV HAALLALDENDSPRTSLGYDIMCLERINDYDRE LEKREESGHEIKDVLWWINDQVHHVQSIGLEGTSNALIR LIKLELATQRABARAAPAPPTSRGGRAPAPPTSPTTTGGPAPACGRAP PAPALROPTHGRAPARSKRAPPAPALSHGTAAAALSPASAGD TORKLODGDDXVFRRAPSKRKRFPPEBHGGGGMLSASAFTLPA GFRVSTLGTILD TPONTOARCHESPINLLIAGE TORKLODGDDXVFRRAPSKRKRFPPEBHGGGGMLSASAFTLPA GFRVSTLGTILD TPONTOARCHESPINLLIAGE TORKLODGDDXVFRRAPSKRRFPPALSHGTVAAAALSPASPACP APPALROPTHGRAPARSSAAPAPAPALSHEHPAPARSASSOQ QTPGWBGSCLLQGVAGABELGARABGDTVAAAANESPACGRAPPA ADPALROPTHGRAPARSSABAPARAPALSHEHPAPARSASSOQ QTPGWBGSC				LLSFGGLQVVINGLNSTEPLVKEYAAFVLGAAFSSNPKVQVEAI
ORMSPEKLQOYRGUHLI-GEMEGGNCETTVILLALPERDAREKY	1	}	1	EGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLK
Introvilitacidayroliciasurol		İ		LGGLQVLRTLVQEKGTEVLAVRVVTLLYDLVTEKMFAEEEAELT
DEGYFOELLGSVINSLIKEUR			1	QEMSPEKLQQYRQVHLLPGLWEQGWCEITVHLLALPEHDAREKV
DEGYFOELLGSVINSLIKEUR			1	
KOLARKEGS I PTSLTULSLASASPPLGGRSTPKLITERSAAQDLDR MGVMTLPSDLRKHRRKLLSPVSREENREDKATI KCETSPPSSPR TLRIEKLGHPALSQEEGKSALEDQGSNPSSNSSGODSLHKGAKR KG IKSSIGRIFGKEKGRLIQLGERDGATGHVLUTDSEFSNQEPM VPAKLGTQAEKDRRIKKHGQLEDARKKEMPPAQMDGPTUSML ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISMALHR LKLRIAI JGEWSLITSPSAPPSRRTSAWVSTHEMETTELTSTK TDSEGGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYPMECLV DARMLDHLTKKDLRVHLKNVDSPHRTSLQYGIMCKRLNYDKRE EKKREESGNEI KDVLWYNTDQVUHWOSIGLRDYAGNLHESGV HGALLALDENPDINTLALILQIPTONTQAQVMEEFNNLLAIG TDRKLDDGDDKVFRRAPSWRKFRFPREHGGGMLSASABTLPA GFRVSTLGTLQPPPAPPKKIMPBAHSHYLYGHMLSAFRD 5650 1172 3006 MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNI KQLRKRGS I PTSLTULSLASASPPLEGGSTFEKLTSRSAQDLDR MOVMTLPSDLRKHRKLLSPVSREENREDKATI KCETSPPSSFR TLRIEKLGHPALSQEEGKSALEDQGSSSNSSGOSLHKGAKR KGIKSSIGRLFGKKERGRLIQLSRDGATGHVLLITDSFFSNGEPM VPAKLGTQAEKDRRLKKKHOLLEDARSSNSSSGOSLHKGAKR KGIKSSIGRLFGKKERGRLIQLSRDGATGHVLLITDSFFSNGEPM VPAKLGTQAEKDRRLKKKHOLLEDARSSNSSSOSLHKGAKR KGIKSSIGRLFGKKERGRLIQLSRDGATGHVLLITDSFFSNGEPM VPAKLGTQAEKDRRLKKKHOLLEDARNDFNEEMSTLETSTK TDSEGSSWAQTLAYGNMENEN GIREKMP PAQNDGTVUSML ELWYGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR LKLRLAIQENVSLTSPSAPPTSRTSSGNWVHTEEMSTLETSTK TDSEGSSWAQTLAYGNMENEN GIREKUPSALGLPQYRGFYFMECLV DARMLDHLTKKOLRVHLKWUDSFHRTSLQYGIMCLKKILNYDRE ELKYRERSGGEIKDLUVINTNOOVUNGJGLRDYNGANLEGGV HGALLALDENFOINTLALILQIPTONTQARQVMEREFNNILLAIG TDRKLDDGDDKVFRRAPSWRKFFPREHHGRGGMLSASATLPA GFRVSTLGTLQPPPAP PKKIMPERHSHTLYGMISAFRD AGRGGGTVAGELTALALAGASAAAA)APPTRGGPAPASASASO QTPCWPGGSCCLAQGWQAEPLGAPGABASHAYPAPALSHGASASASO QTPCWPGGSCCLAQGWQAEPLGAPGABADAPPPHPAPAPARGSASASO QTPCWPGGSCCLAQGWQAEPLGAPGABACHQASASASO QTPCWPGGSCCLAQGWQAEPLGAPGABACHQASASASO QTPCWPGSGLGLARGGIDDAYARRAGCGGRAPP WPADLRVUTTIGRAPAADGGSTLPAAPPHPAPAPARGSASASO QTPCWPGGSCCLAGGWAGEPLGABACGGGGCRTIPASA CMPSPPVEGSLGLARGGGGNAPPAPARGCASPAPPHPAPAPAPACSGRAPP WPADLRVUTTIGRAPARAGGGFTAARRAGGTPVAAAPNCRV*GSA CMPSPPVEGSLGLARGGGGNAPPAPARGAGGTGAAFRHLVPLIPPL LGPRGTGRPSSPB 5652 735 343 HHKKYQHTHQKSFSCPEPACKSFNFKKHLKHSDTRDYI CFCARSFRTSSILVLILLDILLGAGGGORVSHKKGGFTAPAL CFCARSFRTSSILVLILLDI			[
KOLAKKGSI PTSLTULSLASASPPLGGRSTPKLITGRSÄAGDLDR MGYMTLPSDLRKHRRKLLSPVSRERNEDKATI KCETSPPSSPR TLRIEKLGHPALSQEGGKSALENQGSNPSSNSSQDSLHGGAKR KGIKSSIGRIFGKKEKGRLIQLERDGATGHVLUTDSEPSMPERM VPAKLGTOARKDRIKKKHQULEDARKKMMPFAQMDGFVVSML ELWVGMPAWYVAACRANVKSGALMSALSDTEIQRSIGISNALHR LKLRIALJOEWSLTIPSJSAPPTSRTSJAVGTMUKVSTEMETTELTSTK TDSEGGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYPMECLV DARMLDHLTKKORVHLIMNUDSPHRTSLQYGIMCLKRIANYDKE ELKKRESSQHEI KOVLWYTINDQVVHWYDSIGLRDYAGNLHESGV HGALLALDENFDINTLALILQIPTQNTQARQVMEREFNNLLALG TDRKLDDGDDKVYRRAPSWRKRFRPREHKGRGMLSASABTLPA GFRYSTLGTLQPPAPPKKIMPEAHSHYLYGHMLSAFRD 5650 1172 3006 MLQEQLDAINEEIRMIQEEKESTELRAEEIFTRVTSGSMEALNI KQLRKRGS IPTSLTULSLASASPLEGRSTFEKLTSRSAAQDLDR MOWNTLPSDLRKHRKLLSPVSREENREDKATIKCETSPSSSR TLRIEKLGHPALSQEGGKSALEDQGSNPSSNSSQDSLHKGARR KGIKSSIGRIFGKKERGRLIQLSRDGATGHVLLITDSFFSWGPBM VPAKLGTQAEKDRIKKKHOLLEDARKOMPPAQWDGTVUSML ELWVGMPAWYVAACRANVXSGAIMSALSDTEIQREIGISNALHR LKLRIAIQEMVSLTSPSAPPTSRTSSGNWUTHEMETLETSTK TDSEGSKAQTLAYGMMHEMIGNEMUPSLGLPQYRGFYNECLV DARMLDHLTKKOLRVHLKMVDSPHRTSLQYGIMCLKKINNYDRE ELKKRESSGEIKDULVINTNDQVVHWGJGLRDYNGNLHESGV HGALLALDENFOINTLALILQIPTONTQARQVMEREFNNLLALG TDRKLDDGDDKVFRRAPSWRKFRPREHHGRGGMLSASATLPA GFRYSTLGTLQPPPAP PKKIMPEAHSHYLYGHMLSAFRD AGRGGGTPWG*EARRAGGATSASTAPRAALSFRGGMLSASATLPA GFRYSTLGTLQPPPAP PKKIMPEAHSHYLYGHMLSAFRD AGRGGGT*ASGLTLAAGASAAAA,PPTPRGGPAPASCRAPP WPALRVPTTIGRAPAPBRRAAPRAPALSHGTAAAALSPASPAGP APP*LPGFSSGSPFRG*RRGGGMLSASASTLPA GFRYSTLGTLQPPPAP PKKIMPEAHSHYLYGHMLSAFRD APP*LPGFSSGSPFRG*RRGGBABASASASQ QTPEWPGSCCLAQGWQAEPLQAPRAWSPAPPTPGSTPL AGRGGGT*ASGLTAAGASAAAAA,PPTPRGGPAPASCRAPP WPALRRVPTTIGRAPAADGGSTPLAAGASASASQ QTPEWPGSCCLAQGWQAEPLGAPGABACGCRAPP WPALRRAPAADGGSCLAQGPTAARRAAGGTPVAAAPNCRV*GSA CMPSPPVEGSIGLISARGHGDLPSQAR*GHTCPACKSLMW HORKHAETVAALRFPCEFCGKREKPDSVAAHRKSHPALLLA CFFCARSFRISSINLVHRR HTGEKFLQCEIGGFTCRQKASIMW HORKHAETVAALRFPCEFCGKREKPDSVAAHRKSHPALLLA CFFCARSFRISSINLVHERHTHTSKHSHPALLSHLLGFPTLKSUGMPTAFLL CFFCARSFRISSINLVHERHTHTSKHSHPALLSHL HKKYQHTHQKSTSCPPPTTATSLUDGGGGORVSHKKKGGFTAFAL CFFCARSFRISSINLVHERHTTSKHSPERLGLELDFLAGGGFTAFALLSH	5649	1172	3006	MLOEOLDAINEEIRMIOEEKESTELRAEEIETRVTSGSMEALNL
MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPSSPS TLRLEKLGHPALSQEEGKSALEDQGSNPSSNSSQDSLHKGAKR KGIKSSIGRIFGKKEKGRLIQLSRGATSHVALITDSPSNGEM VPAKLGTQARKDRRLKKHQLLEDARRKGMPFAQMDGPTVSWL ELWYGMPAWYAACRANVKGAĞIMASDTETQREIGISISNALHR LKLRLAIQEWSLTSPSAPPTSRTSGSNWWYHEEMSTLETSTK TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGJPQYRSYPMECLV DARWLDHLTKKDLRVHLKMUDSPHRTSLQYGIMCLKRLNYDRKE LEKKREESGNEI KDVLVWTNDQVHWQSIGLRDYAGNNLEESGV HABLLAIDEMPDINTLAILIQLIPTONTQARQWMEREFNNLALG TDRKLDDGDDKVPRRAPPWKRFPPREHHGRGGMLSASABTLPA GFRVSTLGTTLQPPPAPPKKIMPEBAHSHYLYGHMLSAPRD 5650 1172 3006 MLQEQLDAINEETRMIQEEKESTELBREEIERTVTSGSMEALNI KQLKRRGSIPTSLTDLSLASASPPLSGGRSTPKLTGSNAADLDD MCQEQLDAINEETRMIQEEKESTELBREEIERTVTSGSMEALNI KQLKRRGSIPTSLTDLSLASASPPLSGGRSTPKLTGSNAADDLDR MCVMTLPSDLRKHKRKLLSPVGREENREDKATIKCETSPSSPR TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM VPAKLGTQABKDRRLKKKGOLLEDARRKGMPFAQWIDDFTVUSWL ELWVGMPAMYVAACRANVKSGALMSALSDTETQRIOISMALHR LKILRLAIQEWSLITSPSAPPTSRTSQNWVTHEMBETLETSTK TDSEGSWAQTLAYGDMNHEWIGNEWLPSLGLDYGRSYPMECUV DARMLDHLTKKDLRVELKMVDSPHRETSLQYGIMCLKRLINVDRKE LEKRRESQHEIKDVLWYNDQVHWVQSIGLRDYAGNLHESGV HGALLALDENFONNTLALILQIPTQTTQARQWMEREFNNLLALG TDRKLDDODKVYRRAPSWRKFRFPREHHGRGGMLSASABTLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD TORKLDDODKVYBRAPSWRKFRFPREHHGRGGMLSASABTLPA GFRVSTLGTLQPPPAPPKKMPEAHSHYLYGHMLSAFRD APPAPPGFSSQSPFRG*RWGRSFSPPPPEPPGTL ANGEGAGIR*ASGITAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTTGGRAPARSRAAPRAPALSHITAAAALSPASPAGPA PAPALRPGFSSGSPFRG*RWGRGRDLPSGASASASO QTPGMPGSCCLAQGWQABPLAARGAGD,PVPPORGPPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGOTPVAAAPNCRV*GSA APALHRAPAAADPGSPLQAPPRAWASPAAAPHCBHATCHYGLG GFRASGSPSBS CMPSPFVEGSIGLISRGGGDLPSQAR*GHHECRRARHLIVPLPFL LGPGRTTGPSSBS ACMFSPVEGSIGLISRGGGDLPSQAR*GHHECRRARHLLYDLPFL LGPGRTTGPSSBS TGRGLGSRGFTLGALULLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL			1	<u> </u>
KGIKSSIGRLFGKKERGRLIQLGRDGATGHVLLIDSEPSMQEPM VPAKLGTQABKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWIL ELWVGMPAWYVAACRANVKSGATMASALSTTEIQREIGISNALHR LKLRIAIQEWVSLTSPSAPPTSRTSSGNVWYTHEEMETLETSTK TDSEGSWAQTIAYGDMHEBHIGHBLGLDPYRSYPMECLV DARMLDHLTKKDLRVHLKMVDSPHRTSLQYGIMCLKKLNYDRSE LEKRREBQHBIKOVLVWINDQVUHWVQSIGLRDYAGNLHESGV HGALLALDEMPDHNTLALILQIPTQNTQARQWGREFFNNLLALG TDRKLDDGDDKVFRRAPSWRRFRPREHHGRGGMLSASABTLDA GFRVSTLGTTQPPPAPKKIMPEAHSUTGGMLSASABTDA GFRVSTLGTTQPPPAPKKIMPEAHSUTGGMLSASABTDA KQLKRGSIPTSLTILDSLASASPPLEGGRSTALITGGBTSSTELRGEEITRVTSGSMEALNL KQLKRGSIPTSLTLDSLASASPPLEGGRSTALITGGBTSSTELRGEEITRVTSGSMEALNL KQLKRGSIPTSLTLDSLASASPPLEGGRSTALITGGBTSSTSGMLNALAIG MOVMTLPSDLRKHRRKLLSPVSREEMREDKATIKCETSPSSFR TLRLEKLGHPALSQEGKSALEDQGSNPSSSNSSODSLHKGARR KGIKSSIGRLFGKKREGRLIQLSRGATGHVLLTDSSFSSFSMCBM VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL ELWVGMPAMYVAACRANVKSGATMSALSDTEIQRGISNAHGARR KGIKSSIGRLFGKKERGRLIQLSRGATGHVLLTDSSFSSSFSMOBM VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL ELWVGMPAMYVAACRANVKSGATMSALSDTEIQRGISNAHGARR KGIKSSIGLAGVBAGTULAYDMNHBWIGNBULPSLGLGPGISNAHGARR TDSEEGSWAQTILAYGDMNHBWIGNBULPSLGLGPVGSTYFMECLV DARMLDHITKKDLRVHLKMVDSPHRTSLQYGIMCLKKLINVDRKB LEKRRESQHEIKDVLVWINDQVVHWVQSIGLRDYAGNLHESGV HGALLALDEMFPHNTLALILQIPTQTQARQWMREFRNNLSGU TRKLDDGDDKVFRRAFGARSSFSVENFREHIGGGGMLSASASTLPA GFRVSTLGTLQPPPAPKKIMPBAHSHYLYGMMLSAFRD TRKLDDGDDKVFRRAFGARSSFSVENFREHIGGGGMLSASASTLPA ARQGGROPWG*GEARAGRASSFSVENFREHIGGGGMLSASASTLPA ARQGGROPWG*GEARAGRASSFSVENFREHIGGGGMLSASASTLPA ARQGGROPWG*GEARAGRASSFSVENFREHIGGGGMCKTASASASTQ APAPCHSGSGSTGAAPGARGARSFAPAPHEPHPAPAGGGRAPP WPAPLRVPTHGRAPARGRAAPRAPALSHGTAAAALSPSAPAPP WPAPLRVPTHGRAPARGRAAPRAPALSHGTAAAALSPSAPAPP WPAPLRVPTHGRAPARGRAAPRAPALSHGTAAAALSPSAPAPP WPAPLRVPTHGRAPARAGAGTPYAAAAPTCHY*GSG ARMSGISBELLGAAGLSDNWARCGGPGAPG*GCCTTIPASA CMPSSPVEGSGGGARGAAPGAAGATPVAAAAPTCHY*GSG PAGSWAGLIAGYG*GAAPGTAATAFAAGGTPVAAAPRCTY*GSG ACMPSSPVEGSGLGLARGGGROPGCATTPASA CMPSSPVEGSGLGLARGGGGROFTAFBLUKPLPLFL LGPRGRTGTSSSSS GEGGGARGGGGGGGGGGGGGGGGGGGGGGGCTTABAGGGPGCACTTPLTKDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG			1	_ ·
VPAKLGTQABKDRRLKKKUGLLEDARRKGMPFAQMOCPTVUSWL ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR LKLRLAIQEWVSLTSPSAPTSRTSSGNVWTHEEMSTLETSTK TDSEGGSWAQTLAYGMNNEWIGNBWLPSLGLPQYRSYPMECLV DARMLDHLTKKOLRVHLKWUDSFISLQYGIMCLKRLNYDRKE LEKRRESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDEBPDHNTLALILQIPTONTQARGVWEREFINILALG TDRKLDDGDDKVFRRAPSWRKRFPREHHGRGGMLSASABTLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSASABTLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSASABTLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD MULGQLDAINEEIRMIQEBKESTELRAEEIETRVTSGSMEALNI KQLRRGGIPTSLTDLSLASASPPLSGRSTFKLITSRSAAQDLDR MGWMTLPSDLRKHRRKLLSPVSREENRBDKSTIKCETSPPSSFR TILBEKLGHPALSGEBGSALEDGSPSSNSSOSDSLHKGAKR KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM VPAKLGTQABEDBRIKKRKULGDARRKGMPFAQWGPTVVSWL ELWVGMPAWYVAACRANVXSGAIMSALSDTEIQREIGISNALHR LKLRLAIQEWSLTSPSAPPTSRTSSGNVWVTHERMSTLETSTK TDSEGGSWAQTLAAGMONHEWI GANDEPSLGLDQYNSYFMECLV DARMLDHLTKKDLRVHLWNDSFHRTSLQYGIMCLKRLNYDRKE LEKRESGSHACTLAAGMONHEWI GANDEPSLGLDQYNSYFMECLV DARMLDHLTKKDLRVHLWNDSFHRTSLQYGIMCLKRLNYDRKE LEKRESGSHACTLAAGMONHEWI GANDEPSLGLDQYNSYFMECLV TDSKLDDGDDKVFRRAPSWRKFFRREHRGRGGMLSASASTLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD AGGGGGTR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WAPLIKUPVTHGRAPAPARSRAPAPAHPHPHAPAGSASASO QTPGMPGSCCLAQGWQABEJGAPGAGADAPACCRY-GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGTVAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASO QTPGMPGSCCLAQGWQABEJGAPGAGACTYVAPAPCKRY-GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGTVAAAADPACKRY-GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGTTVAAAPACKRY-GSA PALHRAPAADPGSPLQAPPRAWASPAAAGTGPOTATAPACKTY-GSA PALHRAPAADPGSPLQAPPRAWASPAAAGTTVAAAPACKRY-GSA PALHRAPAAADPGSPLQAPPRAWASPAAGGGLSSSDYCGGLGA GWRAGISPBLLGAGLSDNWARCCPGPGPAE*GGQPCCRTIPASA CMPSSPVEGSLGLSGRKRHGLDLSQAR*GWHECRRARKLVPLEPL LGPRGRTGRPSSPS 5652 735 343 HKKVQHTHQKSFSCPPAGGKSFWFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGEKPLQCEICGFTCRQKASLNW HGRKHAETVAALRFPCEFCGKFERPDSVAHRSKSHIPAALLLA CPPQPCGGTRRGRRSLKEATEPQLAWABEFVTLKDVGMOPTL CPPQPCGGTRRGRRGRSLKEATEPQLAWABEFVTLKDVGMOPTL CDWEQLGLEGGOTFWUTALNDCQLLFLDPPPRWATSHDDED LEPLAGGSPEATSSDVTETKNSP	1			TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR
ELWVCMPAWYVAACRANVKSGAIMSALSDTBIQREIGISNALHR LKRIAIQEMVSLTSPSAPTSRTSSGVWVTHEEMETLETSTK TDSEGSWAQTLAYGDMNIEWIGNBWLPSLGLPQYRSYFMEGLV DARMLDHLTKKDLRVHLKWDSFHRTSLQYGIMCLKRLINYDRKE LEKRRESQHEIKDVLVWTINDQVVHWVQSIGLRDYAGNLHESGV HGALLALDEMPINNTLALILQIPTQNTQARQVMEREFINNLLAG TDRKLDDGDDKVFRRAPSWRKFRFREHHERGGMLSASABTJPA GFRVSTIGHTQPPAPPKKIMPEAHSHVLYGHMLSAFRD 5650 1172 3006 MLQEQLDAINEETMIQEBKESTELRAESIETRVTSGSMEALNI KQLRKRGSIETSLTDLSLASASPPLSGRSTFKLTSRSAAQDLDR MGVMTLPSDLRKHRRKLLSBPVSREENRBDKATIKCETSPPSSFR TIRLEKLGHPALSQEBGKSALEDQGSNPSSSNSSODSLHKGAKR KGIKSSIGRLFGKKKKGLLEDARRGMFFAQMDGPTVVSML ELWVGMPAWYVAACRANVXSGAIMSALSDTBIQREIGISNALHR LKIRLAIQEMVSITSPSAPPTSGSVWVTHEMBMTLETSTK TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKWDDSFHRTSLQYGIMCLKRLMYDRKE LEKRRESQHBIKDVLWVINDQVVJWVQSIGLRDYAGNHESGV HGALLALDENDHNTLALILQIPTQNTQARQVMEREFINILALG TDRKLDDGDDKVFRRAPSWRKFFRREHERGGMLSASAETLPA GFRVSTTLGTLQPPPAPPKKIMPEAHSHVLYGHMLSARRD 5651 646 1869 ARGGGRDFWG*BARAKGPASESPRV*ESGGEGPASP*TPGSTL AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGRPAPAGCGRAPP WPAPLRVDTHGRAPARPSRAAPRAPALSHTGPAPAGCGRAPP WPAPLRVDTHGRAPARPSRAAPRAPALSHTGPAPAGCGRAPP WPAPLRVDTHGRAPARPSRAAPRAPALSHTAYAGHGTPAAAALSPASAGO QTPGMPGSCCLAGWQABELGARPGALSYPYVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRWMSPAAAGGGLSSSNYCGGLGA GRAGISPELIGAGALSDWNARCPGPAB*GGGGCTTPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARLVPLPRL LGPRGSCCLAGGALSDWNARCPGPAB*GGGCCTTPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARLVPLPRL LGPRGSTGRSSPS AGHAGLSSBLGAGAGSDMNARCPGPAB*GGGGCTTPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARLVPLPRL LGPRGTTGRSSPS 5652 735 343 HKKKYGHTHQKSFSCPPPAGGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRHTGBKPLQCEICGFTCROKASLNW HQKHABTTVAALRFPCEFGGKFEKPDSVAAHRSKSHPALLLA CFPQCPGTTRGRRSSPS 66 1401 RGRLQSRGRTTLGULLLLDLILGARQHGGRVSHGWKGGFLTAPL CPPQCPGTRRGRRSLKEATEPQLAMAEFFVTLKDVGMDFTL CGPQASPGRTSSDVTTKNSFTLEDPTFEBGFSQEIT/SRDVIG CDWEQLGLEQGDTFWDTALDNCQLILDPPPRNLTSHPDGSED LEPLAGGSPEATSSDVTTKNSFTLEDPFFEBGFSQEIT/SRDVIG CDWEQLGLEQGDTFWTTALDDTALDNCQDFFEBGFSQEIT/SRDVIG CDWEQLGLEQGDTFWTTALDDTALDDCDFPRNLTSHPDGSED	ļ		1	KGIKSSIGRLFGKKEKGRLIOLSRDGATGHVLLTDSEFSMOEPM
ELWVCMPAWYVAACRANVKSGAIMSALSDTBIQREIGISNALHR LKRIAIQEMVSLTSPSAPTSRTSSGVWVTHEEMETLETSTK TDSEGSWAQTLAYGDMNIEWIGNBWLPSLGLPQYRSYFMEGLV DARMLDHLTKKDLRVHLKWDSFHRTSLQYGIMCLKRLINYDRKE LEKRRESQHEIKDVLVWTINDQVVHWVQSIGLRDYAGNLHESGV HGALLALDEMPINNTLALILQIPTQNTQARQVMEREFINNLLAG TDRKLDDGDDKVFRRAPSWRKFRFREHHERGGMLSASABTJPA GFRVSTIGHTQPPAPPKKIMPEAHSHVLYGHMLSAFRD 5650 1172 3006 MLQEQLDAINEETMIQEBKESTELRAESIETRVTSGSMEALNI KQLRKRGSIETSLTDLSLASASPPLSGRSTFKLTSRSAAQDLDR MGVMTLPSDLRKHRRKLLSBPVSREENRBDKATIKCETSPPSSFR TIRLEKLGHPALSQEBGKSALEDQGSNPSSSNSSODSLHKGAKR KGIKSSIGRLFGKKKKGLLEDARRGMFFAQMDGPTVVSML ELWVGMPAWYVAACRANVXSGAIMSALSDTBIQREIGISNALHR LKIRLAIQEMVSITSPSAPPTSGSVWVTHEMBMTLETSTK TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKWDDSFHRTSLQYGIMCLKRLMYDRKE LEKRRESQHBIKDVLWVINDQVVJWVQSIGLRDYAGNHESGV HGALLALDENDHNTLALILQIPTQNTQARQVMEREFINILALG TDRKLDDGDDKVFRRAPSWRKFFRREHERGGMLSASAETLPA GFRVSTTLGTLQPPPAPPKKIMPEAHSHVLYGHMLSARRD 5651 646 1869 ARGGGRDFWG*BARAKGPASESPRV*ESGGEGPASP*TPGSTL AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGRPAPAGCGRAPP WPAPLRVDTHGRAPARPSRAAPRAPALSHTGPAPAGCGRAPP WPAPLRVDTHGRAPARPSRAAPRAPALSHTGPAPAGCGRAPP WPAPLRVDTHGRAPARPSRAAPRAPALSHTAYAGHGTPAAAALSPASAGO QTPGMPGSCCLAGWQABELGARPGALSYPYVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRWMSPAAAGGGLSSSNYCGGLGA GRAGISPELIGAGALSDWNARCPGPAB*GGGGCTTPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARLVPLPRL LGPRGSCCLAGGALSDWNARCPGPAB*GGGCCTTPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARLVPLPRL LGPRGSTGRSSPS AGHAGLSSBLGAGAGSDMNARCPGPAB*GGGGCTTPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARLVPLPRL LGPRGTTGRSSPS 5652 735 343 HKKKYGHTHQKSFSCPPPAGGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRHTGBKPLQCEICGFTCROKASLNW HQKHABTTVAALRFPCEFGGKFEKPDSVAAHRSKSHPALLLA CFPQCPGTTRGRRSSPS 66 1401 RGRLQSRGRTTLGULLLLDLILGARQHGGRVSHGWKGGFLTAPL CPPQCPGTRRGRRSLKEATEPQLAMAEFFVTLKDVGMDFTL CGPQASPGRTSSDVTTKNSFTLEDPTFEBGFSQEIT/SRDVIG CDWEQLGLEQGDTFWDTALDNCQLILDPPPRNLTSHPDGSED LEPLAGGSPEATSSDVTTKNSFTLEDPFFEBGFSQEIT/SRDVIG CDWEQLGLEQGDTFWTTALDDTALDNCQDFFEBGFSQEIT/SRDVIG CDWEQLGLEQGDTFWTTALDDTALDDCDFPRNLTSHPDGSED				VPAKLGTOAEKDRRLKKKHOLLEDARRKGMPFAOWDGPTVVSWL
LKLRLAIOEMVSLTSPSAPPTSRTSSGNVMVTHEEMSTLETSTK TTSEEGSWAQTTLAYGMNHEWIGNEHPSLGLPQYRSYMECLV DARMLDHLTKKDLRVHLKWUDSFHRTSLQYGIMCLKELNYDRKE LEKRRESGHEIKDVLWYNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENPDHNTLALILQIPTQNTQARQHRESFNNLLALG TDRKLDGDDKVFRRAPSWRKRFRPREHHGRGMLSASABTLPA GFRVSTLGTLQPPPAPPKKIMPEARISHIVLYGHMLSAFRD GFRVSTLGTLQPPAPPKKIMPEARISHIVLYGHMLSAFRD MAGEQLDAINESIEMIGOERGETERABEIETRYTSGSMBALNI KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAQDLDR MOVMTLPSDLRKHRRKLLSPVSREENREBLATIKCTTSSPSSFR TLRLEKLGHPALSGESGKSALEDQCSNPSSSNSSODSLHKGAKR KGIKSSIGRLFGKKEKGRLIQLSRCAGTGHVTL/TDSEFSMGFM VPAKLGTQAEKDRIKKKKGULEDARRGMPFAQMOPTVUSML LEHWCMPAWYVAACRANVKSGALMSALSDTEIQREIGISNALHR LKLRLAIQEWVSLTSPSAPPTSRTSSGNVWVTHEMSTLETSTK TDSEGSGAGOTLAGYGMNHEWIGHDEPSLCLPQTRSYFMELV. DARMLDHLTKKDLRVHLKWODSFHRTSLQYGIMCLKRLNYDRKE LEKRRESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENPEHNTLALILQIPTONTQARQVMREBERNNLLALG TDRKLDDGDDKVFRRAPSWRKFFRPEHHGRGGKLSASASTLPA GFRVSTIGGTLQPPAPPKKIMPEAHSHVLYGHMLSAFRD 5651 646 1869 ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AMGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WAPLRVPTHGRAPAPARSRAPAPAHSHGTAAAALSPASPAGP ADP*LPGHSSGSPPAPARSRAPAPAHSHGTAAALSPASPAGP ADP*LPGHSSGSPPBPARRRAPARAGGTVVAAAPPKCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGGTLSGCATAP ACHEROPAPAGGARAPAACHTAAAPRCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGGTLSSDYCGGLGA GWRAGISPBLIGAAGLSDNWARCOGPPAP*GCGCTTPASA CMPSPPVEGSLGLSRKHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS AGSAGLAGYG*AGALSDNWARCOGPPAP*GCGCTTPASA CMPSPPVEGSLGLSRKHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS AHKKVHTHQKRSFSCPPPAGGKSFNFKKHLKEHMKLHSDTRDYT CEFCARSPRTSSNLVIHRRIHTGEKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGRFEREPDSVAHRSKSHPALLLA CEFCARSPRTSSNLVIHRRIHTGEKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGRFEREPDSVAHRSKSHPALLLA CFPQPQPGTRRGRRSLEKATEPQLAMBESCPTLKDVFGDFLL CPPQPQPGTRRGRRSLEKATEPQLAMBESCPTLTKDVGMOFTL CDPQPQPGTRRGRRSLEKATEPQLAMBESCPTLTKDVGMOFTL CDPQPQPGTRRGRRSLEKATEPQLAMBESCPTLTKDVGMOFTL CDPQPQPGTRRGRRSLEKATEPQLAMBESCPTLTKDVGMOFTL CDPQPGGBGGRGTTTPATAGGTPTHKDTFTHDGSED LEPLAGGSPEATSSDVTTKNSFTLMOFFEGSFGGEI/SRDVI CDPGLGLEGG	ļ			
TISSEGSWAQTLAYCOMNHEWIGNEWLPSIGALPQYRSYMECLV DARMIGHLTKKDLRVHLKWTDSPHTSLQYGIMCLKRLNYDRKE LEKKREESGHEI KDVLWTMDQVVHWQSIGLRDYAGNLHESGV HGALLALDENPPHNTLALILQIPTQNTQARQVWERSFNNILALG TDRKLDDGDDKVFRRAPSWRKFFREHHGRGGMLSASABTLPA GFRVSTLGTLQPPPAPPKKLMPERHHGRGGMLSASABTLPA GFRVSTLGTLQPPPAPPKKLMPERHSHYLYGHNLSAFRD 5650 1172 3006 MLQEQLDAINEEIRMIQBEKSSTELRABEIETRVTSGSMEALNL KQLRKRGSIPPISJTDLSLASASPPLSGRSTPKLYTSGSMEALNL KQLRKRGSIPPISJTDLSLASASPPLSGRSTPKLYTSGSMEALNL KQLRKRGSIPPISJTDLSLASASPPLSGRSTPKLYTSGSMEALNL KQLRKRGSIPPISJTDLSLASASPPLSGRSTPKLYTSGSMEALNL KQLRKGSIGRLFGKKEKGRLJQJSRDSSNSSQDSLHKGAKR KGIKSSIGRLFGKKEKGRLJQLSRDATGHVLLTDSEFSWGRPM VPAKLGTQAEKDRRKKKKGLLDGSBTPSSNSSQDSLHKGAKR KGIKSSIGRLFGKKEKGRLJQLSRDATGHVLLTDSEFSWGRPM VPAKLGTQAEKDRRKKKKGLLDGSBTSSNSSQDSLHKGAKR LELWCMPANYVAGCRANVKSGAIMSALSDTEIQREIGISNALHR LELWLAIQEMWSLTSPSAPPTSSTSSGNWWTHEMETETSTK TDSEGSWAQTLAYGDWHHWIGNEUPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKWNDS PHRTSLQYGIMCLKRLNYDRKE LEKKREESGHEIKDVLWWTNDQVVHWQSIGLRDYXGNHEEGT HGALLALDBNFDHNTLALILQIPTONTQAQVWEREFNILALG TDRKLDDGDDKVYRRAPSWRKRFPRRHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPKKIMPERHSHYLYGHMLSAFRD FRVSTLGTLQPPPAPKKIMPERHSHYLYGHMLSAFRD FRVSTLGTLQPPPAPKKIMPERHSHYLYGHMLSAFRD FRVSTLGTLQPPAPAPKGRGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAPRAPALSHGTAAAALSPASPAGP AND*LPGHSSGSLGAGSFRFKKMPERAPALSHGTAAAALSPASPAGP AND*LPGHSSGSLGAGAGAFTAAAALSPAPATHEHPAPAGSGASASQ QTPGMPGSCLGAGWQAEPLGABGABGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAPAPALSHGTAAAALSPASPAGP ADP*LPGHSSGSPPRG*RWGSPARAFRAPALSHGTAAAALSPASPAGP ADP*LPGHSSGSLGAGAGAGPATAPAAAGGTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPGARBGPAPAGCGRAPP WPAPLRVPTHGRAPAAPGSPLOAPRAFGGGPACTTPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGTTGRSSPS 5652 735 343 HHKKYGHHQKSFSCPBPAGGKSFNFKKHLKEHMKLHSDTRDYI CFFCARSFRTSSNLVIHRRIHTGRKPLQCEICGFTCROKASLNW HQKKHAETVAALRFPCEFGCKRFEKPDSVAAHRSKSHPALLLA CPPQPCQPGTRRGRSLKEATEGOLAMAREFYTLKOVGMDFTL GDWGQLGLEQGDTPWDTALDNCQLIFLLDPPRPNLTSHPDGSEL CPPQPCQPGTRGRGRSLKEATEGOLAMAREFYTLKOVGMDFTL GDWGQLGLEQGDTPWDTALDNCQLIFLLDPPRPNLTSHPDGSEL DEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSGET/SRDVI				_ · · · · · · · · · · · · · · · · · · ·
DARMLDHLTKKDLRVHLKMVDSPHRTSLQYGIMCLKRLNYDRKE LEKRREESQHBI KDVLWWTNDQVHWVQSIGLRDYAGNLHEGGV HGALLALDENPHPHTILALII QI PTQNTQARQVWEREFNNILALG TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASABTLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHNLSAFRD 5650 1172 3006 MLQEQLDAINEEIRMIQEBEKSSTELRABEIETRVTSGSMEAINL KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAQDLDR MCVMTLPSDLRKHRKLLSPVSREENREDKATIKCETSPPSSPR TLRLEKLGHPALSQEEGKSALEDQGSNPSSNSSODSLHKGAKR KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQFPM VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWGFTVVSWL ELWVCMPANYVAACRAVKSGAIMSALSDTEIQREIGISNAHR LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLMYDRKE LEKREESQHBI KDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENFDHNTLALILQI PTQNTQARQVMEREFNNLLALG GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD ARGGQGQPWG*EARAKGPASSPVY*EGSGWEGPASP*TPGSTL AWGGGAGIR*ASGLTAAGAASAAAA/PPTTRGGPAPAGGGRAPP WPAPLRVPTHGRAPAPRSRAAPARAPEAHPAPAGSASASQ QTPGMPGSCCLAQGWQAEPLGAPGABGASAAAA/PPTTRGGPAPAGGGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPLSHTHAAAALSPASPAGD ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGMPGSCCLAQGWQAEPLGAPGABGDQTVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAMASPAAAGGTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAMASPAAAGGTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAMASPAAAGGTPVAAAPNCRV*GSA GWRAGISPELLGAAGLSDNWARCPGPGPAB*GGQPGCRTIPASA CMPSPPVRGSLGJSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGTGRPSSPS 5652 735 343 HHKKYQHHQKSFSCPEPAGGKSFNFKKHLKEHMKLHSDTRDYI CFFCARSFRTSSNLVIHRRIHTGGKPLQCEICGFTCCRKASLNW HQKHAETVAALRFPCEFGGKFFKKPDSVAAHRSKSHPALLLA CFFQAPGGFTLGLVLLLLDILGARQHGGRVSHGWGGFLTAPL CFPQPQPGTRRGRRSLKEATEQLAMAEEFYTLKDVGMDTTL GDWGULGLEQGDTFWDTALDNCQDLFPLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIC	ļ	ł		-
LEKRRESQHEIKDVLVWTNDQVVHWQSIGLRDYAGNLHESGU HGALLALDENPHNTLALILQIPTONTQARQWEREFNNLLALG TDRKLDDGDDKVFRRAPSWRKFFRPEHHIGRGGMLSASABTLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLVGIMLSAFRD MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALINL KQLRKGSIPTSITDLSLASASPPLSGRSTPKLITSRSAAQDLDR MGYMTLPSDLRKHRKRLLSPVSREENREDKATIKCETSPPSSPR TLRLEKLGHPALSQEEGKSALEDQGSNPSSNSSQDSLHKKGAKR KGIKSSIGHFGKKEKGRLIQLSRNGATHVLLITDSEFSMQERM VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQMGPTVUSWL ELWVGMPAPVVAACRANVASGAIMSALSDTEIQREIGIBNALHR LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWTHEEMETLETSTK TDSEGSSWAQTLAYGDMNHEWIGNBEUPSLGLDQVRSYFMECLV DARMCDHLTKKKKDLVHLKWUDSFHRTSLQYGIMCLKRLMYDRKE LEKRRESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENFPHNTLALILQIPTONTQARQVMEREFNNLLALG TDRKLDDGDDKVFRRAPSKRFFRFEHHERGGMLSASABTLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGIMLSAFRD 5651 646 1869 ARQGQRQWG*EARARGPASSESRV*EGSGWEGAPSP*TPGSTL AMGGGAGIR*ASGLTAAAAAAAPPAPPTRGSPAPAGCGRAPP WPAPLKVPHGRAPAPRSBAAAPAPAPHEPHPAPAGSAASA QTPGWFGSCCLAQGMQAEPLGAPGAEDG\PVPPQAGCGRAPP WPAPLKVPHGRAPAPRSBAPRAPALSHGTAAAALSPASPAPA ADP*LPGHSSQSPPRG*MGMSRSAPAPAPHEPHPAPAGSAASA QTPGWFGSCCLAQGMQAEPLGAPGAEDG\PVPPQAGFFLGTLGS PAGSWAGLAGYG*AGAPGTOATAPRAAGTTPVAAAPNCRV*GSA GMRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRSPSS 5652 735 343 HKKKYQHINGKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CFFCARSFTSSNLVHRRIHTGEKPLQCEICGFTCROKASLNW HQRKHAETVAALRFPCEFCGKREKPDSVAAHRSKSHPALLLA FORDGSGRITTGLVLLLLDILGARQHGRVSHGMKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFYTLKDVGMDFTL GDWGQLGLEQDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKMSPLMEDFFEEGFSGEI/SRDVIG GDWGQLGLEQDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKMSPLMEDFFEEGFSGEI/SRDVIG		1	1	-
HGALLALDENPOHNTLALILQIPTONTQARQVMEREFNNILALG TDRKLDDGDDKVFRRAPSWRKRFREHHGRGGMLSASABTLD GFRVSTLGFILQPPAPPKKIMPEAHSHYLYGIMLSAFRD 5650 1172 3006 MLQEQLDAINEEIRMIQEBKESTELRAEEIETRVTSGSMEALNI. KQLRKRGSIPTSLITDLSLASASPPLSGRSTPKLITSRSAAQDLDR MGVMTLPSDLRKHRKLLSPVSREENREDKATIKCETSPSSSR TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR KGIKSSIGRLFGKKEKGRLIQLSGROATGHVLLITDSEFSMGEPM VPAKKLGTQAEKORRIKKKRLDEDARRKGMPFAQMGPFTVSWIL ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR LKIRLAIGEMVSLITSPSAPPTSRTSSGWVWTHEBEMETLETSTK TDSEEGSWAQUTLAYGDMNHUBUTGNEWLPSLGLPQVRSYFMECLV DARMLDHLTKKDLRVHLKWDSFHRTSLQYGIMCLKRLNYDRKE LEKRRESGHEIKDVLVWTNDQVVJENGFMILLALG TDRKLDDGDDKVFRRAPSWRKFFPREHGGGMLSASABTLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGIMLSAFRD 5651 646 1869 ARGGGRQPWG*SEARAGFAPSESPRV*EGSGWEGPASP*TFGSTL AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPADLRVFTHGRAPAPRSRAAPRAPABHGTAAAALSPASPAGP WPADLRVFTHGRAPAPRSRAAPRAPABHGTAAAALSPASPAGP ADP*LJGHSSGSJPBG*SRMGRSRSAPAPAHPEHPAPAGSASASO QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTOATAPRAAGGTPVAAAPNCRV*GSA AGHRAPAAADPGSFLAAPDFRAAGGTPVAAAPNCRV*GSA AGHRAPAAADPGSFLAAPDFRAAGGTPVAAAPNCRV*GSG AGRAGISPELLGAAGLSDNWARCPGPGPAB*GGQPGCRTIPASA CMPSPPVEGSLGLSKRGHGDLPSQAR*GWHECRRARHLVPLFRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHTHQKSFSCFEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVHRRIHTGRKPLQCEICGFTCRCKASLNW HCRKHAETVAALRFPCEFGCKFEKPDSVAAHRRSSKHPALLLA FCEFCGRFFTSSNLVHRRIHTGRKPLQCEICGFTCRCKASLNW HCRKHAETVAALRFPCEFGCKFEKPDSVAAHRRSSKHPALLLA CFPQPCQPGTRRGRRRSLKEATEPQLAMAEEFVTLKDVCMDFTL GDWGLGLEQGDTFWDTALDNCQDLFLLDPPRNTLTSHPGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ				_
TORKLDDGDDKVPRRAPSWRKRPRPREHHGRGGMLSASABTLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD 5650 1172 3006 MLQEQLDAINEETRMIQEBEKSTELRAEEIETRVTSGSMEAINL KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR MOVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR TLRLEKLGHPALSQEESGKSALEDQGSNPSSSNSSQDSLHKGAKR KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVUSWL ELWVGMPAWYVAACRANVKSGALMSALSDTEIQRRIGISNALHR LKIRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK TDSEEGSWAQTLAYGDMNHEWIGMEUPSLGLPQVRSYFMECLV DARMLDHLTKKDLRVHLKWUDS PHRTSLQYGIMCLKRLNYDRKE LEKRRESGHEIKDVLWWITDQVVHWVQSIGLRDYAGKLHESGV HGALLALDENFDINTLALILQIPYONTQARQWMEREFINILALG TDRKLDDGDDKVPRRAPSWRKFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD 5651 646 1869 ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGEGGGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRAAPAAPAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRAAPARPAALGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAPHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPAGFTLGTLGS PAGSWAGLAGYG*AGABGAADAOATDVAAAPHORURV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSDYCGGLGA GRAGISPBLLGAAGLSDNWARCPGPGPAB*GQGPGSTTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPAGGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLV1HRRIHTGEKPLQCEICGFTCRQKASLNW HQRKHAETVAALKFPCEFGCKRFEKPDSVAAHRSKSHPALLLA FGRQGGGPTTWDAALHONCQDLFLUDPPRNLTSHPDGSED LGPLGAGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ GDWGULGLEQGDTFWDTALDNCQDLFLUDPPRNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ	į			
GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD 5650 1172 3006 MLQECLDAINEEITRMIQEEKESTELRAEEIETRVTSGSMEALNL KQLRKEGS 1PSIJTDLSLASASPPLSGRSTPKLITSRAAQDLDR MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR TLRLEEKIGHPALSQEEGKSALEDGGSNPSSSDNSGDSLHKGAKR KGIKSSIGHFGKKEKERKLLQSRDGSNPSSSDNSGDSLHKGAKR KGIKSSIGHFGKKEKERKLLQSRDGSNPSSSDNSGDSLHKGAKR KGIKSSIGHFGKKEKERKLLQSRDGSNPSSSNSGDSHKGAKR VPAKLGTQAEKDRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL ELWYGMPAMYVAACRANVKSGALMSALSDTEIQREIGISNALHR LKURLAIQEMVSLTSPSAPPTSRTSGSCNWVTHEEMETLETSTK TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKMYDSPHTSLQYGIMCLKRINYDRKE LEKRRESQHEIKDVLWTMDQVVHWVQSIGLRDVAGNLHESGV HAALLALDENFDHNTLALILQIPTQNTQARQVMEREFMNLLALG TDRKLDDGDDKVFRRAPSWRKFFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHLYGHMLSAFRD 5651 646 1869 ARQGQRQFWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGEGGGIR*ASGITAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPARSRAPRAPLSHGTAAAALSPASPAGP ADP*LDGHSSQSPPRG*ERGRARAPAAPALSHGTAAAALSPASPAGP ADP*LDGHSSQSPPRG*AWGSRSAPAPAHPEHPAPAGSASASQ QTPGWEGSCCLAQGWQAEPLGAPGAGEDG\PVPPQRGFFLIGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTVAAAPNCRV*GSA PALHRAPAAADPGSSLQAPPRAWASPAAAGPGLSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAB*GQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYT CEFCARSFRTSSNLV1HRRITHTGKERPLQCEICGFTCRKASLNW HCRKHAETVAALRFPCEKGKFFKENDSVAAHRSKSHPALLLA 5653 66 1401 RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CPPQPCQPGTRRGRRRSLKBATERQLAMAEEFYTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ				
S650 1172 3006 MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL KQLRKRGSIPTSITDLSLASASPPISGRSTPKLTSRSAQQLDR MGWMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSER TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKK KGIKSSIGRLFGKKEKGRLIQLSRGATGHVLLTDSEFSMCPM VPAKLGTQAEKDRRLKKKHQLSEDGATGHVLLTDSEFSMCPM VPAKLGTQAEKDRRLKKKHQLSEDGATGHVLLTDSEFSMCPM VPAKLGTQAEKDRRLKKKHQLSEDGATGHVLLTDSEFSMCPM VPAKLGTQAEKDRRLKKKHQLSEDGATGHVLLTDSEFSMCPM VPAKLGTQAEKDRRLKKKHQLSEDGATGHVLTTSEFSMCPM VPAKLGTQAEKDRRLKKHQLSEDGATGHVLTTSEFSMCPM VPAKLGTQAEKDRAKKKHQLSEDGATGHVLTTSEFSMCPM VPAKLGTQAEKDRAKKKHQLSEDGATGHVAWHEETILETSTK TDSEEGSWAQTLAYGDMNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKMDSPHRTSLQYGIMCLKRINYDRKE LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENFDINTLALLIQIPTQNTQARQVMEREFINILALG TDORKLDGAGGAGATARA TOPANTAGAGAGATAPA VPAHLAGAGAGAGAA VPAHLAGAGAGAGAA VPAHLAGAGAGAGAGAGAGAA VPAHLAGAGAGAGAGAGAAAA VPAHTRGGAPAAGAGGRAPP WFAPLRVPTHGRAFAFRSRAPARPALSHGTAAAALSPAFAPA WFAPLRVPTHGRAFAFRSRAPARPALSHGTAAAALSPAFAPA WFAPLRVPTHGRAFAFRSRAPARPALSHGTAAAALSPAFAPA ADP*LPGHSSQSPPRG*RWGRSSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAFGABAG VVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGGTPVAAAPNCRV*CSSA PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCGPGPAB*GQPGCTTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GMHECRRARLVPLPRL LGPRGTTGRSSFS LGPRGTGRSSFS LGPRGTGRSSFS LGPRGTKRSSFS LGPRGTGRSSFS LGPRGTKRSKHALLAL HGKKHAETVAALKFPCEFCGKREKPNSVAAHRSKSHFALLL HGKKYQHIHKKSFCFEFCGKREKPNSVAAHRSKSHFALLL GDWEQLGLEQOTTWDTALDNCQDLFTLUDPRPNLTSHPDGSED LGPLQGPGTTWDTALDNCQDLFTLUDPRPNLTSHPDGSED LGPLQGPGTTWDTALDNCQDLFTLUDPRPNLTSHPDGSED LGPLQGPGTTWDTALDNCQDLFTLUDPRPNLTSHPDGSED LGPLQGGPGTTWDTALDNCQDLFTLUDPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ LEPLAGGSPEATSPD	Ì		1	
KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR MGVMTLPSDLRKHRKLLSPVSREENREDKATIKCETSPPSSPR TLRLEKLGHPALSQEGKSALEDQGSNPSSSNSSODSLHKGAKR KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMGPM VPAKLGTQAEKDRRLKKKHQLLEDARKKGMPFAQMDGPTVVSWL ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR LKLRLAIQEWUSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE LEKRREESQHEIKDVLVWINDQVVHWVQSIGLRDYAGNLHESGV HGALLALDEMFDHNTLALLIQIPTONTQARQVMEREFINNLALG TDRKLDDGDDKVFRRAPSWRKFFRPEHHGRGGMLSASAETLPA GFRVSTLGTLQPPAPPKKIMPEAHSHTYJGHMLSAFRD 5651 646 1869 ARGGQRQPWG*EARAKGPSESSPTV*EGSGWEGPASP*TPGSTL AWGEGGGIR*ASGITAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPLSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGFSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGABDG\PVPPARGFFLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRRWASPAAAPGFLSSDVCGGLGA GWRAGISPELLGAAGLSDMWARCPGPGPAE*GQQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRARHLVPLPRL LGPRGTTGPSSPS 5652 735 343 HKKKYGHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGEKPLQCEICGFTCROKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA FGFGARSFRTSSNLVIHRRIHTGEKPLQCEICGFTCROKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA GGWQLGLEQGDTWALDLOCDLETLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ	5650	1172	3006	
MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPSSPR TLRLEKIGHPALSGEEGKAALEDQGSNPSSSNSSODSLHKGAKR KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVILTDSEFSMQEPM VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK TDSEEGSWAQTLAYGDMNHEWIGDKEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE LEKRRESQHEIKDVLWWTNDQVIHVVQSIGLRDYAGALHESGV HGALLALDEMPDHNTLALILQIPTOMTQARQVMEREFNNLALG TDRKLDDGDDKVFRRAPSWRKFFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD 5651 646 1869 ARQGQRQFWG*EARRAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGEGGGIR*ASGITAAGAASAAAA/PPPTRGGPAPACCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGABCGTVPAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAGPGLSSDVCGGLGA GWRAGISPELLGAAGLSANWARCPOPGPAE*GQCPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPBPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGEKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA FGRUGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ GWBQLGLEQGDTWADLDNQCDLFLDPPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ				1 7 7
KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM VPAKLGTQAEKDRRLKKKHQLLEDARRKGMFFAQWDGPTVVSWL ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR LKIRLAIQEMVSLISPSAPPTSRTSSGNVWTHEEMETLETSTK TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLITKKDLRVHLKMVDS FHRTSLQYGIMCLKRLNYDRKE LEKRRESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENFPHNTLALIIQIPTONTQAQVMEREFNNLLALG TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD 5651 646 1869 ARQGQROFWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGGRAGIR*ASGLTAAGAASAAA/PPDTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPAPALSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWCGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAEPLGAPGAEDG\PVPPQRGFPLGTLGS PALHRAPAAADPGSPLQAPPRAWASPAAAGGTLYVAAAPNCRV*GSA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGTTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLV1HRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA FGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ	l			MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR
KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM VPAKLGTQAEKDRRLKKKHQLLEDARRKGMFFAQWDGPTVVSWL ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR LKIRLAIQEMVSLISPSAPPTSRTSSGNVWTHEEMETLETSTK TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLITKKDLRVHLKMVDS FHRTSLQYGIMCLKRLNYDRKE LEKRRESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENFPHNTLALIIQIPTONTQAQVMEREFNNLLALG TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD 5651 646 1869 ARQGQROFWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGGRAGIR*ASGLTAAGAASAAA/PPDTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPAPALSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWCGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAEPLGAPGAEDG\PVPPQRGFPLGTLGS PALHRAPAAADPGSPLQAPPRAWASPAAAGGTLYVAAAPNCRV*GSA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGTTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLV1HRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA FGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ				TLRLEKLGHPALSQEEGKSALEDOGSNPSSSNSSODSLHKGAKR
VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL ELWVGMPAWYVACRANVKSGAI MSALSDTEIQREIGISNALHR LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECUV DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE LEKRRESQHEIKDVLJWHNDQVJHWVQSIGLRDYAGNLHESGV HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNNLLALG TDRKLDDGDDKVFRRAPSWRRFFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD 5651 646 1869 ARQGQGDWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGEGGGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPAPALSHGTAAAALSPASPAGP WPAPLRVPTHGRAPAPRSRAAPAPALSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTFVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRARHLVPLPRL LGPRGTTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLV1HRRIHTGBKPLQCEIGGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA FGRLQSRGRLTLGLVLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ	ł			
ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR LKLRLAI QEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKWVDSFHRTSLQYGIMCLKRLNYDRKE LEKRRESQHEIKDVLWWTNDQVYHWVQSIGLRDYAGNLHESGV HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNNLLALG TDRKLDDDDDKVPRRAPSWRKRFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD ARQGQRQDWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS APAGSWAGLAGYG*AGAPGTQATAPRAAGGTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHTHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFGGKFFKPDSVAAHRSKSHPALLLA FGFQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMGFFL GDWEQLGLEGGDTFWDTALDNCQDLFLLDPPRPNITSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ			, '	1 · · · · · · · · · · · · · · · · · · ·
TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKKMJDS FHRTSLQYGIMCLKRLNYDRKE LEKRREESQHEIKDVLWWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNNLLALG TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASABTLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD 5651 646 1869 ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP ADP*LPGHSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAB*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA FGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNITSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ	l			- · · · · · · · · · · · · · · · · · · ·
TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKKMJDS FHRTSLQYGIMCLKRLNYDRKE LEKRREESQHEIKDVLWWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNNLLALG TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASABTLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD 5651 646 1869 ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP ADP*LPGHSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAB*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA FGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNITSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ			"	
DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDEMFDHNTLALILQIPTQNTQARQVMEREFNNLLALG TDRKLDDGDDKVFRRAPSWKRFFPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD 5651 646 1869 ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAFGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA GWRAGISPBLLGAAGLSDNWARCPGPGPAB*GQQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLV1HRRIHTGKPLQCEICGFTCRQKASLNW HQKKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA 5653 66 1401 RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ	J		1	1
LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNNLLALG TDRKLDDGDDKVPRRAPSWRKRFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD 5651 646 1869 ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGEGGGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA FGRUQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPQCQFTRRGRRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ				
HGALLALDENFDHNTLALIQ I PTQNTQARQVMEREFNNLLALG TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD 5651 646 1869 ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGEGAGIR*ASGLTAAGAASAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGTTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA FGRUGSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGPLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ	1			-
TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD 5651 646 1869 ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPLSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGEKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA FGLQSRGRLTLGLVLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ	1		,	
GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD 5651 646 1869 ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGEKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA 5653 66 1401 RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ				
5651 646 1869 ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAGPGLSSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGEKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA 5653 66 1401 RGRLQSRGRITLGLVLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ	1	1		•
AWGEGAGIR*ASGLTAAGAASAAAA/PPPTTGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWAS PAAAGPGLSSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ	5651	646	1869	<u> </u>
WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAGPGLSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ]	-305	
ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAB*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIPQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ			1	·
QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ				· ·
FAGSWAGLAGYG*AGAPGTQATAPRAAGQTTVAAAAPNCRV*GSA PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA FOR SGRLQSRGRLTLGLVLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ				· ·
PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA FOR SGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ			1	
GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA F0563 66 1401 RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ				
CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA 5653 66 1401 RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ	1			
LGPRGRTGRPSSPS 5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA 5653 66 1401 RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ	{	l	1	_
5652 735 343 HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA 5653 66 1401 RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ				•
CEFCARSFRTSSNLVIHRRIHTGBKPLQCEICGFTCRQKASLNW HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA 5653 66 1401 RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEGFSQEI/SRDVIQ	FCE3	735	343	
HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA 5653 66 1401 RGRLQSRGRLTLGLVLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ	3652	/35	343	1
5653 66 1401 RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ]	J]	·-
CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ	F. 555	 	ļ	
GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ	5653	66	1401	
LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ		1		
i i i	1			
[GWLLELQFRRSLYRGHLVR*FARRSRKSSEV*YCHQRGKSHGMQ	1		i	•
	l .			TOWN FOR ADDRESS VOCATION FRADDEDKESKY/KVCHADCKSUCMA

	1 Day 32		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	1	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
			ES*IKERTQSCVHRFHGRRFHG\DNVSEKTLTPAKSKEYRGEFF
	1		SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTQHWITHTREK
			PTVHQECEQGFDRKASHSGYPKTHTGYKFYVCNEYGTPFSQSTY
1			LWHQKTHAGEKPCKSQDSDHPPSHDTQSGEHQKTHTDSKSYNCN ECGKAFTRIFHLTRHQKIHTRKRYECSKCQATFNLRKHLIQHQK
			THAANV
5654	3	598	TLPLFPGRRFRGWRRCGAVAARKNSTGGNVSINQRRDSVRMSAL
555*		350	NWKPFVYGGLASITAECGTFPIDLTKTRFQIQGQTNDAKFKEII
1			YRGMLHALVRIGREEGLKALYSG*VGLHAFLCHCSLFHMGIDFR
ľ			PRLHRSQVKSLRCV*KEQIA**/MFSLLISTLISKYIYYAADVL
]			EKLFYYIOVOTDNNKKICLFKNI
5655	2	867	RPPGIRAPRQLHPAAGRRPDASARPRFRPTVLLHDPFOLSFPPP
]	PLSYPSVFPAVARVLPQRSGDYRAAGMPQLSGGGGGGGGDPELC
			ATDEMIPFKDEGDPQ\REKIFAEIVNPEEEGDLADIKSSLVNES
j			EIIPASNGHEVARQAQTSQEPYHDKAREHPDDGKHPDGGLYNKG
	1	•	PSYSSYSGYIMMPNMNNDPYMSNGSLSPPIPRTSNKVPVVOPSH
ĺ			AVHPLTPLITYSDEHFSPGSHPSHIPSDVNSKQGMSRHPPAPDI
1			PTFYPLSPGGGGQITPPLGWQGQP
5656	228	1066	PRRVPPLPEFASGPGAAFFHSGRLQRSLTKDSAGCFSQCRSRAM
j]		LVLRSGLTKALASRTLAPOVCSSFATGPROYDGTFYEFRTYYLK
ł			PSNMNAFMENLKKNIHLRTSYSELVGFWSVEFGGRTNKVFHIWK
			YDNFPHRAEVRKALANCKEWQEQSIIPNLARIDKQETEITYLIP
İ			WSKLQKPPKEGVYELAVFQMKPGGPALWGDAFERAINAHVNLGY
	·		TKVVGVFHTEYGELNRVHVLWWNESADSRAAVRHKSHEDPISWG
1			GVRESVNYL\VSQQNM
5657	105	1052	GQRLQSPRVQMPVQPPSKDTEEMEAEGDSAAEMNGEEEESEEER
			SGSQTESEEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEKL
	İ		FRERLSQLRLRLEEVGAERAPEYTEPLGGLQRSLKIRIQVAGIY
			KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQERIQR
			LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG
		÷	PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ
			GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL
-			ALVWTPPL.
5658	2346	3541	TERRVYNPWPEPDPD\CIQEDPWNLPNSIKTLVDNIQRYVEDGK
			NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY
1	·		RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE
			RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA
			LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS
		•	PGSQAAEDLQQDINAQSLEKVQQYYRKLRAFYLERSNLPTDAST
			TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC
	•		IMOATDIMRKOGPRVEILAKNLRVKDOMPOGAPRLYRLCOPKMN
			GDL COPERAGE
5659	2	696	WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP
	-	0,70	GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\
			EREGEGORGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA
			AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG
1			EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL
			FRRLQKWELNTYL
5660	229	853	PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL
			CGODLNKTSROQIPESOGVISGAVFLIILFCFIPFPFLNCFVKE
	ŀ	•	QRKAFPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP
			TAASLPLLMVYFINFGNTIIVVPKPFRPILGLHLDLGR*SYHCC
	1		PYGTYFREPFLVLHILLQVFLFCLCVFPDPFW
5661	2	473	LNLYPSPCGGIPKLPGLPREAAAALGASFLAEAPLPVTVRGSGL
"	-		AGMAVTCDPKAFLSICFVTLVFLQLPLASICON*GTDSCASRGK
]		ADFDVTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP
	j		SLAVHMHERGMDMDGEQKWQYRGRT
5662	2	1318	LRKEGRCRRGSNRGVWAAPAEGLGGRGMLGVRCLLRSVRFCSSA
	}		PFPKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	location corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LHVNDGSSLESLQVVADSGLDSRELTFGSSVEVQGQLIKSPSKR
			QNVELKAEKIKVIGNCDAKDFPIKYKERHPLEYLRQYPHFRCRT
		1	NVLGSILRIRSEATAAIHSFFKDSGFVHIHTPIITSNDSEGAGB
			LFQLEPSGKLKVPEENFFNVPAFLTVSGQLHLEVMSGAFTQVFT
		}	FGPTFRAENSQSRRHLAEFYMIBAEISFVDSLQDLMQVIEELFK
			ATTMMVLSKCPEDVELCHKFIAPGQKDRL*HMLKNNFLIISYTE
			AVEILKQASQNFTFTPEWGADLRTEHEKYLVKHCGNIPVFVINY
			PLTLKPFYMRDNEDGPQELEGSVA*HSLGLMILLSIVVIGQP PADIGRSTAKTPGPPRSLEMDDPRYGMCPLKGASGCPGAERSLL
5663	119	698	PADIGRSTAKTPGPPRSLEMDDPRIGMCPLKGASGCPGALKSIIS VQSYFEKGPLTFRDVAIEFSLEEWQCLDSAQQGLYRKVMLENYR
			VQSYFEKGPLTFRDVATEFSLEEWQCLDSAQQGBIRKVMLLKTK NLVFLGIALTKPDLITCLEQGKEPWNIKRHEMVAKPPVICSHFP
			ODLWAEQDIKDSFQEAILKKYGKYGHANFQLQKGCKSVDECKVH
			KEHDNKLNGCLIPKKKK
	110	572	SLSMESNHKSGDGLSGTQKEAALRALVQRTGYSLVQENGQRKYG
5664	118	3/2	GPPPGWDAAPPERGCEIFIGKLPRDLFEDELIPLCEKIGKIYEM
			RMMMDFNGNNRGYAFVTFSNKVEAKNAIKQLNNYEIRNGRLLGV
			CASVDNCRLFVGGIPKTKK
5665	347	702	VVOHLIILLHCERTSPAMITSELPVLQDSTNETTAHSDAGSELE
3003	1	1	ETEVKGKRKRGRPGRPPSTNKKPRKSPGEKSRIEAGIRGAGRGR
			ANGHPOONGEGEPVTLFEVVKLGKSAMQRC
5666	213	540	VSCLPTSCKMITLNNQDQPVPFNSSHPDEYKIAALVFYSCIFII
			GLFVNITALWVFSCTTKKRTTVTIYMMNVALVDLIFIMTLPFRM
		1	FYYAKDEWPFGEYFCQILGA
5667	1	695	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP
			SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR
			VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD
			ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR
			PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL
			PSPVTTLSQLQ CSFLFCIPDLFLQFLLGRKEEEAVLVGGEWSPSLDGLDPQADPQ
5668	691	894	VLVRTAIRCAQAQTGIDLSGCTKW
	407	<u>i</u>	DSGAPEGLSPLMSTQEGLSMHAHPQAYTPFIYLHARKRRGEIGD
5669	407	1	ADSRFNDRYAHKSAQLYFLYFVCWIFQDVYYFTIKEKNHFFFPK
			ARGAPTKYSGSPIGSPTTTPPTRPPSFNLHPAPHLLASMQLQKL
			NSO
5670	3	373	SSECT.TMAWIPLILIPLITICTVSVASYELAOPSSVSVSPGQTAK
3070			ITCSGDVLAKKYARWFQQKPGQAPVLVIYKDTERPSGIPERFSG
		1	STSGTTVTLTISGAQVEDBADYFCYSATDNFLWVF
5671	280	524	KFPPKKTPPHLGMESAITLWQFLLQLLLDQKHEHLICWTSNDGE
		İ	FKLLKAKKVAKLWGLRKNKTNMNYDKLSRALRLLFMT
5672	2	557	FVPATPDPGVWLPPSRDPAMAKRSSLYIRIVEGKNLPAKDITGS
	}		SDPYCIVKVDNBPIIRTATVWKTLCPFWGEEYQVHLPPTFHAVA
			FYVMDEDALSRDDVIGKVCLTRDTIASHPKGKFSLPSHTGLPSH
			WPPSHSETSPLGSVWSPAQGKPFLLSPEAGATFCTPGLCSAACS
			QAWLLLPLP
5673	327	696	ITVADQISHWSAGRIKNRTRIPECIHSSAATTLAGPHTMEGESV
			KLSSQTLIQAGDDEKNQRTITVNPAHMGKAFKVMNELRSKQLLC
			DVMIVAEDVEIEAHRVVLAACSPYFCAMFTGDMS
5674	17	984	GGGSMEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGEVKGI
			AKNSITDSQMDDVEVVYTIDIQKYIPCYQLFSFYNSSGEVNEQA
			LKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSN DLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLA
	1		DLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHKVPLVVAKUK MSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEEDGSLKEVHKII
		1	MSEARC I VLACON INCOME INCOME I NECESSARIO MENTE INCOME I NECESSARIO MENTE INCOME I NECESSARIO MENTE INCOME I NECESSARIO MENTE INCOME I NECESSARIO MENTE INCOME I NECESSARIO MENTE INCOME I NECESSARIO MENTE INCOME
		í	
			EMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRG
			QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKI
			QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKII MFLKVAVTTTTISM
5675	80	753	QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKII MFLKVAVTTTTISM EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFRGVSECRRPP
5675	80	753	QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKII MFLKVAVTTTTISM EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFRGVSECRRPPG KSGVPVSAPGSDGKWWEERPGMFSLMASCCGWFKRWREPVRKV
5675	80	753	QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKI MFLKVAVTTTISM EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFRGVSECRRPI

	1 5 32 1		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ſ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ĺ			SEMLRHPRISGKPILVLANKQDKEGALGEADVIECLSLEKLVNE
			HKCL
5676	2	930	FVSSPPPRPVQPARPGGFGLSGRRSLLCQVASTPAHVGVMRSPV
•			RDLARNDGEESTDRTPLLPGAPRAEAAPVCCSARYNLAILAFFG
ŀ	j		FFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVH
ļ			HNQTGKKYQWDAETQGWILGSFFYGYIITQIPGGYVASKIGGKM
1			LLGFGILGTAVLTLFTPIAADLGVGPLIVLRALEGLGEGVTFPA
		j	MHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMN
			WTYVFYFFGTIGIFWFLLWIWLVSDTPQKHKRISHYEKEYILSS
			L
5677	1	1028	PPRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA
			VTAETHPLPLLAPLAVCQSVKSPAACQVRPRPRAVALPAALGGP
			GRSLPGLTAATMSSFSESALEKKLSELSNSQQSVQTLSLWLIHH
		Į.	RKHAGPIVSVWHRELRKAKSNRKLTFLYLANDVIONSKRKGPEF
	j		TREFESVLVDAFSHVAREADEGCKKPLERLLNIWOERSVYGGEF
	•		IQQLKLSMEDSKSPPPKATEEKKSLKRTFQQIQEEEDDDYPGSY.
			SPQDPSAGPLLTEELIKALQDLENAASGDATVRQKIASLPQEVQ
			DVSLLEKITDKEAAERLSKTVDEACLRNRGPGTS
5678	3	593	SSSPPSSTPSLPLPFYLLLGQLRLQLLWGTAHLSGAGEAAPCPG
3070		333	
		[GSGRTAAPRTRADPAAQSLMIMNKMKNFKRRFSLSVPRTETIER
		İ	SLAEFTEQFNQLHNRRNENLQLGPLGRDPPQECSTFSPTDSGEB
			PGQLSPGVQFQRQNQRRFSMEVRASGALPRQVAGCTHKGVHRR
F 670			AAALQPDFDVSKRLSLPMDI
5679	2	623	LNSRVDDFVAVPGAIMDEDYYGSAAEWGDEADGGQQEDDSGEGB
		1	DDAEVQQECLHKFSTRDYIMEPSIFNTLKRYFQAGGSPENVIQL
	1		LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLLIKH
			FDPRKADSIFTEEGETPAWLEQMIAHTTWRDLFYKLAEAHPDCL
			MLNFTVKVGRVLELRRKVFMNVYFWLLVCFL
5680	258	592	RRLTSTSEKLQNRNSHTPLESLIHPQPSYKGFGIMFGKKKKKIE
			ISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMV
			DPSCITPIQLAPMKTIVRGNKPC
5681	45	869	LLCAKTLGVRTKESQAEGYNRSGINNHQAEDPRFCPSFCWMRSA
-			RQTRPQRLRKEAARPPTPGSCPGGTGMDGKKCSVWMFLPLVFTL
			FTSAGLWIVYFIAVEDDKILPLNSAERKPGVKHAPYISIAGDDP
		:	PASCVFSQVMNMAAFLALVVAVLRFIQLKPKVLNPWLNISGLVA
		'	LCLASFGMTLLGNFQLTNDEEIHNVGTSLTFGFGTLTCWIQAAL
			TLKVNIKNEGRRVGIPRVILSASITLCVGPLLHPHGPKHPHVCS
			QGPVGPGHVL
5682	39	622	PSRSCLGTMRKWRHREVNLPEVTQQDAVCPAPIPSPGLSAQTGL
	l .		QKIWGTIHCQVCPGAPAWPGSPWHEEMGLLLLVPLLLLPGSYGL
	'		PFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFTYQ
			GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIG
			LRHRSFGDYQGRVHLRQD
5683	89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMORA
			HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAORAVAEEESKGS
	[ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM
			NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK
			· · · ·
			EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD SEDEEHDLC
5684	195	699	
2004	123	677	TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT
			AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY
			QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET
			LDQLPLTNPEHFGTPVIGKKTNRGRRYE
5685	779	1262	LLLQQPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPQ
			VKQEHPHTDSDLMHVKPQHEQRKEQEPKRPHIKKPLNAFMLYMK
			EMRANVVAECTLKESAAINQILGRRWHALSREEQAKYYELARKE
			RQLHMQLYPGWSARDNYVSPSSIPVALHS
5686	128	1181	CTWWQVNITLLDINDNHPTWKDAPYYINLVEMTPPDSDVTTVVA
			VDPDLGENGTLVYSIQPPNKFYSLNSTTGKIRTTHAMLDRENPD
			PHEAELMRKIVVSVTDCGRPPLKATSSATVFVNLLDLNDNDPTF

		1 - 11	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	
	sequence		\=possible nucleotide insertion)
			QNLPFVAEVLEGIPAGVSIYQVVAIDLDEGLNGLVSYRMPVGMP
			RMDFLINSSSGVVVTTTELDRBRIAEYQLRVVASDAGTPTKSST
			STLTIHVLDVNDETPTFFPAVYNVSVSEDVPR\GSGWSG*AARN
		ĺ	NDVGLNAELSYFITGGNVDGKFSVGYRDAVVRTVVGLDRETTAA
			YMLILEAIDNGPVGKRHTGTATVFVTVLDVNDKRPIILQSSYV
5687	17	917	AAPPAPPDG/PPP/PPPAPPT/PGPAA/APASSCQPRLSAGRAA
			QGDGGAAAVGHVLVVPAVGPVRVNPGLQTPVPRPELLPGP\SSS
	1	}	LHSDSSYPPDAGLSDDEEPPDASLPPDPPPLTVP/ADA/PMPVT
	1		SGCRMPSTSASE/AAGGQGACTHAKGSETPPPASPQTSEPAPSP
			LPPHLTGGPGMYSSEAKLPNSFSCLGLAGTGAGI*GTASAHGTG
			PPVLPHVCTPSLANPQP\AVGPEASSLPLGVSGIGMSA/SAPIS
			SSPFVAIGSCWLRGIPPPGSGFLCPGRAPGPVPITTHGQEGQGP
			ATDI
5688	1	420	LTKWDLFGNCYRLLKTGIEHGAMPEQVGVYWYS/CLYDSRKLFF
2000	1		*SHMIIRSLL*KVIDDSLGQLPLLRELLL**LNVIDRCIILAYV
		1	LRVEKTFAITYLKNFTVKVDFSLLGEIPLISMAAILKLWIMKID
		1	DGYIPAVF
F 500	1504	3	HELSGKHISMVSGNTCNWHPGGHSPGGGGGGGTTSKDRGEIPAL
5689	1504)	IWA/RKPIGTWTATKPTHRAG*GGAEEYQPPPQPCEGPRSTSRG
			GEG*GHAVGPGREIGKEGSLPFLGPKALGF*SASCQRAFEGGAH
`			GSTARKPAPATPGTRHPRTMETREVAQGWPAGPRSQFWDQHPHS
			PGEHRPSG\SPLPACPPRAWPKAGAVASATGTG\PQLPGSRGKQ
	į.		
			KLPRTREPPLLQAGWAVRKPPWSEAKEGLGQAGRPSGMDSSAS\
			PQTPGGRGSLEWGLPLYLGPHHDVK*RSDRLG*PP*GGQGGGH
			GAPSTPGPGGEAW*LPQQTSRPKPGPQAY*GE\GSPGLQCPCSK
	Ì		EL*RVPPGSLGPSTQCMYEPTDKHS\GGADAQLEVSTAGSRSTF
			GQELKGPLDAGRLWPGAPSASSSHR*GG*ERARAGAGHRGST*A
		İ	SSKIEQGRPRPGPTSDALADVEGGAES/GPHPWPLPGTLPNR/P
ļ	İ		GSPPPA*ASAGRKGTVSTLGGGLL
5690	1424	58	PSPPAGVCAAPAPLPLLALARRDRRPCSPGAEAAPWQTGGPAID
	,		GAWRTSVSALRRGATG/APCSPGAEAAPWQTGGPAIDG\DGELP
		}	*VRSEEAPRGCGAEGGGPGSGPVRRPGAGRGAHAGQGRQQDPEP
[İ	DGLRHRQHGAASHARHRLQRLRPGHHQNRHVRRDPQAPPGGPAP
i			GHAAALPERTRGVAEPPAWAHAGSDAWRAGR*SQRT*ERARPRH
ļ	· .		PTFQGRAGS\GQPGYQPPNPHPGPSSPPAAP\GPRGA*GNPQLE
l		· ·	KAPRSDRNPSQGLRTRIRRPETPDCGPPSPAGSSASASTFRCTS
1		. 1	SLSLLGP/PGAHNLDTAPQDR*HGP*GDKRGAPGVAGEDPRPP*
Į.	1		GNFVR*LLLMP/GVA*RHGTSPFLGPSLGENGGQWDSGNLFGTP
1			KG*SHPAFTKST*SMEAEKSYWNHPHR\DRGRQGVRINCLRVGE
			SEMWGPYSAPRPGTVFLSSFLSPASEEH\PEGSSSFNTPFPPAG
	1		PEGDPGLNSPGLLP
5691	107	550	ISNDPSPGYNIEQMAKRGKKLVELPYTVKGMDVSFSGILSFIED
2031	107	1	VAHRMLATGECTPEDLCFSLQVMQ*KTGTESWG*RFYIVEQN*S
		l	GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG
			GVGVYVLLESVPLSYS
EC00	. 1193	548	TQAWTRAEKDRKGSVRALRLHLERGPPT*RGSHPL\QSVPCIQK
5692	1133	248	PSIFSSYPI/GLPQSGGEPGPVGEQQPVRRPEQPSCGPASRMPL
1	ľ		TSRSVPPGRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQ
			RLNLPVMGATRSNLQPPRKVAVPGPTR*RDQDSKQDFSSKPLQS
			VPGLASTQQTLTPADSGPGTGGRDATRAGLPGVETMGNGVD
			VPGLASTQQTLTPADSGPGTGGRDATRAGDPGVETMONGVD ALTVVPVRKGTTWWAQPHGCSNLVSRARLDLSSRPSQNTEPQAP
5693	1258	1330	ALTVVPVRKGTTWWAQPHGCSNLVSKAREDESSRPSQNTBPQAP *OAGPPSSLRPP\SRRR*APEWPKRATGSRCRGLSAPPWPWPAA
			*QAGPPSSLRPP\SKRK*APEWPKRATGSKCKGLSAPPWPWPAA
1			RGE/PGSAPSHAP/PNSPRPSGTRHP/PGPSSRVLYSPSLPRNS
1			PEAIVWRSSRFPLWFPLRCCFWVSGFKDPNPVLRFF
5694	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
	1	1	QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
		1	
			SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
			CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
			SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV

SEQ	Predicted	[D 32 - L - 3 3	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ĺ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	
İ	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
ļ- -	sequence		\=possible nucleotide insertion)
1			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1	<u> </u>		VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
İ	1		PTATKLAELPPTPLRATAKSFVKPPSLAŅLDKVNSNSLDLPSSS
5695	<u> </u>	1222	DTTQCI
2632	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
			SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
į		· ·	CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
	1		KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
İ	į		IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
1			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
			PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
			DTTQCI
5696	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
İ		_	QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
1		·	SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
 			CDDSSKGGBLKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
			KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
			IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
1			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
i i			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
	·		PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
			PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
1			DTTOCI
			_
5697	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATRAAPPPPEPVPAA
5697	1147	47	_
5697	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA
5697	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS
5697	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL
5697	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT
5697	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATBAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP
5697	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATBAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKYGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE
	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKYGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK
5698	1147	666	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKYGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR
			PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA
			PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT
			PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ
			PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSBEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI
5698			PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF
			PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPFAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLBKTHPGDQAYE
5698	2	666	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE FNQ
5698	2	666	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLBKTHPGDQAYE FNQ RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA
5698	2	666	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE FNQ RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD
5698	2	666	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLBKTHPGDQAYE FNQ RVRQPPGLWVRTTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS
5698	2	666	PSEALSPPACPSAPAPRRSIISRLFGTSPATBAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPWVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLBKTHPGDQAYE FNQ RVRQPPGLWVRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIOTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRSGWPSGCSDIGWALAGWNHS*HLDPNT
5698	2	666	PSEALSPPACPSAPAPRRSIISRLFGTSPATBAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLBKTHPGDQAYE FNQ RVRQPPGLWVRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIOTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN
5698	2	666	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSBEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLBKTHPGDQAYE FNQ RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP
5698	2	666	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSBEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLBKTHPGDQAYE FNQ RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA*
5698	2	666	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPFAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVTSKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLBKTHPGDQAYE FNQ RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA* GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA
5698	2	666	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPFAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLBKTHPGDQAYE FNQ RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA* GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA GWQPRRPGFAGRAALPGPPAPFGPRRLAAGAHTSASARCPPAAAA
5698	2	666	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLBKTHPGDQAYE FNQ RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA* GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA GWQPRRPGFAGRAALPGPPPPPSS*RELGGLPGPGW*TLDPLPA HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL
5698	2	1448	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLBKTHPGDQAYE FNQ RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIOTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA* GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA GWQPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL FPPGRG
5698	2	666	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE FNQ RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN VPILFQNPSGALRSRRTEPAGWVPPTHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA* GGSLGCR/SMLPASSGPPPAPGPRLAAGAHTSASARCPPAAAA GWQPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL FPPGRG NGHKGVWEINIY*RRSNIHKNSKSESHLNQDHSFPPTPNSARS
5698	2	1448	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVBSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE FNQ RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWYSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA* GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA GWQPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL FPPGRG NGHKGVWEINIY*RRSNIHKNSKSESHLNQDHSFPPPTPNSARS KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD
5698 5699 5700	2 923	1448	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVBSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE FNQ RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWYSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VPAPARGPTAEHGHCELTTESQYSNN VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA* GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA GWQPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL FPPGRG NGHKGVWEINIY*RRSNIHKNSKSESHLNQDHSFPPPTPNSARS KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD E*CSIASSLIKAILRVSVLSE
5698	2	1448	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSBEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLBKTHPGDQAYE FNQ RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN VPILFQNPSGALRSRRTEPPAGWVPPTRHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA* GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA GWQPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL FPPGRG NGHKGVWEINIY*RRSNIHKNSKSESHLNQDHSFPPPTPNSARS KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD E*CSIASSLIKAILRVSVLSE IFEKICSDTQEFISPEINPQICSWLIFDKGAK/NHATGKDSLPN
5698 5699 5700	2 923	1448	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR RRQQRPPRSRERTAA GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVBSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE FNQ RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWETPVPWS*AQPGWYSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VPAPARGPTAEHGHCELTTESQYSNN VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA* GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA GWQPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL FPPGRG NGHKGVWEINIY*RRSNIHKNSKSESHLNQDHSFPPPTPNSARS KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD E*CSIASSLIKAILRVSVLSE

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	location	to first	L=Leucine, M=Methionine, N=Asparagine,
1	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į.	to first		S=Serine, T=Threonine, V=Valine,
1	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	residue of	amino acid	Codon, /=possible nucleotide deletion,
į	amino acid	sequence	\=possible nucleotide insertion)
[sequence		\=possible nucleotide insertion/
5702	. 3	1517	ETFVDPSQCGGIPSDSPHPVITPSRASESSASSDGPHPVITPSR
ļ			ASESSASSDGPHPVITPSRASESSASSDGLHPVITPSRASESSA
•		1	SSDGPHPVITPSRASESSASSDGPHPVITPSRASESSASSDGLH
ŀ			PVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTN
			IEVINCSITEIETTTSSIPGASDTDLIPTEGVKASSTSDPPALP
İ		,	DSTEAKPHITEVTASAETLSTAGTTESAAPHATVGTPLPTNSAT
ļ			EREVTAPGATTLSGALVTVSRNPLEETSALSVETPSYVKVSGAA
1			PVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETLTMDI
ļ			TTKGPFPTSRDPLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKP
f			PTATPTTARTRPTT\A*VQVKMEVSSSCG*VWLPRKTSLTPEWQ
			KG*CSSSTGNSTPTRLTSRSPYCVSGEANG/PSAAARHVPYAKR
			GCCP*PGPPPTDCSCVTVLRGTQKVPMKGSMSKPLTPDVATGPS
			LTSTGVYVWGGASPVPRGVLGLTLAHVLCFSKEKT
5703	14	1117	HHKDSRSOGLPRTOECARPELRPLLCPRALWPVTRLSYRCPWQA
5/03	**		PKAGIGTKAKPSESHLKLHPGWPSLDRQGEPATLGTGTGHCSDS
	1		RILRWHP*HTAAR*PRWRRLPSSHRWTRHLGVLRVQDKS**VSL
 -	<u> </u>		DPSCRPRFLRTC**YGMRSVASSSNPPPGWSGPGASVFPARPVS
	Ì		ALPTGPRCW*APRGRTRQPCGWPRLSSPHATADWGPGCPLSPSR
		1	GSWETAPGS*WCPWL*AARWTGWRTASGASAGLGRAADRPSAWA
		İ	RRVAGLLPGQGLTVRR*H*TAGAPASVRSSQGATRSPAPGGDQC
		ii	ACGRGPGSC*HPPPWPVSPSSPVPCPSGR*HLRGPLLSAARPRA
1			AGWPRHSPHDTQTPBP
			GDYEFDSPYWDDISQAAXDLVTRLMEVEQDQRITAEEAISHEWI
5704	23	562	GDYEFDSPYWDDISQAARDDVIRDHEVEQDQRIIABEAISHEWI
l			SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE
l			QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA
ľ			KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE
İ			SPQP
5705	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
ŀ			SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE
İ			QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA
1	1	ļ	KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE
i			SPQP
5706	1161	610	QLGRFXAQDTVAIRKVKEVFGTGAMRHVVILFTHKED*GGQALD
1			DYVANTONCSLKOLVRECERRYCAFNNWGSVEEQRQQQAELLAV
ļ .			IERLGREREGSFHSNDLFLDAQLLQRTGAGACQEDYRQYQAKVE
			WQVEKHKQELRENESNWAYKALLRVKHLMLLHYEIFVFLLLCSI
j		1	LFFIIFLF
5707	28	609	GSPAPTPGPRRPGRGTPSPGTRHHQGRAEPEPDAPERAPLRR*
3,07	20		MFAIQPGLAEGGQFLGDPPPGLCQPELQPDSNSNFMASAKDANE
		1 .	NWHGMPGRVEPILRRSSSESPSDNQAFQAPGSPEEGVRSPPEGA
1		1	EIPGAEPEKMGGAGTVCSPLEDNGYASSSLSIDSRSSSPEPACG
		1	TPRGPGPPDPLLPSVAQA
F 77.5	44	1925	SFSWEETISPCFPKMPAEPWWLSPVSLGAAGWPGQPRPYLDLPA
5708	44	1923	QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPQAKPKP
			PRCPFTAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAP\GPA
}			GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSFSLGAPGAPSPL
			RVSPASGGPRKEGRQGSGG*AGGGGP\ARTHADLPCVGFVCSPP
1]		LLK*SDSPVKQLPA\SGQGSGAGMPPVGSSDILRPRPTSVSGTG
			LLK*SDSPVKQLPA\SGQGSGAGAPPVGSSDTLKFRFTSVSGC RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S
			KAAG*CSWQPAACCIPKSQ*WAVARSPSRCSRW*RQSGR*RG*S
			SRRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR*
1			LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS*
			AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH
			GRGRAMGSRCVCTCTGLPCPGIPLSGASPGGSGETGAGRSHTLK
			AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS
1			QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPPP
1	ı	1	PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GEAPA
	1		
		İ	PPPRPEPPPPPARRP
5709	2	2031	ITLCPLPOTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG
5709	2	2031	

SEQ	Predicted	Predicted end	I Amino soid account containing signal nontide
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
"0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ľ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bequence	\=possible nucleotide insertion)
	5044055		LEQYDPPELADSSGRVVREKRSADMWRLGCLIWEVFNGPLPRAA
ł			ALRNPGKIPKTLVPHYCELVGANPKVRPNPARFLONCRAPGGFM
1	•		SNRFVETNLFLEEIQIKEPAEKQKFFQELSKSLDAFPEDFCRHK
1]	VLPOLLTAPEFGNAGAVVLTPLFKVGKFLSAEEYOOKIIPVVVK
	1	İ	MFSSTDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVVHGFLDT
			NPAIREOTVKSMLLLAPKLNEANLNVELMKHFARLOAKDEOGPI
			RCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPFAPSRVAGV
			LGFAATHNLYSMNDCAOKILPVLCGLTVDPEKSVRDOAFKAIRS
`			FLSKLESVSEDPTQLEEVEKDVHAASSPGMGGAAASWAGWAVTG
1		}	VSSLTSKLIRSHPTTAPTETNIPQRPTPEGVPAPAPTPVPATPT
ŀ			TSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVLAQQD
			DWSTGGQVSRASQVS\TPTTNPPNPQSPTGAAGK\RGLLGTGLA
			GAKLPGATS*RYTAGORV
5710	1	562	IPGSTISCEVELMARMAKTIDSFTONOTRLVVIIDGLDACEODK
	<u> </u>		VLQMLDTVRVLFSKGPFIAIFASDPHIIIKAINQNLNSVPSGFK
	,		\LNGHDYMRNIVHLPVFLNSRGL/RQ/LQENFS*LQQQMETFHA
			QILQGYRKMLTEEFHRTALGR*QNLVARQPSIDG*DAIGFELYV
			CIAIQFNTNKDDAT
5711	1526	1130	RRHPFQWTTVTQEAFSHHDVAFTSTPVLFYPDSAOPFIVKSESS
			SQIAKAVLSQORPSLFHECAFHFFS*SLORHTINLDQGIF*LLM
İ			LSEERQHLFESS/IWTTPHNLK*/FEIHEHLGSHEGHWTLFFLL
			OIL
5712	3	1391	GRKLFQSLDISERLKFLLTLDCVDDTLIVLAEEHGCLDIIKELP
	_		ETVIDLLNKCLTFHPSKRPTPDELMKDKVFSEVSPLYTPFTKPA
		,	SLFSSSLRCADLTLPEDISQLCKDINNDYLAERSIEEVYYLWCL
	1		AGGDLEKELVNKEIIRSKPPICTLPNFLFEDGESFGQGRDRSS/
			TFR*YHWDIVVMPAKK*IERCWGRSILPITLKMTSLILPYSNSN
			NELSAAATLPLIIREKDTEYOLNRIILFDRLLKAYPYKKNOIWK
			EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDROI
1			EVDIPRCHQYDELLSSPEGHAKFRRVLKAWVVSHPDLVYWQGLD
İ			SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIQEY
			LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL
			HKIFHLW\DTLLLGEFLFPILYWE
5713	634	284	PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGPMEGH
ŀ			TACRCSRRGAQVQHLPREDIRAAE*DPHLREVWPGLPTSSATSP
1			*RAVLTSPCSHLGSADAASSHWLCGVSFH
5714	212	613	WGLGLGPTMSSLGGGSQDAGGSSSSTNGSGGSGSGSKAGAAD
I .			KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS
1			HYSSFGSSGGSGGSMMGGESADKATAAAAASLLANGHDLAAA
1			MA
5715	131	1979	ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE
1			QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\
			GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN
			DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS
1	ĺ		PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS
1			QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR
]			TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL
1			YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG
			L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT
			PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP
			VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE
			EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT
			GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E
1			RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL
			TDLTEAQTSQH
5716	1711	1370	RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD
].			*LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC*
			RCPLVL*SGFFTIIVGGYSCCMPLKT
5717	44	1489	LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD
L			EGPGALVLESDLLLGQDLEFEEEEEEEEGDGNSDQLMGFERDSE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			GDSLGARPGLPYGLSDDESGGGRALSAESEVEEPARGPGEARGE
	Ì		RPGPACQLCGGPTGEGPCCGAGGPGGGPLLPPRLLYSCRLCTFV
			SHYSSHLKRHMQTHSGEKPFRCGRCPYASAQLVNLTRHTRTHTG
			EKPYRCPHCPFACSSLGNLRRHQRTHAGPPTPPCPTCGFRCCTP
			RPARPPSPTEQEGAVPRRPEDALLLPDLSLHVPPGGASFLPDCG
			Q\CGVKGRASAGLDQNHCQS/SLFPWTCRGCGQELEEGEGSRLG
			AAMCGRCMRGEAGGGASGGPQGPSDKGFACSLCPFATHYPNHLA
			RHMKTHSGEKPFRCARCPYASAHLDNLKRHQRVHTGEKPYKCPL
	1	1	CPYACGNLANLKRHGRIHSGDKPFRCSLCNYSCNQSMNLIRHM
			VAHALSLPAESYGNDVSMTHPQLPPTQLAWDLCRTCLPLSYNFT
5718	120	284	
	_		S**STADPLHL
5719	48	428	ELNNGPFQMPLCNGGNLAVTGSWADRSPLHEAASQGRLLALRTL
			LSQGYNVNAVTLDHVTPLHEACLGDHVACARTLLEAGANVNAIT
			IDGVTPLFNACSQGSPSCAELLLEYGAKAQP\ESCLPSP
5720	1	1051	LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK
2,20	1 -		\RCT\YYE\TCGGTYGLQMWSVSFQDVAQKVVAL\RKKQQ\LAI
	1		GPCK\SLPN\SPSH\SAVSAASIPARAPINQGHE/SGGGSAFSD
			Y\SSSVPSTPSISQRELRIETIAASSTPTPIRKQSKRRSNIFTS
			RKGADP\DREKKAAGCKVDSIGSGRAIPIKQGILLKRSGKSLNK
	1		EWKKKYVTLCDNGLLTYHPSLHDYMQNIHGKEIDLLRTTVKVPG
		i	KRLPRATPATAPGTSPRANGLSVERSNTQLGGGTGAPHSASSAS
		!	LHSERPLSSSAWAGPRPEGLHQRSCSVSSADQWSEATTSLPPGM
			QHPASG RHSSPCCSLRRTERSSNAAVST/TTVQQFKRFIENYRRHIGCVA
5721	97	492	RHSSPCCSLRRTERSSNAAVST/TTVQQFRRFTENTRRITGCVA
	Ì	Ì	VFYAIAGGLFLERAYYYAFAAHHTGITDTTRVGIILSRGTAASI
			SFMFSYILLTMCRNLITFLRETFLNRYVPFDAAVDFHRLIASTA
5722	88	1043	VALDVLAGSSPGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
ļ			GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP
			QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR
			GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG
i.			GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPA
			PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG
			RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
			KSSTREIPEMI
		1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
5723	88	, 1043	GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP
1			QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRPGAGVGAPRR
1			GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG
!	1		GRARGOAGILLGROGGGGGGGAERERAADGALGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
			PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG
1			RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
	l		KSSTREIPEMI
5724	3	1841	FTNEAPPAPLPDASASPLSPHRRAKSLDRRSTEPSVTPDLLNFK
	1		KGWLTKQYEDGQWKKHWFALADQSLRYYRDSVAEEAADLDGEID
ł			LSACYDVTEYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIQTI
	1	İ	MKHVHPTTAPDVTSSLPEEKNKSSCSFETCPRPTBKQEAELGEP
		1	DPEQKRSRARE\RRREGRSKTFDWAEFRPIQQALAQERVGGVGP
1			ADTH\DPWRPEAEHGELERERARREERRKRFGMLDATDGPGTE
1]	DAALRMEVDRSPGLPMSDLKTHNVHVBIEQRWHQVETTPLREEK
1		1	OVPIAPVHLSSEDGGDRLSTHELTSLLEKELEQSQKEASDLLEQ
		1	NRLLQDQLRVALGREQSAREGYVLQATCERGFAAMEETHQKKIE
i		į.	DLQRQHQRELEKLREEKDRLLAEETAATISAIEAMKNAHREEME
1			RELEKSQRSQISSVNSDVEALRRQYLEELQSVQRELEVLSEQYS
			QKCLENAHLAQALEAERQALRQCQRENQELNAHNQELNNRLAAE
İ			QKCLENAHLAQALBAEKQALKQCQKBNQCDINAHNQEDINKRIAAB
			ITRLRTLLTGDGGGEATGSPLAQGKDAYELEVPSGARPCLTQLC
			TQEPQGSAAWPLSYRVVGGTDLRQQESQGPGRSKSPEGGEEQ
	3	1049	VNGHSEETSQSPNRTEPHDSDCSVDLGISKSTEDLSPQKSGPVG
5725			· · · · · · · · · · · · · · · · · · ·
5725			SVVKSHSITNMEIGGLKIYDILSDN\DLSSHLQPLK/FTSAVDG
5725			SVVKSHSITMMEIGGLKIYDILSDN\DLSSHLQPPK\FTSAVDG KNIVRSKAATLLYDQPLQVFTGSSSSSDLISGTKAIFKFDSNHN PE/GAKYNKRPHKWAHNLHLKYMVLHSIISNTVAV\RSQRHFVA

Deginning location		1 8 - 17 - 5 - 3		
Notation Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence Sequence	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first anin acid to first anin acid amino acid residue of amino acid amino acid amino acid sequence s		, ,		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Leleucine, M-Methionine, N-Asparagine, amino acid residue of samino acid sequence Serine, T-Threonine, V-Valine, General control sequence Serine, T-Threonine, V-Valine, M-Trytopian, Y-Tyrosine, N-Cubrown, *-stop Codon, /=possible nucleotide deletion, \-possible nucleotide sequence Serine, T-Threonine, V-Valine, M-Trytopian, Y-Tyrosine, X-Unknown, *-stop Codon, /=possible nucleotide deletion, \-possible nucleotide sequence Serine, T-Threonine, V-Valine, M-Trytopian, Y-Tyrosine, X-Unknown, *-stop Codon, /=possible nucleotide deletion, \-possible nucleotide sequence Serine, T-Threonine, V-Valine, M-Trytopian, Y-Tyrosine, X-Unknown, *-stop Codon, /=possible nucleotide deletion, \-possi	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first anion acid residue of anion acid anion acid residue of anion acid anion acid anion acid anion acid anion acid anion acid sequence sequence sequence (Codon, /mpossible nucleotide delection, 1-possible nucleotide delection, 1-possible nucleotide linsertion)				H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence sequence Sequence Codon, //possible nuclectide delection, //possible nuclectide insertion) LOTKSPRRPCQTSSSEAPS/VDGRAQ/INGSYAKKSSANNFSNR NURANTAPHILDRICAPSCAPSSEAPS/VDGRAQ/INGSYAKKSSANNFSNR NURANTAPHILDRICAPSCAPSCAPSSEAPS/VDGRAQ/INGSYAKKSSANNFSNR NURANTAPHILDRICAPSCAPSCAPSCAPSCAPSCAPSCAPSCAPSCAPSCAPS				L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence (Codon, /=possible nucleotide deletion, \				P=Proline, Q=Glutamine, R=Arginine,
residue of amino acid sequence (Codon, /=possible nucleotide deletion, \			residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence Codon, /-possible nucleotide insertion) LOTKSPNERCOFSSSAPS/WOGRAG/INGSYASHSANNESNIN NURANTAYHLINGLOPARHGEWAR ISPNERLIPATISTICROS SYSSTASVALODROSTRRAGIEGOVIS/SYREPHSAGRIPPHMIC SCRIBBARTYSIDGEONASROSARPSINEIPERTMYSVDPINYS TOP SERSISMWHNSGLPASSHSSKLPVTWGFSGCYRELRIGREPLAN TOP THANGOVIPCILGPLERGIFPEGSGVITL/SSYGRATPHMIC STAGE		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence		amino acid	sequence	Codon, /=possible nucleotide deletion.
LOTKSPNER/COFSSSAPS/VOGRAC/TINGSYAKHSANNINFSNIK NNANTAYHLINGLAPAHGEWAH ISPINALIPAYHISTIONG SYSSTASVALIDEGSTERACJEGOVILS/REFFISAGETPPMOR GORDISARTYSIOGENASROSARPSINEIPERTMYSVDPNYS TOP 5726 2 486 SRSLSMWNSGLPASHISSKLPVTVGFSGCVERLERGEPLAST TENGGVTPCILGPLERALIFPEGSGCVITL/SSVGAGITOPSSAG GOSPOGSGGEDPLESSFSQLPADHOGATHPUGALIFRATERPLAYI 5727 21 221 FRILITLEFTERLEVATORY AVENTAGEATHPUGALIFRATERPLAYI 5728 2 877 GTRAGGAPPPYLOLOVTEROVILLRADDG GIPHLIGARTPSTATULOLOVTEROVILLRADDG GIPHLIGARTPSTATULOLOVTEROVILLRADDG GIPHLIGARTPSTATULOLOVTEROVILLRADDG GIPHLIGARTPSTATULOLOVTEROVILLRADDG GIPHLIGARTPSTATULOLOVTEROVILLRADDG GIPHLIGARTPSTATULOLOVTEROVILLRADDG GIPHLIGARTPSTATULOLOVTEROVILLRADDG GIPHLIGARTPSTATULOLOVTEROVILLRADDG GIPHLIGARTPSTATULOLOVTEROVILLRADDG GIPHLIGARTPSTATULOLOVTEROVILLRADDG GIPHLIGARTPSTATULOLOVTEROVILLRADDG GIPHLIGARTPSTATULOLOVTEROVILLRADDG GIPHLIGARTPSTATULOLOVTEROVILLRADDG GOPAGAGGDAD/ILLRADGSGAGODGSCOVILLRADGGSCVLTVKK AGANTSTYNHISSKRRSSLIDNG GOPAGAGGDAD/ILLRADGSGAGODGSCOVILLRADGGSCOVILLRADGG GOPAGAGGADA/ILLRADGSGAGODGSCOVILLRADGGSCOVILLRADGG GOPAGAGGADA/ILLRADGGERAGODGSCOVILLRADGGSCOVILLRADGG GOPAGAGGADA/ILLRADGGERAGODGSCOVILLRADGGSCOVILLRADGG GOPAGAGGADA/ILLRADGGAGADGGSCOVILLRADGGAGDADDA/ILLRADGGAGADGADGADGADGADGADGADGADDA/ILLRADGGAGADGADGADGADGADGADGADGADGADGADGADGA	·	sequence	-	
NVRANTAYHLIGKLOPARHGEWAL SENDRIJPENTSTIGGGS SVSSTASVNILGBOEDSTRRAGIFEGDULSTREFHSAGKTPPMMC SQRPLSARTYSIDGENASRRQSARPSINEIPERTMSVSDPTVSS TSP 5726 2 486 SRSLSMWINSGLPASSHSKEJVTVGFSGCVEKLELIGEPLGAN CREATER CONTROL OF THE CONTROL OF TH				LOTKSPNRPCOFSSSADS/VDOPAO/TNOSVAVUSANMNFSNUM
SYSSTASVILIDEOSTRRAGIFEDDYLGYBEFFISAGRIFPISAGRIPPIMOS SORPLISARTYSI DEDMASROSARPSINSI PERTMYSVSPNYSS TSP SREJSMWNNSGLPASSHSSELDVTVGFSGCVYRLEHGOPLGAI TRINGCVTPCILIGPLEAGLFPPGSGGVYTL/SSVGAGTEGPSRAG GSPOGSGGGPDFSSSPQLPADLIGAT.PDVGLLEHGPLGAI TRINGCVTS POLITICAGATTPOLOLOTEROVILLEADDO REFLIL LIKEFFELLPHATGY SAVINAGASTHNEDGAS CEVILVKKK AGANTS TPNRNS SKRRS LENGE TO GTRINGGFB PRREGAMESS LENGE S72 2 877 GTRINGGFB PRREGAMESS LENGE GR VMAGGR PRIVOSGVLGSRVCGPLYSTSSAGG/SGGLESPPANE GR VMAGGR PRIVOSGVLGSRVCGPLYSTSSAGG/SGGLESPPANE GR VMAGGR PRIVOSGVLGSRVCGPLYSTSSAGG/SGGLESPPANE FREYOVERAGEGLAVPABEGGGGT ETGALOCKEN/GAEDPARE EPPOVERAGEGLAVPABEGGGGT ETGALOCKEN/GAEDPARE EPPOVERAGEGLAVPABEGGGGT ETGALOCKEN/GAEDPARE FREYOVERAGEGLAVPABEGGGGT ETGALOCKEN/GAEDPARE FREYOVERAGEGLAVAREGGGGT ETGALOCKEN/GAEDPARE FREYOVERAGEGLAVAREGGGGGT-CADAVCRICCKN/GAEDPARE FREYOVERAGEGLAVAREGGGGGT-CADAVCRICCKN/GAEDPARE FREYOVERAGEGLAVAREGGGGGT-CADAVCRICCKN/GAEDPARE FREYOVERAGEGLAVAREGGGGGT-CADAVCRICCKN/GAEDPARE FREYOVERAGEGLAVAREGGGGGT-CADAVCRICCKN/GAEDPARE FREYOVERAGEGLAVAREGGGGGT-CADAVCRICCKN/GAEDPARE FREYOVERAGEGLAVAREGGGGGT-CADAVCRICCKN/GAEDPARE CODULYRTCRTLIGGET-TYRLILMOLKSSISSLKEBGGLYKOB GULDALAMGGRICTHREEL-PYRND-LOPILAGGGAGT-TORH-LIPVE CODYLOGFG-LICULHOGS-GGGGGGGAA-LICADVCRICCHS-CADAVCRICCKN/GAEDPARE GRADALAMGGRICTHREEL-PYRND-LOPILAGGS-GGLESPG-WILLFTVAE COLOCAL ADALLSTAN GAEGA-CADAVCRICCHS-CADAVCRIC				NVPANTAVHI.UODI CDADUCEMWA I COMDDI I DAUTECTIODOC
SQRELSARTYSIDDEMASREQSARPSINEIPERTMSVSDFMYSS TSP 5726 2 486 SRIJAMWINGGLASHRSKLPUTVGFSGCVRURLHIGRURD GENERALT TEMAGVTPCILADPLEAGLEPPESGGVTUL, BEYGRUT LPGENAL GOSPOGSGGSPLPLSSRSQUTLADPATLDWULLELEVRPLAVI GLIPHLOARTPYVLOLQVTEKGVLLRADDO 5727 21 221 RFILLURETPELPMATGYASVINAGKSTHNEDGASCEVLTVKK ANATSIPMINSSKENSSLENBE 5728 2 877 GTRINGGFBRRGANEGSAGGLRAPGAAAGGFGVQFRGSG/LPG GRANGGGRAPVENGLAVANDSTENSSLENBEN GRANGGRAPVENGLAVANDSTENSSLENBE GRANGGRAPVENGLAVANDSTENSSLENBE GRANGGRAPVENGLAVANDSTENSSLENBE GRANGGRAPVENGLAVANDSTENSSLENBE GRANGGRAPVENGLAVANDSTENSSLENBE GRANGGRAPVENGLAVANDSTENSSLENBE GRANGGRAPVENGLAVANDSTENSSLENBE GRANGGRAPVENGLAVANDSTENSSLENBER GRANGGRAPVENGLAVANDSTENSSLENBER FPPOVPEAGEBAVPAREGRANGGFRANSCFOWIFFEGGLAPPA GRANGGRAPVENGLAVANDSTENSSLENBER FPPOVPEAGEBAVPAREGRAPSTENDSLEVENGGSBEPAGE GOPAGAAGGDAO/LEGRCGSARWEAGSRAASCFOWIFFEGGLAPPAGE GOPAGAAGGDAO/LEGRCGSARWEAGSRAASCFOWIFFEGGLAPPAGE GOPAGAAGGDAO/LEGRCGSARWEAGSRAASCFOWIFFEGGALPPAGE HEPPOVPEAGEBAVPAREGRAPSTENGAGGFANSCFOWIFFEGGALPPAGE FPPOVPEAGEBLAVANDGTUTTHELIADLICASISLSKEPGGLVENBE GOPAGAAGGTAVANDGTUTTHERSTENSBERFFANSCFOWIFFEGGALPPAGE CDVILGGFLICHLIDGSTVORARBELGARENGGESCVILSBERFANDS GRANGGRAFTLANDGTVICHLIDGSTVORARBELGARENGGESCVILSBERFANDS KSEPOMMULOSFORTATERSTENGGESVILKERFANGESCHARDE GRANGGRAFTHANGGTARTHERSSLAVENGBERFANDSTENGGGAR FPPOVPSFPLIKHDATSPRINGERFANGGSCALATALADLIVTCGTFSPPPSA LLACTTGEBILAQVILQQQQPOWMSSHLLLTPCRVAPPYPHLPS SCSPOMMULOSFORGAAVESVEYFG SCSPOMMULOSFORGAAVESVEYFG		1		
5726 2 486 SRSLSHWWNSGLPASSHSKKLPVTVGPSGCVRLRLHGRPPJAN TRMGVTPCILGPLEAGLPPRGSGVTTL/ESVGAGITGPSGAG GGSPGGSGRPLESSPGDLPADLPATLPDVGLESVRPLAVZ GLIPHLOQAFTPYLQLQVTEKQVLLRADDO 5727 21 221 PIPLILKEFTELDRAGKSTHNEQASCEVLTVKK AGAVTSTPRENSSKENSSLPNGG 5728 2 877 GTENGGFEPRGRAWSGSGLRAPGAANGGPVQFRGSG/LPC NAIRAGVNPGRGPASFPWLSLIJEWDLNPPPTDHAPGARPFPAVE GR\WAGGRPPWYGGVLGSRVCGPLYSTSPAGPS/GGGLEAPGAAGGRPVQFRGSG/LPC GRAGGLAGIA-LJGGRCSPARWAGSGRAGGPQAPGAGPSGS/LPC RNIRAGVPPRGGRASFPWLSLIJEWDLNPPPTDHAPGARPFPAVE GR\WAGGRPPWYGGVLGSRVCGPLYSTSPAGPS/GGGLEAPHABGGG GGPAGAGGLAG-LJGGRCSPARWAGSGRAGCPTETOAQVCWERHABGAGG GGPAGAGGLAG-LJGGRCSPARWAGSGRAGCPTETOAQVCWERHABGAGG GGPAGAGGLAG-LJGGRGSPAGPAGPGSGGLAGPAGAGGAGG KOSPRILADPQDLFAGGWSLAPFFPPVAAVIRSKK GSPRILADPQDLFAGGWSLAPFFPPVAAVIRSK SFRRIADPQDLFAGGWSLAPFFPPVAAVIRSK GCARREVILTIGLGFRAFFVGGARWAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG				
SRELSHMWNSGLPASSHSSKLPTVGVSGCVRERLEGGPLCAN TEMAGVTPCILIDERAGLEPPOSGCVITL, BSVGGGI TIPGSBAN GGSPGGGGGPPLSDSQPLPADLPGATLPDVGLEEVRPLAVI OLI PHLOGARTPPTLQLOVTEKQVLLKADDG S727 21 221 RFILILEFTRERSSKRSSLFNGS S738 2 877 CTRRGGFEPTRERMSSKRSSLFNGS GFNAGGFEPTRERMSSKRSSLFNGS S748 S77 CTRRGGFEPTRERMSSKRSSLEADGASGFGVQPRGSG/LEC NAIRAGWNGGGPASFFUDLSLFWDLWFPFTDHAPGAPDFFG GR\AGGAPTSTTRRMSSKRSSLFNGS GFNAGGGPPAFFECTRERSSKRSSLFNGS GRAGGAPTSTTRRMSSKRSSLFNGS GRAGGAPTSTTRRMSSKRSSLFNGS GRAGGAPTSTTRRMSSKRSSLFNGS GRAGGAPTSTTRRMSSKRSSLFNGS GRAGGAPTSTTRRMSSKRSSLFNGS GRAGGAPTSTTRRMSSKRSSLFNGSFTARAGGFGVQPRGSG/LEPSC GGPAGAGGDAG/LEGCCPSAPWRAGSRPAASGCPWIFOGGGISPSC GGPAGAGDAG/LEGCCPSAPWRAGSRPAASGCPWIFOGGGISPSC GGPAGAGDAG/LEGCCPSAPWRAGSRPAASGCPWIFOGGGISPSC GGPAGAGDAG/LEGCCPSAPWRAGSRPAASGCPWIFOGGGGSCAGGAPTSTQAADGVICERPPAGAPTSTAAGGGPPARE EPFQVPFAGEEDAVPABEGPGGTPSTQAADGVICERPPAGAPTSTAAGGGPPARE EPFQVPFAGEEDAVPABEGPGGTPSTQAADGVICERPPAGAPTSTAAGGGPTATAGGTPTATAGGTPTATAGGTTTPATALTAGGTTTPATLTLAMBLAGGG KSSPRIADPQDIJAGGGNATATAGGSTVATAGGTPTATAGGAPTAGATTAGATTAGATTAGATTAG		1		
TRMGUTPCILAPLEAGLEPEGSGUTTL/BSVGAGITPGEGSG GGSGSGUTPLESSRQULPBALPGATLPWGLELEVRPLAY GLIFHLGQARTPPYLOLQYTEKQVLRADDG 5727 21 221 221 221 221 RFILILEFTREDWATGTASVINAGKSTHNEDGASCSVLTVKK AGAVTSTPRINSSKRSSLANG 5728 2 877 GTRNGGFBPRKGRANGGSAGGLEAGAAAGGFGVQPRGSG/LK NAIRAGNUNGRGARASFFWLISLUMLNEPFTHAPGAGSFPKAY GR\PMAGGRPPWYSGVLGSRVCGPLYSTSPAGGS/GGLEPSG GGPAGAGGDAG/LGGCRSAPMARGSRSAGGLEAGAAAGGFGVQPRGSG/LK GR\PMAGGRPPWYSGVLGSRVCGPLYSTSPAGGS/GGLEPSG GGPAGAGGDAG/LGGCRSAPMARGSRSAGGLEAGAAGGFGVQPRGSG/LK GR\PMAGGRPPWYSGVLGSRVCGPLYSTSPAGGS/GGLEPSG GGPAGAGGDAG/LGGCRSAPMARGSRSAGGLEAGAAGGFGVQPRGSG/LK GR\PMAGGRPPWYSGVLGSRVCGPLYSTSPAGGS/GGLEPSG GGPAGAGGDAG/LGGCRSAPMARGSRSAAGGFGVQPRGSG/LK GR\PMAGGRPPWYSGVLGSRVCGPLYSTSPAGGS/GGLEPSGAG HHNTTS/GPSGLGSGSAGGEGVADAGGGGAGDPAAF EPPQYEAGAGGDAG HHNTS/GPSGLGSFGSYGGAGGEGVADAGGGAGDPAAF EPPQYEAGAGGBAAGAGGGEGAAGAGGGAGDPAAF EPPQYEAGAGGAGAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGA	550			
GSPGSGSGPLASPISGPLADLICAGILEVQLELEVQLANDIO 5727 21 221 RFILILKETRELIPAGTGYAEVTNAGKSTHNEDQASCEVLTVKKY AGAVTSTPRINSSKRSSLING 5728 2 877 CTRINGGPEPREGARMSSSKRSSLING 5728 2 877 CTRINGGPEPREGARMSSSKRSSLING GRAMAGGRIPWEVSGVLIGARDGAAAGGROVQFRGSGT/LEF GRAMAGGRIPWEVSGVLIGARVGGLIYSTBAGGGFOVQFRGSGT/LEF GRAMAGGRIPWEVSGVLIGARVGGLIYSTBAGGGFOVQFRGSGT/LEF GGPAGAGGDAG/LEGGCSSAWRAGSRRAASCPDWIEGGGLISPS GGPAGAGGDAG/LEGGCSSAWRAGSRRAASCPDWIEGGGLISPS GGPAGAGGDAG/LEGGCSSAWRAGSRRAASCPDWIEGGGLISPS GGPAGAGGDAG/LEGGCSSAWRAGSRRAASCPDWIEGGGPAGE EPPQVPEAGBEDAVPABEGGGTPETQADQVRERPEAHLABGGG KGSPRELADPQDLAGQUSLAPPPPVAAAVISKA 5729 1 1525 AGGARBULTLQLGHFAGFVGAHWMQQDAALGAATDSKEPPPAL FOLVENTETTLANDLAGGTVTPLLIAUDALGSLESK,EEGGLIYRDK KSINGKGSSPLPPATTPRELIPITAGSTVTPLLIAUDALGSLESK,EEGGLIYRDK KSINGKGSSPLPPATTPRELIPITAGSTVTPLLIAUDALGSLESK,EEGGLIYRDK KSINGKGSSPLPPATTPRELIPITAGSLIYAHLHPRSI CHIOKYNHOGRAGRLEARFQGSSVLKEPKYGEBLEDPLLIFYTY CHOGGPILCHDOGSGVGAARAEALLODEVSGRGITTWGLLE GPYHRGGAGRILATGCGPSGVVLRGFRYGGBLEDPLLIFYTY CHOGGPILCHDOGSGVGAARAEALLODEVSGRGITTWGLLE GPYHRGGAGRILATGCGPSGVVLRGFRYGGGTGGTWGLIGAG PEPPSFPYLHVADATPHCHSALTALATLUTVCHSGSIGGLI PEPPSFPYLHVADATPHCHSALTALATLUTVCHSSIGGSIGHE PEPPSFPYLHVADATPHCHSALTALATLUTVCHSCRGGTTY AUGUSTAMATATATATATATATATATATATATATATATATATAT	5726	2	486	
CLIPHLIQARTPPYLOLOVTEKOVLIKADDO 5727 21 221 RPILLIKETERIPMATYSHAVINAGKSTHNEDQASCEVLTVKKK AGATYSTPRINISKKRSSLPNOE S77 GTRNQGFEPRKGRAWEGSAGGIRAPGAAAGGPGVQPRGSG/LPC ANTRAGNINGCOPASFEWDLSLPMDLINPPTTHAPGAGDFAW GR\PWAGGRPMPVSGVLGSRYCCPLYSTSPAGPG/SGGLPSG GGPAGAGGGAG/LPGRCPSAPRHAGSSPARAGSPAGGPAGGPPAG GGPAGAGGGAG/LPGRCPSAPRHAGSSPARAGSPAGEPPAGE EPPQVPEAGEEDAVPRAEGPGATFETGADVGKEPPEAHLASGG EPPQVPEAGEEDAVPRAEGPGATFETGADVGKEPPEAHLASGG EPPQVPEAGEEDAVPRAEGPGATFETGADVGKEPPEAHLASGG KGSPRIADPQDLPAGMSLAPFPPVAAVIRSIK GSPRRIADPQDLPAGMSLAPFPPVAAVIRSIK GSPRRIADPQDLPAGMSLAPFPPVAAVIRSIK GSPRRIADPQDLPAGMSLAPFPPVAAVIRSIK GSPRRIADPQDLPAGMSLAPFPPVAAVIRSIK GLOBALAMOGGALTTHKEBLYKPNPVLOPLASIGSGVARAGELLQDEYSGGVRW KGSPRRIADPQDLPAGMSLAPFPPVAAVIRSIK GLOBALAMOGGALTTHKEBLYKPNPVLOPLASIGSGSGLKEGGLYRD GLOBALAMOGGALTTHKEBLYKPNPVLOPLASIGSGSGLK GUDAALAMOGGALTHKEBLYKPNPVLOPLASIGSGSGLKEGGLYRD GGPYRRGGAGRIYTRILINTAFGLVRILTHABSSLVCPLSIGSGGKG GPYRRGGAGRIYTRILINTAFGLVRILTHABSSLVCPLSIGSGGGLPS GGPYRRGGAGRIYTRILINTAFGLVRILTHABSSLVCPLSIGSGGGLPS GPYRRGGAGRIYTRILINTAFGLVRILTHABSSLVCPLSIGGSIGLB FPPVSSPPLIADATLP GEVALATION GENERAL STANDARD FPTPLISACCEPSGTRCPAGYVLIGGIDARCHYST STRICTSGCTPGTPPPS GENERAL STANDARD FPTPLISACCEPSGTRCPAGYVLIGGIDARCHYST STRICTSGCTPGTPPS GENERAL STANDARD FPTPLISACCEPSGTRCPAGYVLIGGIDARCHYST STRICTSGCTPGTPPPS GENERAL STANDARD GENERAL STANDARD GENERAL STANDARD GENERAL STANDARD GGRANDARD		1		
S727 21 221 RPILIKETRRIPMATOYAEVINAGKSTINEDQASCEVLTVKKE AGAVTSTYRHENSKRRSSKIPNOE		İ	ļ	QGSPGGSGEGPPLSSPSQPLPADLPGATLPDVGLELEVRPLAVT
5728 2 877 GTRNGGFERRARGSLAGGEGVQERGSG/LPG GRVWLAGGREPHRUSLEPHOLIMPEPTHAPGARDFPANE GRVWLAGGREPHRUSLEPHOLIMPEPTHAPGARDFPANE GRVWLAGGREPHRUSLEPHOLIMPEPTHAPGARDFPANE GRVWLAGGREPHRUSGFERRAGGEGVEGGLEPSG GGPAGAGGAGA/LPGRCFSAFRWLGSLEPHAGGEGVEGGLEPSG GGPAGAGGAGA/LPGRCFSAPRWLAGSRPAASGEPMATGEGVEGHW HNNTS/GPPSQIGGAEGGDEGVADAPGICCKN/GAGAEPPAGE EPPQVPEAGEBEDAVPAEGGFGTFETGADOVEREPERHALBAGG KGSPRILADPODLPAGGMSLAPPPPVAAVIESNK SGSPRILADPODLPAGGMSLAPPPPVAAVIESNK GGREVITIGIGHFAGFVGAHWNQODAALGRANDSEPGEI CPULFRGTTHAGGETYTPRILIMDLKGSISJKEEGGLYRG LDAA IAWGGKLTHKRELYPKNPYLOPLESAGEVLSSEGWRW KSIPNGKGSSPLPTHTTPRILIPELAGERUSPHHHPTSI CHICKYNHIGGBAGKLAFFQGGSVLKEPKYGEELEDRLHPTYVE CDYLGGFGILCHLIGGFGGGKVLKEPKYGEELEDRLHPTYVE CDYLGGFGILCHLIGFGGGGKVLKEPKYGEELEDRLHPTYVE CDYLGGFGILCHLIGFGGGGKVLKEPKYGEELEDRLHPTYVE CDYLGGFGILCHLIGHGGGGGAVAKABELLOPGVHHHPTYGE CPYHRGBAGRNIYRLINTAFGLVHITHAHSSLVCPLSLGSIGLA PEPPVSFPYLHVDATLPFHCSAILATALDTHTCRVAPPYPHLEF SCHYMIGBAGGEGAGAKABELLOPGVHTSGLTGFGGAT WITHLAGAGEPSGTRCFAGSVVLKGSAILATALDTHTCRVAPPYPHLEF SCSPFGMVLLOSPKGAAVESVEVUG 1258 1713 KKFQAPARBITCHCCQKTVYPBRILLANQQVFHISCFRCSYCNNK LSLGTYASLHGRIYCKPHTNQLFKSKGNDGEFGHPPHKDLMAT KIETEGFWERFRINFENGGREPLKSFGGDCPSC*GCGGSNY*AQ GSSGREKGGASWNPKLRVA GSSGREKGGASWNPKLRVA SSSREKGGASWNPKLRVA REHGELIPRDSCYMKKPFRFFKKRRGG/CALPGGCLTFKDVAT EPSLEBWKCLNPAGRALYRAPMLENTRULESVGLTSKOSWYMKK KGGRGRKKGRRGEWFFLRVY FPSRSCGSPRKSRRAHTVTLVCGFTSFSFSLPLYLCGCLKF PERTCSGLQQADWAPDFGFSSFVPSWAATATGARKFLLAHTI\N LLGTKEDAHRIALALBREGGGGKOPGGRLKVGGGFYLDEKNIA ALDDAA FPSRSCGSPRKSRRAHTVTLVCGFTSFSFSLPLYLCGCLKF PERTCSGLQQADWAPDFGFSSFVPSWAATATGARKFLLAHTI\N LLGTKEDAHRIALALBREGGGKOPGGFGLKVGGGFYLDEKNIA ALDDAA FPSRSCGSPRKSRRAHTVTLVCGFTSFSFSLPLYLCGCLKF PERTCSGLQQADWAPDFGFSSFVPSWAATATGARKFLLAHTI\N LLGTKEDAHRIANAWTATATYPERKREGHTHATY GSLPLANKLTALALBREGGGKOPGGFRLKVGGGFYLGEKNAM AQVOYSMWNTKRNAWTATATYPERKREGHTHATY GSLPLANKLTALALBREGGGKOPGGRLKVGGAFYDERBERGHTHATY GSLPLANKLATALALBREGGGGADGFRGESCHACHGGGFYLGEKNAM AQVOYSMWNTKRNAWTATATYPURKERGFTAGARAFYLS SWYGGGGAPPQAVGVKPQNILGVLQKVQLDSHKQAMEKVGSY GSVLLSAESFCKLFNSLDDSVKRHPPREFGGFFT		}		GLIFHLGQARTPPYLQLQVTEKQVLLRADDG
5728 2 877 CTRNOGPEPREGRAWEGSAGCIRAPGGGGUDEGGGLEG NAIRAGUNDGGPASPPMULSLPWOLMPDHAPGDPPAVE GR\PWAGGRPWPUSGVLGSRVCGPLYSTSPAGPG/SGGLEPSC GGPAGAGCDAG/LEGRCPSAWRAGSRPAASCPMITGPGGLMI HENPTS/GPPSJGIGGGAGGDGVADAPGJCRM/GAEDPPAKE EPPGVPBAGEEDAVPAREGPGGTPETOADQVERRPSRHABGGR KSSPRILAPDQDLPAGMGSLAPPPPVAAVHOODALGRATDSKERPGEL EPPGVPBAGEEDAVPAREGPGGTPETOADQVERRPSRHABGGR KSSPRILAPDQDLPAGMGSLAPPPPVAAVHOODALGRATDSKERPGEL EPPGVPBAGEEDAVPAREGPGGTPETOADQVERRPSRHABGGR KSSPRILAPDQDLPAGMGSLAPPPPVAAVHOODALGRATDSKERPGEL FPGVPBAGEEDAVPAREGPGGTPETOADQVERRPSRHABGGR KSSPRILAPDQPLPAGMGSLAPPPTLIMDLKSKERGGULFUS GDUANALAWGGKLTTHKREILYPRIPYLODFLSAEGULGSBUGNER GDUANALAWGGKLTTHKREILYPRIPYLODFLSAEGULGSBUGNER KSIPMGGSSPLPTATTPKPLIPTEASIRVENGEDRIKVHLHPRSI CHIQKYNHUDGRAGRLEAFGQGESVLKEPFVGBELBRUHFTYLHLIPT CHIQKYNHUDGRAGRLEAFGQGESVLKEPFVGBELBRUHFTYLHLIPT CHIQKYNHUDGRAGRLEAFGQGESVLKEPFVGBELBRUHFTYLHLIPT CHIQKYNHUDGRAGRLEAFGQGGSVLKEPTGBLEVHLHPSICTSLSSPVG MYHL\ADMLSGCKKVUTAGGUNTSLUTHGTBPPSA LHACTTGEELLAQVILQQQDGWASSHLLIPTSLSGSDLGM PEPFVSFPVLSTPLATTERLAVILLOQUPGMSSSHLLIPTSLSGSPUS SCSPPGMVLLOSPKGRAVESVPVGG SCSPPGMVLLOSPKGRAVESVPVGG SCSPPGMVLLOSPKGRAVESVPVGG SCSPPGMVLLOSPKGRAVESVPVGG LEACTTGELAQVILQQQPGMSSSHLLIPTCAPAPPYHIFS SCSPPGMVLLOSPKGRAVESVPVGG SCSPPGMVLLOSPKGRAVESVPVGG SCSPPGMVLLOSPKGRAVESVPVGG SSSREKGGGANMPKLKUT SCSSPEKGRAVAMLENVRALESVGLTSKOMWMRK KIGTAGASAMPKLKUTO SSSREKGGGANMPKLKUTO SSSREKGGGANMPKLKUTO SSSREKGGGANMPKLKUTO SSSREKGGAAMSPKLTUTULQGGTSFSFSIPLYLCGCLTF PPRTCSOLQOADMAPDFGPSSFVPSMGATATGRKFLILHHI\M LLGTKEQAARIALAMGKQYENDARTLFEPTSGVNDTESPTIYKDES MCGGGAFCAAVCHONLLQVLQKVGLDSSHKAMMAAAQVQYSMWVTRAMATATHYTULQGTSFSFSIPLYLCGCLTR PPRTCSOLQOADMAPDFGPSSFVPSMGATATGRKFLILHHI\M LLGTKQQARIALAMUTONADPRINKEGGHTAVUTEDEKKMVAS FDEI\VY\SFTIGKTDSVLSEDPM SKYGGGAFCAAVCHONLLQVLQKVGLDSSHKAMMARKVGSY GSVLSAEBFGKENENDLGSVVKHEPPREFEGYGFFLGSAGFLEG HYYTDYLGNLLALAMLVSICVFLVLIDADVLEARDDTILEDILKNO VFUYYLLEMLLKLKVFLGLGKGYLSYPSNYFGGLITVVLLULEIS TIL\VCTDCHTGAGGRRWJKRILSUMTRMLMINILIVFRENTIDING YPVPFWLITNYESEBLDLITLEGNFSVLMPLHTITAGRTYNDLING YPVPFWLITNYESEBLDLITLEGNFSVLMPLHTITAGRTYNDLING	5727	21	221	RPILILKETRRLPWATGYAEVINAGKSTHNEDQASCEVLTVKKK
NAIRAGVNPGRGPASPFMDLSLIWDLWPPFTDLRAGADIPFANY GR\PMAGGRPPWDSGULGSRVCGDLYSTSPAGPG/SGGLSPS GGPAGAGGDAG/LPGRCPSABWRAGSRPAASCPDWIPGPQGLWI HRNPTS/GPPSQIGBAEQGGBCWADARQIQCGN/GAEDPPASI EPPQVPEAGEEDAVPAEGGGTPETQADQVRERPEAHLABGG KGSPRILADPQDLPAGOMSLAPPFPPVADAVIRSNK AGGARBULTUGJGHFAGFVGAHWWNQDALGSKIASSILKEEGGLYRDW GGSPRILADPQDLPAGOMSLAPPFPPVADAVIRSNK SOMMAGKLTHKIEGLYVGPYLODAGAGNALGSRTDSKEPPGEI CPULYRFGSTLHIGGETYTPRLILIMDLKGSLSSILKEEGGLYRDW KSIPRGKASSPLDTATTEKPLIPTEASIRVMSDPLRVHLHPRSI CMIQKYNHDGBAGRLEAFGGGSVULKEPKYQBELBERLHFYVEE CPYLYGFQTILCDLHGGSGGVULKEPKYQBELBERLHFYVEE GPYHRGBAGRITYRLLATAGSULVTCS\YRUGSSPUL EPPVSFPYLYDATLPFHCSALLATALDTYCS\YRUGSSPUL EPPVSFPYLHYDATLPFHCSALLATALDTYCS\YRUGSSPUL EPPVSFPYLHYDATLPFHCSALLATALDTYCS\YRUGSSPUL EPPVSFPYLHYDATLPFHCSALLATALDTYCS\YRUGSSPUL EPPVSFPYLHYDATLPFHCSALLATALDTYCS\YRUGSSPUL EPPVSFPYLHYDATLPFHCSALLATALDTYCS\YRUGSSPUL EPPVSFPYLHYDATLPFHCSALLATALDTYCS\YRUGSSPUL EPPVSFPYLHYDATLPFHCSALLATALDTYCS\YRUGSSPUL EPPVSFPYLHYDATLPFHCSALLATALDTYCS\YRUGSSPUL EPPVSFPYLHYDATLPFHCSALLATALDTYCS\YRUGSSPUL EPPVSFPYLHYDATLPFHCSALLATALDTYCS\YRUGSSPROHIPPPSA MYHTISACGPPSTRCPPYCGPCHSYLWGAGNETHAGRACHYCS\YRUGSSPUL EPPVSFPYLHYDAGSPRAGVURGSVULRGIDAGCHGGFTPPPSA LHACTTGEBILAQYLQQQPDWASSHLLLTPCCVAPPYPHLFS SCSPPGMVLDGSPKGRASSPULAGAGVURGFHKIDLWAT KIETGGFWEP PRNFROGGPLKSFGGGSGGCGGGGGCGSYNYAQ GSSRERGGQASWNFKLRVA SSRERGGQASWNFKLRVA SSRERGGGASWNFKLRVA SSRERGGGASWNFKLRVA SSRERGGGASWNFKLRVA SSRERGGGASWNFKLRVA EPSLEEWKCLNPAQBALYRAVMLENYRNLESVGLTSKDGWYMRK KPORGRGKORQEWPFLRVY FPSRSCGSPRRKSRRRAHVTVYTLVCGFTSFSFSLPLYLCGCLFF PERTCSGLQQADMAPDGGSSFVPGMATAGGRKLTANN LLGTREQARH IALINARGGGKOQDGFMATAGGRKLTANN LLGTREQARH IALINARGGGKOQDGFMATAGGRKLTANN LLGTREQARH IALINARGGGKOQDGFMATAGGRKLTANN LLGTREQARH IALINARGGGKOQDGFMATAGGRKTLANN AQVYSMWTRNAWYRANDTPMKRGGLISTVVLUKJEDEKTM\AS PESLYWPSCGGAPQAGWGKAPOALTUFARDFVLY SYNOBGGAPQAGWGKAPOALLQULGKYGLDSSKKQAMMEKYGSY GSSPLISABFOKLFNELDRSVVKEHPPRPESGPPLGGATGFRFT NYFDYLGKLKARANIALLATLTSQFRGTLMSGTSLTYPLULIGET VFITYNLLBHALLKYFALGRGVISTGGAFTGGFFT SYNOBGGARPAGFT SINFETHAMITATIGGPTYVILLE				AGAVTSTPNRNSSKRRSSLPNGE
NAIRAGVNPGRGPASPFMDLSLIWDLWPPFTDLRAGADIPFANY GR\PMAGGRPPWDSGULGSRVCGDLYSTSPAGPG/SGGLSPS GGPAGAGGDAG/LPGRCPSABWRAGSRPAASCPDWIPGPQGLWI HRNPTS/GPPSQIGBAEQGGBCWADARQIQCGN/GAEDPPASI EPPQVPEAGEEDAVPAEGGGTPETQADQVRERPEAHLABGG KGSPRILADPQDLPAGOMSLAPPFPPVADAVIRSNK AGGARBULTUGJGHFAGFVGAHWWNQDALGSKIASSILKEEGGLYRDW AGGARBULTUGJGHFAGFVGAHWWNQDALGSKIASSILKEEGGLYRDW GDAALAWGKLTHKEELLYKDRYPLOJEASGVLSSGUMRP KSIPRGKASSPLDTATTPKPLIPTEASIRVMSDPLRVHLHPRSI CMIQKYNHDGBAGRLEAFGGGSVULKEPKYQBELBERLHFYVEE CDYLQGFQILCDLHGGGSGVUKEPKYQBELBERLHFYVEE GPYHRGBAGRNIYRILATAGGUTHTAHSSLVCPLSIGGSLGLK GPYHRGBAGRNIYRILATAGGUTHTAHSSLVCPLSIGGSLGLK GPYHRGBAGRNIYRILATAGGUTHTAHSSLVCPLSIGGSLGLK GPYHRGBAGRNIYRILATAGGUTHTAHSSLVCPLSIGGSLGLK GPYHRGBAGRNIYRILATAGGUTHTAHSSLVCPLSIGGSLGLK GPYHRGBAGRNIYRILATAGGUTHTAHSSLVCPLSIGGSLGLK GPYHRGBAGRNIYRILATAGGUTHTAHSSLVCPLSIGGSLGLK GPYHRGBAGRNIYRILATAGGUTHTAHSSLVCPLSIGGSLGLK GPYHRGBAGRNIYRILATAGGUTHTAHSSLVCPLSIGGSLGLK GPYHRGBAGRNIYRILATAGGUTHTAHSSLVCPLSIGGSIGGN MHLIADMLSPCGKKVVTAGAIIPPHGAFTHDEAGGSIDLMGFGGAT FOFTDEAGGPSTRICAGPSVUKGIDAGCHTTAGGSTCPPPPSA LHACTTGEBILAQVILQQQQPGWASSHLLLTPCRVAPPYPHLPS SCSPPGMVLDGSPKGRAVESVPVFG 5730 1258 1713 KRFQGAPARETCVECQRTVYPMERLLANQQVFHISCFRCSYCNNK LSLGTTYASLHGRIYCKPHPQLFKSKGNYDGGGGGCGCPSNY*AQ GSSSREGGGASWNFLRVA SSREEGGGASWNFKLRVA SSREEGGGASWNFKLRVA SSREEGGGASWNFKLRVA SSREEGGGASWNFKLRVA SSREEGGGASWNFKLRVA SSREEGGGASWNFKLRVA SSREEGGGASWNFKLRVA LSLGTTROAHFARAGATATAGATAGATAGATAGATAGATAGATAGATAGAT	5728	2	877	
GR\PMAGGRPPMPVSGVLGSRVCGPLYSTSDAGP\GSGLSPSG GGPAGAGGDAG\LPGRCSPAWRAGSRPASCCPWTPGPGGLMI GRPAGGGDAG\LPGRCSPAWRAGSRPASCCPWTPGPGGLMI HRNPTS/GPPSQIGEGAEQGEGVADAPQIQCKN/GAEDPPAEL EPPGVPEAGEEDAVPAEEGGGTPETQADQVRERPEAHLASGGP KGSPRILADPOQLPAGGGNSLAPPFPPVAAVIRSNK 5729 1 1525 AGGAREVLTLQIGHFAGFVGAHWMQQDAAIGRATDSKEPPGET CPDVLYRRGTHIGGETYTPRILIMD\LSSIGNERGEGIVRDR GLDAAIAWQGKLTHKBELYPKNPYLQDFLSAGGVLSSGVWRN KSIPNGKGSSPLPTATTPKPLIPTEASIRVWSDFLRVHLHPRSI CMIQKYNHDGEAGRLEAFGGGSSVLKEPKYQBELBERLHFYVEE CDYLGGFQILICDLHGGTSGVGAKARELLQDEYSGRGITWGLLE GPYHRGSGAGNITRILATPGIVHLTATATADITTCS\YRICSSPVG MYHLADANDS-FCGKKVYTAGAIIPPHCSAILATADITTCS\YRICSSPVG MYHLADANDS-FCGKKVYTAGAIIPPHCSAILATADITTCS\YRICSSPVG MYHLADANDS-FCGKKVYTYGGAITATADITTCS\YRICSSPVG MYHLADANDS-FCGKKVYTYGGAITATADITTCS\YRICSSPVG MYHLADANDS-FCGKKVYTYGGAITATADITTCS\YRICSSPVG MYHLADANDS-FCGKKVYTYGGAITATADITTCS\YRICSSPVG MYHLADANDS-FCGKKVYTYGGAITATADITTCS\YRICSSPVG MYHLADANDS-FCGKKVYTYGGAITATADITTCS\YRICSSPVG MYHLACTTGGETILAQYVLQQQQRGWASSHLLLTPCRVAPPYHLIPS SCSPPGWVLDGSPKGANVSSVPUG SCSPPGKSGRGCPGSVVLRGIDRACHTSQLTPGTPPPSA LHACTTGGETILAQYVLQQQQRGWASSHLLLTPCRVAPPYHLIPS KKFQAPARETCVECQKTVYYMRELLANQQVFHISGFRCSYCNINK XIETTGGFWERPRNFENGGRELKSPGGCPGSNY*AQ GSSSREKGQASWNFUKNA XIETTGGFWERPRNFENGGRELKSPGGCPGSNY*AQ GSSSREKGQASWNFUKNA XIETTGFWERPRNFENGGRELKSPGGCPGSNY*AQ GSSSREKGQASWNFUKNA FSHRGELIFEDSCYMRKPFRRPKKRRGG/CALPQGCLTFKDVAI EFSLEEWKCLINFAQAALYRAVHLENYRLLESVCLTSKOSYMKR KPGGRGRKORROBEFFILMY SPRTCSQLOADMADFOSPSSFVFWSKATATGARKFLLAFNI\N LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLLGKNILA QVSTNILDFEVTALHTVYBETCRAQLELSLPVVGSQLIGUVPLK ALLDAA PROCESSPERKSRRRAHVYTVLVGFTSFSFSLPJIYKGGCFBAIKSAYM AQVQSMWVTRKNAWYFANDPROMKREGLHYVVIERDEKYM\AS FDEI\VP\EFFIGKMDEVLSRDPM S733 1 460 PALGEVANANAMKQYENDARTLFFFTSSVMTESPITYRDSS SWCEGGAPPQAVGVKPONLLJOVLGVGUNDTESPITYRDSS SWCEGGAPPQAVGVKPONLLJOVLGVGUNDTESPITYPTOTI GSLFLNNLLTATIYSQFRGYLMSSLQTSLFRRAGTRAPETUS GSVLLSABEFQLLTWELDRSVVKEHPPRPSYQSPFLOSAQPLIC VFIVYYLLEMLLKVPAGGRGVLKKAYSLPRVGGGFSCLIPARTISL TL\CCTTCTTQAGGGRRW/FLLSLMDWTRMLMNLLVFFLRIIP SWCEGABPQAUGVKPONREISINFET				NAIRAGVNPGRGPASPFWDLSLPWDLWPPPTDHAPGAPDFPAGE
GGPAGAGGDAG / LPGRCTS APWRAGSPRASCED PROPERLING HRNPTS / GPPSQTGGGSAGGGGGAGVADGCOKN / GABD PARE EPPQVPEAGEEDAVPABEGPGGTPETQADQVRERPEAHLAEGGE KGSPRILAD PQDLPAGGMSLAPPFPVAAVIRSNK AGGAREVLITUGLGHFAGFVGAHWMQQDAALGERTDSKEPPGEI CPDVLYRTGRTLHGGETTTPRLITUMDLKSSLSSLKEEGGLVRON (GLDAAIAWGKLTHKEELPYKEPYLOPELASKOVLKSSUKKEEGGLVRON KSIPNGKGSSPLDTATTPKPLITEASKOVLSSDWRW KSIPNGKGSSPLDTATTPKPLITEASKOVLSSDWRW KSIPNGKGSSPLDTATTPKPLITEASKOVLSSDWRW KSIPNGKGSSPLDTATTPKPLITEASKOVLSSDWRW KSIPNGKGSSPLDTATTPKPLITEASKOVLSSDWRW KSIPNGKGSSPLDTATTPKPLITEASKOVLSSLGSUGGUK KSIPNGKGSSPLDTATTPKPLITAMSSLVCPLSGSUGGUK GPYHRGSAGRINITALASSLVCPLSJGSUGGUK PEPPVSFPYLHVDATLPFHCSALLATALDTVTCS\YRLCSSPVS MYHL\ADMISFCGKKVVTAGAIIPPLAGGSLPJGGSGGIT PWTPLSAGGPSSTRCFQSVVUKGIDAGTGGATPPPSA LHACTTGGEBLAQVLQQQDGVWRSSHLLITPCRVAPPYPHLFS CSPPGMVLDGSPKGANAVESVPVG 5730 1258 1713 KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK LSLGTTYASLHGRIYCKPHFNQLFKSKGNYDGGGGGHSPY*AQ GSSREKGGQASWNFKLRVA KETGGFWGRPNFENGREPLKSPGGGESPCGGCPGSNY*AQ GSSREKGGQASWNFKLRVA SSREKGGJASWNFKLRVA FSHRSELIFBDSCYMRKPPRPKKRGG/CALFGGGLTFKDVAT EPSLEEMKCLNPAQRALYRAVMLENYRNLESVGLTSKDGWYMRK KOGRGGKORGGBPFTLKYV 5731 122 443 RSHRSELIFBDSCYMRKPPRPKRRGG/CALFGGGCLTFKDVAT EPSLEEMKCLNPAQRALYRAVMLENYRNLESVGLTSKDGWYMRK KOGRGGKORGGEOPHPLRVY 5732 226 772 PPSRSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF PERTCSGLQQADWADADFGSSFVFBWGATATGARKLIANNI LGGTKGGAHR IALDIARGGGKOQDGFGHKXVQGGIGWLDGENLA QUSTNLLDFEVTALHTVYEETCERQELSLPVVGSGLVGLVPLK ALLDAA ALLDAA ANDAYSMWTRNAWYFANTDEPMKRRGLLSTUVUSRDEKTM\AS FDST\VP\EFICKMDEVLSRDPM MRTACSPDGLCSDGNGLEKKPFTSRDFMKFRLGFFRAKSAM AQVQSMWTRNAMAVARNIVSTOFTLUFFTVT GSLFLMNLLTAIITSGFRGTLMSCLGTSLFFRLGFFRAKSAM AQVQSMWTRNAMYFANTDEPMKRRGLLSTVVULREDEKTM\AS FDST\VP\EFICKMDEVLSRDPM KGNSPESLTSLLVLLTTANNIEVULTDADVVPGERDEKTM\AS FDST\VP\EFICKMDEVLSRDPM KGNSPESLTSLLVLLTTANNIEVULTDADVVPGEBLTVVLLVLETS TL\VCTDCTTQAGGGRRW/FLLISLLDMDTRHLMMLLVPFFLRIIP GSFLINMLLTAIITSGFRGTLMSCLJAWTRHLAMMLLVPFFLRIIP SKRPMAUVSSTVLGL VFTYVYLLEBLALKMPALSTUPGLITVVLLULGET TL\CTDCTTQAGGGRRW/FLLISLLDMDTRHLAMMLLVPFFLRIIP SKRPMAUVSSTVLGL VFTYVYLLEBLL				
HENDTS/GPSQIGGGASQGDGCAADPQIGCKN/GAGDPPAEL EPPQVPEAGEGDAVPABEGGGTPETQADQVGRRPEAHLAGGG KGSPRILADPQDLPAGQMSLAPPFPPVAAVIRSNK 5729 1 1525 AGGAREVITIQUGHFAGFVGAHWWNQQDAAUGRSTDKEPFGGE CDDVLYRTGTHIGGETYTFRILIMDLKGSUSSLKEEGGLYRDK CDDVLYRTGTHIGGETYTFRILIMDLKGSUSSLKEEGGLYRDK KSIPNGKGSSPLPTATTFYTFRILIMDLKGSUSSLKEEGGLYRDK KSIPNGKGSSPLPTATTFYTFRILIMDLKGSUSSLKEEGGLYRDK KSIPNGKGSSPLPTATTFYRLITPAGATTWSDFLRVHLHFRSI CMIQKYNHDGBAGRLEARGQGSSVLKEPKYQBELEDRLHFYVEE CDYLQGFQILCDLHDGFSGVGAKAAELLQDEYSGRGITMGLLE GPYHRGEAGRNIYRLLHTARGUNHTAHASSLVCPLSLGGSLGLE PEPPVSFPYLHTDATLFPHCSAILATADITVTCS\KYRLCSSPVG MYHL\ADMASPCGKKVVYAGAIIPPHCSAILATADITVTCS\KYRLCSSPVG MYHL\ADMASPCKKVVYAGAIIPPHCSAILATADITVTCS\KYRLCSSPVG MYHL\ADMASPCKKVVYAGAIIPPHCSAILATADITVTCS\KYRLCSSPVG MYHL\ADMASPCKKVVYAGAIIPPHCSAILATADITVTCS\KYRLCSSPVG MYHL\ADMASPCKKVVYAGAIIPPHCSAILATADITVTCS\KYRLCSSPVG MYHL\ADMASPCKKVVYAGAIIPPHCSAILATADITVTCS\KYRLCSSPVG MYHL\ADMASPCKVVYYAGAIIPPHCSAILATADITVTCS\KYRLCSSPVG MYHL\ADMASPCKVVYYAGAIIPPHCSAILATADITVTCS\KYRLCSSPVG MYHL\ADMASPCKVVYYAGAIIPPHCSAILATADITVTCS\KYRLCSSPLYBLIAGGEGGAGPPHCHKOLWAT KIETGGFWERPRNFENGGRFLAGAVVYTJEGTPTPPPPS SCSPPGMVLDGSPKGAVESVPVFG 5730 1258 1713 KKFQAPARETCVECQKTVYYMERELLANQOVYHISGFRCSYCNNK KSGAPARETCVECQKTVYYMERELLANQOVYHISGCFRCSYCNNK KSGAPARETCVECQKTVYYMERELLANQOVYHISGCFRCSYCNNK KSGAPARETCVECQKTVYYMERELLANQOVYHISGCFRCSYCNNK KSGAPARETCVECQKTVYYMERELLANQOVYHISGCFRCSYCNNK KSGAPARETCVECQKTVYYMERELLANQOVYHISGCFRCSYCNNK KSGAPARETCVECQKTVYYMERELLANQOVYHISGCFRCSYCNNK KSGAPARETCVECQKTVYYMERELLANQOVYHISGCFRCSYCNNK KSGAPARETCVECQKTVYYMERELLANQOVYHISGCFRCSYCNNK KSGAPARETCVECQKTVYYMERELLANQOVYHISGCFRCSYCNNK KSGAPARETCVECQKTVYYMERELLANQOVYHISGCFCSYCNNK KSGAPARETCVECQKTVYYMERELLANQOVYHISGCFCSYCNNX KSGAPARETCVECQKTVYYMERELLANQOVYHISGCFCSTCONNX*AQ GSSSEREGGAPWFRCNANA SEGGAPATTATATTATTATTATTATTATTATTATTATTATTATT				
SPPQVPEAGEEDAVPABEEPGGTPETQADQVERPEAHLARGGA KGSPRILADPODLPAAQMSLANPING S729 1	,			HENDER (CERTAROCORCUADA DO TOCKA (CARDADA ED
SSPREIADPODLPAGOMSLAPPFPPVAAVIRSNK				EDDUNDESCREDSIDS DECOCCADESCOS DOS DESCRESSIONS SECTOR DE L'ACTUAL
1 1525 AGGAREVLTLOLGHFAGFVGAHWMNQODALGRATDSKEPDGEV CDDVLYRTGRTLHGGETYTPRLILMDLKGSLSSLKEEGGLYRDK QLDAAIAWQGKLTHKBELYPKNPYLDDFLSAGGVLSSDGWRW KSIPNGKGSSPLPTATTRYPLIPTEASIRWSDFLRVHLHPRSI CNIQKYNHODGAGRLEAFGGGSSVLKEPKYOBBLEDRHHFYVEE CDYLQGFOILCDLHDGFSGVGAKAABLLQDEYSGRGITTWGLLE GPYHRGEAQRNIYRLLNTAFGLVHLTAHSSLVCPLSLGGSLGLE EPEPVSFYLHYDATLPFHGSAILATALDIVTCS\YRLCSSPVS MYHL\ADMLSFCGKKVVTAGAIIPPPLAPQGSLPDSIMQFGGAI FDTDISAGGBPSSTRCFAQSSVVLRGIATALDIVTCS\YRLCSSPVS MYHL\ADMLSFCGKKVVTAGAIIPPPLAPQGSLPDSIMQFGGAI FDTDISAGGBPSSTRCFAQSSVVLRGIATALDIVTCS\YRLCSSPVS MYHL\ADMLSFCGKKVVTAGAIIPPLAPQGSLPDSIMQFGGAI FDTDISAGGBPSSTRCFAQSSVVLRGIATALDIVTCS\YRLCSSPVS MYHL\ADMLSFCGKKVVTAGAIIPPLAPQGSLPDSIMQFGGAI FDTDISAGGBPSTGAVSTRAJUVTGS\YRLCSSPVS MYHL\ADMLSFCGKKVVTAGAIIPPLAPQGSLPDSIMQFGGAI KKFQAPARETCVECQRTVYPMERLLANQQVFHISCFTRPPPPHPLF SCSPPGMVLDGSPKGANVESVPVFG SCSPPGMVLDGSPKGANVESVPVFG KKFQAPARETCVECQRTVYPMERLLANQQVFHISCFRCSYCNNK LSLGTYASLHGRIYCKPHFNOLFKSKGNYDGFGFRPHKKDLWAT KLETGFWHEPNFRFRKGRGPLKSKGPGCPGSNY*AQ GSSSREKGGQASNNPKLRVA SFRGELIPKDSCYMRKPPRFRPKKRRQG/CALPGGCLFFKDVAI EFSLEEWKCLNPAQRALVRAWLENYNNLESVGLTSKDSWYMKK KLGGRGKQRRQBWFPLRVY PPSRSCSOPPRKSRRRAHVTVTLVCGFTSFSFSLDLYLCGCLEF PPETCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTTRQAHRIANLRGGGRKDQFGRLKKVGGIGWYLDEKNLA ALLDAA QVSTNLLDFEVTLALTVYVEETCREAGGLSLPVVGSQLVJCLVLK ALLDAA PALOGVANANLAWGKQYENDARTLFBFTSGVNDTESPITYDBS MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVISRDEKTM\AS FDEI\VYD-PEIGKGMDEVLSRDPM S734 3 968 RCNSPESLTSLUVLTTANNLFVLIPAYSKMRAVAIFPLVFTVFTVT GSLJMMLLTAIIYSGFRGYLMKSLQTSLFRRLGTRAAPEVILS SMVCEGGAFPQAVGVKPQNLQVIQKVQLDSSHKQAMMEKVRSY GSVLLSAEBFQKLFFLDRSVVKEHPPREYSGPFLOSAGFLEG HYYPDVJALEMLLAVAILGTAYINSICTFLJUADDVLPAERDDFILGIINC VFIVYYLLEMLLKVPALGLRGYLSYPSNVFDGGAFTSCGLPOARTIPL SMKPMAVVASTVLGL TL\VCTDCHTQAGGRRWW/RLLSLMDMTRMIMMLIVFRFLIIP SMKPMAVVASTVLGL APPROLVK/SSNNTGRWGREISNFLAFTLITILITINTLILITINTSEBELDLTLDGGPRFLJKFLIAFINTLAGRTYNDLNA YPVPPWULTNYSSBELDLTLDGGRFULSKPIATINTLIGRTYNDLNA YPVPPWULTNYSSBELDLTLDGGRFULSKPIATINTLIGRTYNDLNA LKILT				
CPDVLYRTGRTLHGQETYTPRLILMDLKGSLSSLKEEGGLYRDK QLDAAIANQGRUTTHKEELYPKNPYLQPISAEGULSSDGWRW KSIPNGKGSSPLPTATTPKPLIPTEASIRWMSDFLRVHLHFRSI CMIQKYNHDGBAGRLEAFGGESVLKEPKYQBELEDRLHFYVEE CDYLQGPQILCDLHGFGSGWGSALALQDEYSGRGIITWGLLF GPYHRGEAQRNIYRLLNTAFGLVHLTAHSSLVCPLSIGGSLGLK PEPPVSFFYLHYDATLFFHCSAILATALDTUTCS\YRLCSSPVS WHLLADMLSSCGKVVTAGAITPPLAPQGSLPDSLMQFGGT PHTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTFOTPPPSA LHACTTGEEILAQYLQQQQPGWMSSHLLLTPCRVAPPYPHLFS SCSPPGMVLDGSRGAAVESVPVFG 5730 1258 1713 KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK LSLGTYASALHGILYCKPHTNQLFKSKGNYDEGFGHRPHKDLWAT KIETEGFWERPRNFENQGRPLKSPGGEDCFSC*GGCPGSNY*AQ GSSSREKGGGASMNPKLRVA KSETGGFWERPRNFENQGRPLKSPGGEDCFSC*GGCPGSNY*AQ GSSSREKGGGASMNPKLRVA KSETGGFWERPRNFENGGRPLKSPGGCCALPQGCLTFKDVAI EPSLEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK KVGRGKQRRQEWPFLRVY FORGKORRQEWPLRVY FPSRSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF PERTCSOLQQADWAPDFGESSFVPSWGATATGARKFLIARNI\N LLGTKEOCHEN LALLDRACHGCHOPGRLKKVQG GWYLDEKNLA QVSTNLLDFEVTALHTVYBETCREAQELSLPVVGSQLVGILVPIK ALLDAA 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDONGLELKCPFTSRDFMKRFLGGFBAIKSAYM AQVQYSMVTRKNAWYFANYDPRMKREGLHYVVIERDEKXM\AS SFDEI\VP\EFIGKMDEVLSRDPM 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDONGLELKCPFTSRDFMKRFLGGFBAIKSAYM AQVQXSMVTRKNAWYFANYDPRMKREGLHYVVIERDEKXM\AS SFDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFTVFTVI GSLFILMNLLTAIITSQFGGYLMSLQVTLADAVLPAERDDPILGIINC VFIVYYLLEMLKVFALGLRGVI.SYPSNFFOLLTVVLLULBIS SMVGEGGAPPQAVGVRQNLLQVLQKVQLDSSHKQAMMEKYRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEUSGPFLQSAGFFIG HYYPDYLGNLIALANLVSICVFLULDADVLPAERDDPILGIINC VFIVYYLLEMLKVFALGLRGVI.SYPSNFFOLLTVVLLULBIS SMKPMAVVASTVLGL 5735 2 540 FFTDCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLVK/SSNTYDRWQRGREISNEFYLMFINITAGRTYNDLNQ VPVPWWLTNYESEBLDLTLPONFRDLSKPIGAINPRAAYFYAE RYTWEDDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY VPVPWWLTNYESEBLDLTLPONFRDLSKPIGAINPRAAYFYAE RYTWEDDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY			1.505	<u> </u>
CIDAAIAMOGRLTTHKRELYPKNPYLQDFLSAEGYLSSDGYWRV KSIPNGKGSSPLPTATTPKPLIPTEASIRVWSDFLRYHLHPRSI CNIQKYNIDGEAGREAFGGGESVLKEPKYQBELEDRLHPYVEE CDYLGGFQILCDLHDGFSGGSAKAAELLQDPYSGRGITTWGLLE GPYHRGEAQRNIYHLINTAFGLYLTAHSSLVCPLSIGGSIGIR PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS\YRLGSSIGIR PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS\YRLGSSIGIR PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS\YRLGSSIGIR PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS\YRLGSSPGGAT MYHL\ADMLSFCGKKVVTAGAIIPPPLAGGSLPDSIMQFGGAT DYTPLSACGPPSGTRCPAGSVULNGIDRACHTSQLTFOTPPPSA LHACTTGEEILAQVLQQQPGVWSSSHLLLTPCRVAPPYPHLFS SCSPPGMVLLDGSPKGANVESVPVFG	5/29	1	1525	
KSIPNGKGSSPLPTATTPKPLIPTEASIRVMSDFLRVELHERSI CMIQKYNHDGBAGRLEAFGQGESVLKEPKYQBELEDRIHFYVEE CDYLQGFQILCDLHDGFSGVGAKARELLQDEYSGRGITTMGLLE GPYHRGEAQRNIYRLLMTAFGLVHLTAHSSLVCPLSLGSGLGLR PRPPVSFPYLHYDATLPFHCSAITALDTVTICS VRICSSPYMS MVHL\ADMLSFCGKKVVTAGAIIPFPLAPGQSLPDSLMQFGGAT PWTPLSACGBPSGTRCFAGSVVLRGIDRACHTSQLTTGTTPPBSA LHACTTGEELLAQVLQQQQFGWASSHLLLTTCRVAPPYHLFS SCSPPGMVLDGSPKGAAVESVPVFG 5730 1258 1713 KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK KIETEGFFERPRHFENGGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSREKGGQASWHKLRVA 5731 122 443 RSHRGELIPKDSCYMRKPPRRFKKRRQG/CALPQGCLTFKDVAI EFSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMK KFGRGGKGRRGRQFFLRVY 5732 226 772 PPSRSCQSPRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNIN LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA QUSTNLLDFEVTALHTVYBETCREAQELSLPVVGSQLVGLVPLK ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPILYLCGCLRF PERTCSQLQQAWAPDFGPSSFVPSWGATATGARKFLIAFNIN LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA QVSYNVLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPILYLCGCLRF PERTCSQLQVAGWAVTRANAVATYPTYTEGESPILYLCGCLRF PERTCSQLCSDGNGLELKCPFTSRDFWKRFLGGFBAIKSAYM AQVQYSWMVTRKNAWYFANTDPMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYATFFIVFTVI GSLFLMMLLTAIITYSGFGYLMKSLQTSLFRRRGGTRAPEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKDQLSSHKQAMMEKVRSY GSVLLSABEPGKLFNELDRSVVKEHPPRPEYQSPPLQSAQFLFG HYYFDYLGNILIALANLVSICVPLULDADVLPAREDDPILGIINC VFIVYYLLEMLLKVFALGLRGYISYSNYFFGLLTVVLLUTLEIS TL\CTCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTECVARANFPDQATVKKAYAYSEFSCGLPQARRISL ATPRQLVK/SSNNTPRQWQREISNFEYLMFINTLAGRTYNDLNQ VPVPPWULTNYEGEBLDLTLPONFRDLSKPIGAINPRAAVFYAB RYFWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY VPVPPWULTNYEGEBLDLTLPONFRDLSKPIGAINPRAAVFYAB RYFWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT		(
CHIQKYNHOGEAGRILEAFGQGESULKEPKYQBELBPRLHFYVGEL CDYLQGFQILCDLHDGFSGVGAKAABLLQDEYSGRGIITWGLE CDYLQGFQILCDLHDGFSGVGAKAABLLQDEYSGRGIITWGLE GPYHRGEAQRNIYRLLMTAFGLWHLTAHSSLVCPLSIGGSLGLR PEPPVSFFYLHYDATLPFHCSÄILATALDTUTCS\YRLGSEPGW MYHLADALLSFGKKVUTVAGIIPPCHSQLDDSIMQFGGAI PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTFGTPPPBS LHACTTGEBILAQYLQQQQPGWMSSHLLITPCRVAPPYPHLFS SCSPPGWYLLDGSPKGAAVESVPVFG 5730 1258 1713 KKFQAPARETCVECQKTVYPMERILANQQVFHISCFRCSYCNNK LSLGTYASLHGRIYCKEPHFNQLFKSKGNYDEGFGHRPHKDLWAT KIETTGFFMERPRNFENGGRENSFGGEDFSC**GGCPGSNY*AQ GSSSREKGQASWMPKLRVA 5731 122 443 RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAI EPSLEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMKK KPGRGRGKQRRQEWFFLRVY 5732 226 772 PPSRSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLEF PERTCSQLQQADWAPDFGPSSFVSWGATATGRKFLIARNI\N LLGTTEQAHRIALNLREGGRGKDQPGRLKKVQGIGWYLDEKNIA QVSTNLLDFEVTALHTVYEFTCREAQELSLPVVGSQLVGLVPIK ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFFFTSGWNDTESPIIYNDES MRTACSPDGLCSGONGLELKCPTTSRDFMKFRLGGFBAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKNDEVISRDPM 5734 3 968 RCNSFSESLTSLIVLITTANNIVPULTPAYSKNRAYATFFTVFTVI GSLPLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVCEGGAFPQAVGVKPQNLLQVLQKVQLDSSIKQAMMEXYRSY GSVLLSABEFGKLFNELDRSVKHPPPBFYGSPFLGSHFLIGILNC VFTVYYLLEMLLKVFALGLRGYLSYPSVDFGLLTVVLVLERIS GSVLLSABEFGKLFNELDRSVKHPPPBFYGSPFLGSHFLIGILNC VFTVYYLLEMLLKVFALGLRGYLSYPSVDFGLLTVVLVLBILS SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLFRVGGGTSCGLPQARRISL ATPRQLYKYSSNMTQRWQRESISNFEVLMMEINTIAGRTYNDLNQ YPVPFWVLTNYESSELDLTLPGNFRDLSKFIGAINPRAVFYBE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				
CDYLQGFQILCDLHDGFGGVGAKAABLLQDBYSGRGIITWGLLE GPYHRGBAQRNIYRLINTAFGLVHLITAHSSLVCPLSIGSLGILG BPEPPVSFFYLHYDATLPHCSAILATALDTUTTCS\YRLCSSPVS MYHL\ADMLSPGGKKVVUTAGAIIPPLAPQGSLDDSIMQFGGAT PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTPGTPPPSB LHACTTGEBILAQYLQQQPGVMSSSHLLLTPCRVAPPYPHLFS SCSPPGMYLDGSPKGAAVESVPVFG 5730 1258 1713 KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK KSPGAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK KIETTGFHERPRNFENGGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWNPKLRVA 5731 122 443 RSHRGELIPKDSCYMRKPPRPFKKRRQG/CALPQGCLTFKDVAI EFSLBEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK KVPGRGRGKQRQEWFFLRVY 5732 226 772 PPSRSCQSPRKSRRAHVTUTLVCGFTSFSFSLPLYLCGCLFF PERTCSOLQADWAPDFGPSSFVPSWGATATGRRKFILARNI\N LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNIA ALLDAA 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKRRGGFGALKSAYM AQVQYSMWTRKNAWYFANYDPRKKRGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM SMVEGGGAPPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY SMVEGGGAPPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSABEFGKLFNELDRSVVKEHPPRPBYGSPFLQSAQFLFG HYYFPYLGNLTALANLUSICVFLVLDASLDSHKAQAMMEKVRSY VFIVYYLLEMLLKVPALGLRGYLSYPSNVFGGITSULVLULBIS SMKPMAVVASTVLGL SMKPMAVVASTVLGL 5735 2 540 FFFTCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWCREISNFEVLMFLINTLAGRTYNDLNQ VPVPFWVLINTYESSELDLTLPGNFRDLSKFIGLINPKRAVFYBE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				KSIPNGKGSSPLPTATTPKPLIPTEASIRVWSDFLRVHLHPRSI
GPYHRGEAQRN I YRLLNTAFGLUHLTAHSSLVCPLSLGGSLGLH PEPPVSFPYLHYDATLPFHCSAI LATALDITYTCS \ YRLCSSPVS WHYL\ADMLSFCGKKVVTAGAI I PPILAPQQSLPDSLMQFGGAT PMTPLSACGEPSGTRCFAQSVULRG I DRACHTSQLTFGTPPPSB LHACTTGEEILAQYLQQQPGWMSSHLLLTPCRVAPPYPHLFS SCSPPGMVLDGSPKGAAVESVPVFG 5730 1258 1713 KKFQAPARSTCVECQKTVYPMERLLANQQVFHISCFRCSYCNKK KKFQAPARSTCVECQKTVYPMERLLANQQVFHISCFRCSYCNKK KKFQAPARSTCVECQKTVYPMERLLANQQVFHISCFRCSYCNKK KIETEGFHERPRNFENQGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWNPKLRVA SSSSREKGGQASWNPKLRVA SSSSREKGGQASWNPKLRVA SSSSREKGGQASWNPKLRVA SPHRGELIPKDSCYMKKPPRPFKKRRQG/CALPQGCLTFKDVAI EFSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK KDGRGRGKQRRQEWFFLRVY PPSRSCQSPRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLEF PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNNERQGGGKDQPGRLKXVQGIGWYLDEKALA ALLDAA 5733 1 460 PALGEVNANALAWGKQYENDARTLFBFTSGVNDTESPIIYRDES WRTACSPDGLCSDGMGLELKCPFTSRDFMKFRLGGFBALKSATM AQVQYSMWVTRKNAWYFANYDPMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM STAGSPBSLTSLUVLLTTANNLFVLIPAYSKNRAYAIFFTVFTVI GSLFMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVEGGGAFPQAVGYRONLLQVLLQVQLDSSHKQAMBEKVRSY GSVLLSABEFQKLFMELDRSVVKEHPPRPEYGSPFLQSAQFLFG HYYFDYLGNLIALAALVSICVPLVLDADVLPAERDDFILGILINC VFIVYYLLEMLLKVFALGLRGYLGYPDFLATVALLEIS TL\VCTDCHTQAGGRRWW/RLLSLMDMTRMLMMLIVFRERIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVPFWULTNYESELDLTLPONFRDLSKPIGALMPKRAVFYAB RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	-			CMIQKYNHDGBAGRLEAFGQGESVLKEPKYQBELEDRLHFYVEE
PEPPVSFPYLHYDATLPFHCSÄILATALDTVTCS\YRLCSSPVS WYHL\ADMLSPCGKKVVTAGAII PPPLAPGQSIPDBIMGPGGD PWTPLSACGEPSGTRCFAGSVVLRGIDRACHTSQLTTEGTPPPBS LHACTTGEBILAQYLQQQQFGWSSSHLLLTPCRVAPPYPHLFS SCSPPGMVLDGSPKGAAVESVPVFG KKPQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT KIETEGFERPRNFENQGRFLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWNPKLNY 5731 122 443 RSHRGELIPKDSCYMRKPPRPKKRRQG/CALPQGCLTFKDVAI EFSLEWKCLNPAQRALYRAVWLENYRNLESVGLTSKDSWYMK KPGRGRGKGRGEWFFLNY 5732 226 772 PPSRSQSPRRKSRRAHVTVTLVCGFTSFSFLPLYLCGCLFF PERTCSQLQQADWAPDFGPSSVPYSMGATATGARKFLIAFNI\N LLGTKEQAHIALANLREGGGKDQPGRLKXVQCIGWYLDEKNLA QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWTRKNAMYFANYDPRMKFRGLHYVVIERDEKYM\AS FDEI\VP\EFICKMDEVLSSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFTVFTVI GSLFIMNLLTAIIYSQFRCYLMKSLGTSLFRRRLGTRAAFEVLS SMVGGGAFPQAVGVKPQDLAVGVLQTSLGTSLFRRRLGTRAAFEVLS SWVGEGGAPQAVGVKPQDLAVGVLQTSUJDSHKQAMMEVKRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLTALANLVSICVFLUIDADVLPAERDDFILGIINC CVFILYYYLLEMLLKVPALGLERGYLSYPSNVPGGLITVVLIVLISIS TL\CTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWGRREISNFEYLMFLNTIAGRTYNDLNQ YPVYPWULTNYESELDLTTLPONFRDLSKPIGALMPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKKILT		,		CDYLQGFQILCDLHDGFSGVGAKAAELLQDEYSGRGIITWGLLP
PEPPVSFPYLHYDATLPFHCSÄILATALDTVTCS\YRLCSSPVS WYHL\ADMLSPCGKKVVTAGAII PPPLAPGQSIPDBIMGPGGD PWTPLSACGEPSGTRCFAGSVVLRGIDRACHTSQLTTEGTPPPBS LHACTTGEBILAQYLQQQQFGWSSSHLLLTPCRVAPPYPHLFS SCSPPGMVLDGSPKGAAVESVPVFG KKPQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT KIETEGFERPRNFENQGRFLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWNPKLNY 5731 122 443 RSHRGELIPKDSCYMRKPPRPKKRRQG/CALPQGCLTFKDVAI EFSLEWKCLNPAQRALYRAVWLENYRNLESVGLTSKDSWYMK KPGRGRGKGRGEWFFLNY 5732 226 772 PPSRSQSPRRKSRRAHVTVTLVCGFTSFSFLPLYLCGCLFF PERTCSQLQQADWAPDFGPSSVPYSMGATATGARKFLIAFNI\N LLGTKEQAHIALANLREGGGKDQPGRLKXVQCIGWYLDEKNLA QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWTRKNAMYFANYDPRMKFRGLHYVVIERDEKYM\AS FDEI\VP\EFICKMDEVLSSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFTVFTVI GSLFIMNLLTAIIYSQFRCYLMKSLGTSLFRRRLGTRAAFEVLS SMVGGGAFPQAVGVKPQDLAVGVLQTSLGTSLFRRRLGTRAAFEVLS SWVGEGGAPQAVGVKPQDLAVGVLQTSUJDSHKQAMMEVKRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLTALANLVSICVFLUIDADVLPAERDDFILGIINC CVFILYYYLLEMLLKVPALGLERGYLSYPSNVPGGLITVVLIVLISIS TL\CTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWGRREISNFEYLMFLNTIAGRTYNDLNQ YPVYPWULTNYESELDLTTLPONFRDLSKPIGALMPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKKILT				GPYHRGEAQRNIYRLLNTAFGLVHLTAHSSLVCPLSLGGSLGLR
MYHL\ADMLSFCGKKVUTAGAIIPPPLAPGQSLPDSLMQFGGAI PWTPLSACGEPSGTRCFAQSVULRGI DRACHTSQLTPGTTPPPSA LHACTTGEBILAQYLQQQQQFGWSSSHLLLTPCRVAPPYPHLFS SCSPPGMVLDGSPKGAAVESVPVFG 1258 1713 KKFQAPARETCVECQKTVYPMEELLANQQVFHISCFRCSYCINK KKFQAPARETCVECQKTVYPMEELLANQQVFHISCFRCSYCINK KIETEGFWERPRNFENQGRPLKSPGGEDCPSC*GGCTGSNY*AQ GSSSREKGGQASWNPKLRVA 122 443 RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAI EFSLEEWKCLNPAQRALYRAVWLENYRNLESVGLTSKDSWYMRK KPGRGRGKQRRQEWFFLRVY 5732 226 772 PPSRSCSPRRKSRRAHVTVTLVCGFTSFFSLPLYLCGCLRF PERTCSQLQADWAPDFGPSSFVPSWGATATGRKFLIAFNI\N LLGTKEQAHRIALNLEQGRGKDQPGRLKKVQGIGWYLDEKNIA QUSTNILDFEVTALHTVYETCREAQELSLPVVGSQLVGLVPLK ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSAFFKKFRLGGFEALKSAYM AQVQSMWTYRNAWFFANYPPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVILTPAYSKNRAYATFFTVFTTVI GSLPLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAPQAVGVKPONLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEFQKL FWELDRSVVKEHPPRPEYQSPPLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDDAVLPAERDDFILGILNC VFIVYYLLEMLLKVPALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL SMKPMAVVASTVLGL TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL SMKPMAVVASTVLGL LKILT 5735 2 540 FFTPCVARAFMPPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTLAGRTYNDLNQ YPVPFWULTNYESELDLUTLPONFRDLSKPIGALMPKRAVFYAB RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT		1		
PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTPGTPPPSALLHACTTGEBILAQYLQQQPGVWSSHLLLTPCRVAPPYPHLFS SCSPEGWLLDGSFKGAAVESVPVFG 1258 1713 KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK LSLGTYASLHGRIYCKPHFNQLFKSKGMYDEGFGHRPHKDLWAT KIETEGFWERPFRFENGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWNPKLRVA 5731 122 443 RSHRGELIPKDSCYMRKPPRRPFKRRQG/CALPQGCLTFKDVAI EFSLEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK KPGRGRGKQRRQEWFFLRVY 5732 226 772 PPSRSCQSPRRKSGRRRAHVTVTUVGFTSFSFSLPLYLCGCLFF PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGPEATKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\SFIGKMDEVLSRDPM 5734 3 968 RCNSPSLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFIMNLLTAIIYSGFRGYLMKSLGTSLFRRIGTRAAFEVLS SMVCEGGAPQAVGVKPQNLLQVLQKVQLDSSHKQAMEKVRSY GSVLLSAEEFQKLFNELDRSVVKBHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLBARDDFILGILNC VFIVYYLLEMLLKVFALGKYLSYSDNVFDOLLTVVLLVLUFLIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKRMAVVASTVLGL 5735 2 540 FPTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVPFWVLTNYESEBLDLTLPGWFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	·			
LHACTTGEEILAQYLQQQQFGVMSSSHLLLTPCRVAPPYPHLFS SCSPPGMVLDGSFKGAAVESVPVFG 1713 KKPQAPAREFCVEQGKTVYPMERLLANQQVFHISCFRCSYCNNK LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGRRPHKDLWAT KIETEGFWERPRNFENGGRFLKSFGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWNPKLRVA 5731 122 443 RSHRGELIEKDSCYMRKPPRRFKKRRQG/CALPQGCLTFKDVAI EFSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK KPGRGRKQRRQEWFFLRVY 5732 226 772 PPSRSCQSPRRKSRRRHVTVTLVCGFTSFSFSLPLYLCGCLRF PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANTDPRNKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFTVFTVI GSLFLMNLLTAIIYSGPRGVLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYGSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYISYPSNVFGGLLTVVLLVLBIS TL\CTDCTTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFRIIP SMKPMAVVASTVLGL 5735 2 540 FFTFCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFFYLMFINTIAGRTYNDLNQ YPVPFWULTNYESEELDLTLPGHFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	`			1 .
SCSPPGMVLDGSPKGAAVESVPVFG 1258 1713 KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT KIETEGFWERPRIPENGGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWMPKLRVA 122 443 RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAI EFSLEEWKCLNPAQRALVRAVMLENYRNLESVGLTSKDSWYMRK KPGRGRGKQRQEWFFLRVY 5732 226 772 PPSRSCQSPRRKSRRAHVTVTLVCGFTSFSLPLYLCGCLRF PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLIGTKEQAHRIALNLREGGRGKDQPGRLKKVQGTGWYLDEKNLA QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKRRLGSFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLISRDPM 5734 3 968 RCNSPSSLTSLLVLLTTANNLFVLIPAYSKNRAVAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQAVVKPDPLBSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDSVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGRLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLBIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTFCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFFYLMFLNTIAGRTYNDLNQ YPVFPWULTNYESEELDLTLPGNFRDLSKPIGALINPKRAVFYAE RYFTWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT			•	
1713 KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK LSLGTYASLHGRIYCKPHFNDLFKSKGNYVDEGFGHRPHKDLWAT KIETEGFWERPRNFENQGPLKFSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWMPKLRVA GSSSREKGGQASWMPKLRVA RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAT EFSLEEWKCLNPAQRALYRAVMLENYKNLESVGLTSKDSWYMKK KPGRGRGKQKDRQEMFFLRVY FSTSCQSPRRKSRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI \ N LLGTKEQAHRIALNREQGRGKDQDGRLKKVQGIGWYLDEKNILA QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA ALDAA ALDAA ALQVYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM FDEI\VP\EFIGKMDEVLSRDPM GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEBFQKLFNELDRSVVKEHPPRPBYQSFFLQSAQFLFG HYYFDYLLBMLLVSICVFLVLDADVLPABRDDFILGILNG VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIP SMKPMAVVASTVIGL SMPMAVVASTVIGL SAPPQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWULTNYESEELDLTLPGNFRDLSKFIGALNPKRAVFYAE RYFTYEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				
LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT KIETEGFWERPRNFENQGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWPKLRVA 773	E730	1250	1713	
KIETEGFWERPRNFENQGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWNPKLIRVA 122 443 RSHRGELIPKDSCYMRKPPRPKKRRQG/CALPQGCLTFKDVAI EFSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK KPGRGRGKQRRQEWFFLRVY 5732 226 772 PPSRSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLEF PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGFKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA QVSTNILDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYATFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEBFQKLFNELDRSVVKEHPPRPBYQSPFLQSAQFLFG HYYFDYLGNLTALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWM/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEBLDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	5/30	1256	1/13	
GSSSREKGGQASWNPKLRVA 122 443 RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAI EFSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMK KPGRGRGKQRRQEWFFLRVY 5732 226 772 PPSRSCQSPRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNLREQGRKDQPGRLKKVQEIGWYLDEKNLA QVSTNILDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA 5733 1 460 PALQEVMANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRGFFAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVT GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFÇKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWM/RLLSLWDMTRMLNMLIVFRFLRIIP SKKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEVLMFLNTLAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				<u>-</u>
S731 122 443 RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAI EFSLEEMKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK KPGRGRGKQRRQEWFFLRVY		·.		· · · · · · · · · · · · · · · · · · ·
EFSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK KPGRGRGKQRRQEWFFLRVY 5732 226 772 PPSRSCQSPRRKSRRAHTVTULVCGFTSFFSLPLYLCGCLRF PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFMI\N LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\ETIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLLALANLVSICVFLVLLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALSLRGYLSYPSNVPDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFFYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGNFFDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				<u> </u>
KPGRGRKQRRQEWFFLRVY 5732 226 772 PPSRSCQSPRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPPMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTLAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	5731	122	443	, ,
5732 226 772 PPSRSCQSPRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSGFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGIINC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGMFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				EFSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK
PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA QVSTNLLDFEVTALHTVYBETCREAQELSLPVVGSQLVGLVPLK ALLDAA 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAPPQAVGVKPQNLLQVLQKVQLDSSHKQAMKEVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	i			KPGRGRGKQRRQEWFFLRVY
PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA QVSTNLLDFEVTALHTVYBETCREAQELSLPVVGSQLVGLVPLK ALLDAA 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAPPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	5732	226	772	PPSRSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF
LIGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFTVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFFFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGMFRDLSKPIGALMPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N
QVSTNLLDFEVTALHTVYBETCREAQELSLPVVGSQLVGLVPLK ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLVLLTTANNLFVLIPAYSKNRAYATFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPBYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	ļ			LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA
ALLDAA 5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				
5733 1 460 PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVXEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				
MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY	5733	1	460	
AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT		-	200	-
FDEI\VP\EFIGKMDEVLSRDPM 5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				
5734 3 968 RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPBYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEBLDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				1
GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPBYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				
SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEBLDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	5734	3	968	
GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEBLDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	1			GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS
HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEBLDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	1			SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY
HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEBLDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	Ī			GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG
VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESEBLDLTLPGNFRDLSKPIGALNPKRAVFYAB RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	-			HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC
TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS
SMKPMAVVASTVLGL 5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	1	İ		\$ ·
5735 2 540 FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT				
ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	5735		540	
YPVFPWVLTNYESBELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWBDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT	ا دد،د	f	340	
RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT		1		
LKILT	j	İ		i
	ł			į.
5736 1 382 GTRPSTKKSGYSPOOVAVTHCKGHOKENTAVAHSNOKADSAAOV				
	5736	11	382	GTRPSTKKSGYSPQQVAVIHCKGHQKENTAVAHSNQKADSAAQV

Degianing coation cotation cotation cotation cotation cotation cotation cotation cotresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence cotation c			1	Amino acid segment containing signal peptide
No. location corresponding to first maino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of residue of amino acid residue of	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Corresponding to first amino acid amino acid residue of amino acid residue of amino acid amino acid sequence Peroline, Gedlutamine, Rahquinine, acid amino acid sequence Peroline, Gedlutamine, Rahquinine, acid amino acid sequence Peroline, Gedlutamine, Rahquinine, acid amino acid sequence Peroline, Gedlutamine, Rahquinine, acid amino acid sequence Peroline, Gedlutamine, Rahquinine, acid amino acid sequence Peroline, Gedlutamine, Rahquinine, acid amino acid sequence Peroline, Gedlutamine, Rahquinine, acid amino acid sequence Peroline, Gedlutamine, Rahquine, X-Unknown, *-Stop Codm, Apossible mucleotide insertion Peroline, Gedlutamine, Rahquinine, acid amino acid sequence Peroline, Gedlutamine, Rahquine, Acid Codm, Apossible mucleotide insertion Peroline, Gedlutamine, Rahquine, Codm, Apossible mucleotide insertion Peroline, Gedlutamine, Rahquine, Codm, Apossible mucleotide deletion, Apossible mucleotide insertion Peroline, Gedlutamine, Rahquine, Codm, Apossible mucleotide deletion, Apossible mucleotide deletion, Apossible mucleotide deletion, Apossible mucleotide deletion, Apossible mucleotide deletion, Apossible mucleotide deletion, Apossible, Gedlutamine, Rahquine, Peroline, Gedlutamine, Rahquine, Rahquine, Peroline, Gedlutamine, Rahquine,				Cluramic Acid F-Phenylalanine G-Glycine.
to first maino acid residue of amino acid residue of amino acid residue of amino acid sequence solvente per control of the con	NO:			u-uichidine I-Tsolencine K-Ivsine.
to first amino acid am				I-Lougine M-Methionine N-Asparagine.
amino acid residue of amino acid aequence 5737 290 1041 KARLSVYPPNILDYVSPPQDILDPBVYSTTERLASDLRARNS) QSS**HIDPSGIPTP**TSYLQSTHILRARALPQLLRR QSS**HIDPSGIPTP**TSYLQSTHILRARALPQLRRRN QSS**HIDPSGIPTP**TSYLQSTHILRARALPQLRRRN QSS**HIDPSGIPTP**TSYLQSTHILRARALPQLRRN QSS**HIDPSGIPTP**TSYLQSTHILRARALPQLRRN QSS**HIDPSGIPTP**TSYLQSTHILRARALPQLRRNS QSS**HIDPSGIPTP**TSYLQSTHILRARALPQLRRNS QSS**HIDPSGIPTP**TSYLQSTHILRARALPQLRRNS QSS**HIDPSGIPTP**TSYLQSTHILRARALPQLRRNS QSS**HIDPSGIPTP**TSYLQSTHILRARALPQLRRNS RADGEGGGGGDGDAHHPGPRSSSWRASGRALIPGLGGSHILDAYVG RDLEGGTPAPLQBIPTP*GRISARACHPGRRNS RDLEGGTPAPLQBIPTP*GRISARACHPGRRNS RDLEGGTPAPLQBIPTP*GRISARACHPGRRNS APSPINGGCGGGGGCGGCGCDAPPGGGGGGGGGTTT ATOPAAPLITYPSIPRGVGCT**PTAMTGREJFPGSTVERQLHFF FRILSERAMALCAVETR** 5739 1 1222 SFORRGIRMWYHTHEPBHRAWAGIGGGGGGGGTT ATOPAAPLITYPSIPRGVGCT**PTAMTGREJFPGSTVERQLHFF FRILSERAMALCAVETR** SARVOGVVGAVLSSGSITOTCLY**IFSGTTGLFKARAISHHKT LQCQGFYCLGGWIGBUTYLARACHPGAGGGGAGGGATT VUKSKFGAGGFBGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG			1	D-Decline, M-McChienter, M-Magazagana,
maino acid adjunca equence adjunca equence codom, "possible nuclectide deletion,		1 *		G Coming W-Whenchine V-Valine
anino acid sequence Codom, /=possible nucleotide dalection, -possible nucleotide insertion) 78XLSVTPPNLDPVSFOPDIDEDOMYVSTTTEKLADLEANEN 78XLSVTPPNLDPVSFOPDIDEDOMYVSTTTEKLADLEANEN 78XLSVTPPNLDPVSFOPDIDEDOMYVSTTTEKLADLEANEN 8				S=Serine, I=Intectine, v-varine,
Sequence				werryptopnan, responsible musloctide deletion
TARLES Y FOR ILL PONT STORT THE ASDIGNAMN 089** ILD DOSGIT PI 'T TSTIGSTIFERE THE ASDIGNAMN ORS'* ILD DOSGIT PI 'T TSTIGSTIFERE THE ASDIGNAMN ORS'* ILD COLLEGE AND THE ASDIGNAMN ORS' REAL PROSECTION OF THE ASDIGNAMN ORS' REAL PROSECTION OF THE ASDIGNAMN ORS' REAL PROSECTION OR STREET THE ASDIGNAMN ORS' RETREIT ORS' PROSECTION ORS' RETREIT ORS' PROVINCE PROBLEM OR THE ASDIGNAMN ORS' RETREIT ORS' PROGRAM ORS' RETREIT ORS' PROGRAM ORS' RETREIT ORS' PROGRAM ORS' RETREIT ORS' PROGRAM ORS' PROGRAM ORS' RETREIT ORS' PROGRAM O		1 .	sequence	Codon, /=possible indirection delection,
CREST LIPIDSGIFTP TTSTLQSTHILRRAKLPQLIER S737		sequence		/=possible nucleotide insertion/
S737 290 1041 KACLHLISSFLISHENELPIDISUSYURASGRANGGUERK				TARLSVIPPNLLPIVSPPQPDLPDNPVISITIERLASDLRANKN
LQTURRLAAGFQYSSIKND\$LISAKEKHTDYLNEARGFWIGHUSY RIADSCCROPPOGAHRIFORSSSSWARSEKLIPELGSSIRLDAYVY RDLEGGTTBALQLBIPPOGROFIPASTALTAGASHINDYG RDLEGGTBALQLBIPPOGROFIPASTALTAGASHESYSACGIN APSPTSQCCEGRCDAYPEHRANRITLCSQ PETERPLOGREF SELLENGTURPHICPURPSFY-LSC-PFOLARAKSIPPKTYSNEY VTLWYRPPDILLAGSTDYSTQIDMW-QQUEVAQGPCGKGGGLVTT ATQBAARLFYTPUSPHENGVCLTFWARGFPGTAKGGGLVTT ATQBAARLFYTPUSPHENGVCLTFWARGFPGTAKGGGLVTT ATQBAARLFYTPUSPHENGVCLTFWARGFPGTAGASTALTAGASTAGAS				QES**ILPDSGIFIP*T*TSYLQSTTHERRARDPQLERR
RTADGSCGROPGOAHHROPKSSWRASRLIPEGGSHILDATVE RDLEGGTPAPLUGIB PPOPRIGHDAYDTAPROAWEDSVBAGGKP RDLEGGTPAPLUGIB PPOPRIGHDAYDTAPROAWEDSVBAGGKP APSPTSQGCCGROCADYPHABARTHETLCSQ 5738 8 460 PTISTINGTUSETT PRTSSFTLSFLF PFGLARKS IPTKTYSMEN TATQBARLIPTYPSDJERGVGCTFYEMATGRPLFPGSTVEEQLHFI RTLSEBAWALCAVETIR FRILSEBAWALCAVETIR 5739 1 1222 SFORRGIRWKVITLHERPRAWAGIGRGEGSTALLIGENARGHL FPTILLEFLESLEPDLPALRAWGHLWAAGPGTHPAGISDLALEV SARVDGPVPGYLSSSGSITTCTLY IPTSGTTCLFYRAARISHHXI LQCQGFYQLGGVIGGBUY TLAIPLHIMGGGLIGTVAGGWIGTAVY VLKSKEBAQPWBDCQQHRVTVFQYIGGLCRIVWGPSIGAKER HKWALAVGGGLRPDTWRRFVRRFGLQVLBTTGLTEGNVATINT TQCRGAVGRASWIKHTFFFSLIRTVTTCFEIR FDEGGICWATS PGEGGLLVAPVSQOSPFLAYAGGPELAGGKLIKDVFRPGUSVTY TQCRGAVGRASWIKHTFFFSLIRTVTTCFEIR FDEGGICWATS PGEGGLLVAPVSQOSPFLAYAGGPELAGGKLIKDVFRPGUSVTY TQCRGAVGRASWIKHTFFFSLIRTVTTCFEIR FDEGGICWATS PGEGGLLVAPVSQOSPFLAYAGGPELAGGKLIKDVFRPGUSVTY TQCRGAVGRASWIKHTFFFSLIRTVTTCFEIR FDEGGICWATS PGEGGLLVAPVSQOSPFLAYAGGPELAGGKLIKDVFRPGUSVTY TQCRGAVGRASWIKHTFFFSLIRTVTTCFEIR FDEGGICWATS PGEGGLLVAPVSQOSPFLAYAGGPELAGGKLIKDVFRPGUSVTY TQCRGAVGRASWIKHTFFFSLIRTVTTCFEIR FDEGGICWATS PGEGGLLVAPVSQOSPFLAYAGGPELAGGKLIKDVFRPGUSVTA TQCRGAVGRASWIKHTFFSLIRTVTTGVTTGFEIR FDEGGICWATS PGEGGLLVAPVSQOSPFLAYAGGPELAGGKLIKDVFRPGUSVTA TQCRGAVGRASWIKHTFFSLIRTVTTGVTTGTFLAWAVATSVENDED LQEWNVYGUTV 5741 1 650 PRETMRRGUMTLLQGSMTLPEHGKREURSPPLOGALDAGG TYVRILTVRAVAVANDGEGWITLAVVSYSHATNKYRVDDEDE BEKERHTLGRREVIDLOGAWTLDEWNSCHAFDELGKEQULVALLYG TCYPPALHHAP PGDRCADAYSTYDFPDEALFGKEQULVALLYG TCYPPALHHAP PGDRCADAYSTYDFPDEALFGKEQULVALLYG TCYPPALHAPADFRONGOSTGGRACIKHI PPLKK TALVMAVERGNATMVRDILGCGNPTSICTXG VCKEPKKK*CCLADGRSRNDTGODSGGRACIKHI PPLKK TALVMAVERGNATMVRDILGCGNPTSICTXG TALVMAVERGNATMVRDILGCGNPTSICTXG TALVMAVERGNATMVRDILGCGNPTSICTXG TALVMAVERGNATMVRDILGCGNPTSICTXG TALVMAVERGNATMVRDILGCGNPTSICTXG TALVMAVERGNATMVRDILGCGNPTSICTXG TALVMAVERGNATMVRDILGCGNPTSICTXG TALVMAVERGNATMVRDILGCGNPTSICTXG TALVMAVERGNATMVRDILGCGNPTSICTXG TALVMAVERGNATMVRDILGCGNPTSICTXG TALVMAVERGNATMVRDILGCGNPTSICTXG TALVMAVERGNATMVRDILGCGNPTSICTXG TALVMAVERGNATMVRDILGCGNPTSICTXG T	5737	290	1041	KACLHLLSSFLTSNFLFNPLLPDSLYSVEARSQRANLGPCRRRR
RDLECGTPALALGLETPOPRGHPATITIOGAGPROSGGAGPW ETRPLIDGRE PGLARWAGTATHAGAGNETURESQ \$7338 8 460 DELINCTUBERLETPOPSFALESCE PFOLARAKSI PPKTYSNEV VTLNYRPPDILLGSTDYSTOIDM**GQVEVWQGPCGKGGGLVTT ATQPAAFLITVESLPROVOCITYEMATGRPLPGGSTVERGUTT ATQPAAFLITVESLPROVOCITYEMATGRPLPGGSTVERGUTT ETRILSSEAMALGAVSTER \$739 1 1222 SFORRSIEMIVETHEPPRAVWAGIGGGGS*ALLGRARAPALC FPTLEEFLESLEEDLPALEAWGLHUMAAGPGTHRAGISDLLAEV SAEVDGPVPGYLSSSOSITDTCLYITTSGTTGLFRAARISHLA LQCQGFYQLGGVUGDVITLALPYHMSGGLLGITYGGMIGATY VLKSKFSAGOFWEDCQGHRYTVFQYIGSLCRYLVWQPFSKAERG KKVKLAVGSGLRFDWBRFVVRRFDQVLSTTGLFRAARISHLA LQCQGFYQLGGVUGDVYLTPGYTGSLCRYLVWQPFSKAERG KKVKLAVGSGLRFDWBRFVVRRFDQVLSTTGHTGRAARISHLA LQCQGFYQLGGVUGDVYLTPGYTGSLCRYLVWQPFSKAERG KKVKLAVGSGLRFDWBRFVVRRFDQVLSTTGHTGRAARISHLA LQCSGLAVAYSGTV PGRGLAVARSOOSPELGAGGLLAVGHADCHATG PGRGLAVGRASMLYKHIFPFSLIRTDVTTGEFRRFQGHCMATS PGREGGLAVAPVSOOSPELGAGGLLAVGHADCHATGHTGHTGHTGHTGHTGHTGHTGHTGHTGHTGHTGHTGHT				LQTLMRLAAGFQYSSHKDPSLSAKEKHTDYHNEARGPWPGWVG*
BTRELTDORR POWRYPGMYTANHASTLEPRGAVESYSACGKW APSPTSQGCCEGRCADYPHRAMSTRICSQ 5738 8 460 DTLSINGTLDETLEMTSSFLISTL PFOLARAKSIPTKYTSGN TWENPPDILLAGTOWSGTOWN GOVEWOGGPCKSGGLUTT ATQPAARLPTYPSLERGVGCTFYEMATGRELPFGSTVERGLHFI FILLSEBAMALLOWSTER 5739 1 1222 SFQRRGIRWRYHTLHEPERAWAGIGGHGHGS ALIGRARABAI FPILLESEBAMALCHARAGPOTHPGISDLALEV FPILLESLESDLEPLARAMGILHARAGPOTHPGISDLALEV FPILLESLESDLEPLARAMGILHARAGPOTHPGISDLALEV SARVDEPVPGVISSKSQGITTCTLYIFTSGTTGLPKAARISHIKAI LQCGGFYGLGGVHGEDVIYITALPLHMMGGLLGIVGCMGIGATY VLKSKYSAQPWEDCQGHEVTVFQYTGGLCRILWRPSFSKAERG HKWRLAVSGGLREPTWSRFVRRFGLQVHSTTGLTEGNVATINT TGQRGAVGRASHLKKHIFFSELIRTVTTGETREOGNATINT TGQRGAVGRASHLKKHIFFSELIRTVTTGETREOGNATINT TGQRGAVGRASHLKKHIFFSELIRTVTTGETREOGNATINT TGQRGAVGRASHLKKHIFFSELIRTVTTGETREOGNATING TGRALVCDGGGFLARGFHRATGOPFRKGEDVHSTGLTGLAGAVAR LQSELKKLYDESTGAVGGELAGGKLKKDVFRPGDUFF TRULLVCDGGGFLARGFHRATGOPFRKGENATEVARVEVEALDS LQEWNVYGUTV STA40 255 231 PAYMLKVFTLGLSKRTDLREKASHVSAQLQGEVRGLAGALMM*A VYVERVY*N NISHMVHALGKRHEPAGLSSSMALQLNFCLGMIMM*A LQSELKKLYDESTGAWSGGAGGTP 5741 1 650 PREMMERGUMTLLQGSAWTLFLWIGKRGDFPPLGGALMAN LQSELKKLYDESTGAWSGGAGGTP 5742 2 362 TQSVKBILKRNPNVALDGOGGTHALBVVSYSHATKVKEVDDIDG RGKERHITLSRREVIDLOGNKANPETDPEALFOKEQUILALVYON ACKEPKKK*CLALDSSFRUDTGODSIGRAGIKHIPPLKK* 5742 2 362 TQSVKBILKRNPNVALDGOGGTHALBVVSYSHATKVKEVDDIDG RGKERHTLSRREVIDLOGNKANPETDPEALFOKEQUILALVYON ACKEPKKK*CLALDSSFRUDTGODSIGRAGIKHIPPLKK* 5743 2 415 GKTPGGIGHTSTATGRGSSTREKTREVIDLADGT TYVNIPRGGOTVLLGANKANPETDICALGKYADDIDLAGG TYVNIPRGGGTVLLGANKANPETSICQUEVXPLGRMQTDL KATCRETSSFRKYPEVIDATELIKQLESTGENEVEXPLGRMQTDL KATCRETSSFRKYPEVIDATELIKQLESTGENETSVENDEGENETTEL SPQB 5744 3 703 TRETTTTSPITTRQMITTPAALPTTVTTPELTTGTPLQMITIA SPGBERDLATTULTSSKSKWULDSTSHVWKTSDSVS PQCGASDTAVEGNKTKTGONGGIPMSKKEMPISQLIMITAP SGRVPULKKINGSKKYNDESTGNAKSHVKNIDSDVS PQCGASDTAVEGNKTKTGONGGIPMSKKEMPISQUSSVS SGRSTANTAKSKCKENDILAVKSIG OKKTETVIVSTE KKREKTSSGRINGKKKYNDESTGNAKSTONLINDV VENNLPOMPADRALLGRAKSSGGMOATATGGARSSGANALDV VENNLPOMPADRALLGRAKSSGGMOATATGGARSSGANALDV VENNLPOMPADRALLGRAKSSGGMOATATGGARSSGANALGTUNGLUNG				RTADGSCGRGPDGAHHPGPKSSSWRASRLLPGLGGSHALDAYVG
S738 8 460 DILGINCTIPE PROPERTY SELF LY FIGHARMS IPTKTYSNEY				RDLECGTPAPLQLEIPPQPRGHPAPIPTGQAGPRDSGPGASP*V
S738 B 460 DT.SINCTLPETLPWTSF-LSFL-FEGLARAKSITETYTYNEV VILWYRPPDILLASTDYSTOLDWH-GQUEWOGGCKGGGUTT ATQRAPIFTYPSLPREWGCIFYEMATGRPLFPGSTVEEQLHFI TRILSEEAWALCAVETER SFORRGIRWNHTLEPHPRAVWAGIGRGHGS*ALLGRARAPALC FPTLLEFLESILEPHDEALRAMGLHUMAAOPGTHHAGISULLAEV SAEWDGPVPG/LSSVGSITUTCLYIFTSGTTELPKARRISHIKAI LQCGGFVQLGCUNGBBUYLADLINGPFSKAERG LQCGGFVQLGCUNGBBUYLADLINGPFSKAERG HKWILAVGSGLRPDTWEEFVRRFGFLQCKLIKNOVPFSKAERG HKWILAVGSGLRPDTWEEFVRRFGFLQCKLIKNOVPFSKAERG HKWILAVGSGLRPDTWEEFVRRFGFLQCKLIKNOVPFSKAERG HKWILAVGSGLRPDTWEEFVRRFGFLQCKLIKNOVPFSKAERG HKWILAVGSGLRPDTWEEFVRRFGFLQCKLIKNOVPFSKAERG HKWILAVGSGLRPDTWEEFVRRFGFLQCKLIKNOVPFSKAERG HKWILAVGSGLRPDTWEEFVRRFGFLQCKLIKNOVPFRGDUFFN TRDLLVCDQGFLRFFURTGOFFRKKEERVATTEVARVFEALDF LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU TRDLLVCDQGFLRFFURTGOFFRKKEERVATTEVARVFEALDF LQENNUVGUTU LQENNUGGUTU LQENNUVGUTU LQENNUVGUTU LQENNUGGUTU LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU LQENNUGGUTU LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU LQENNUVGUTU LQENNUGGUTU LQENNUGGUTU LQENNUVGUTU LQENNUVGUTU LQENNUGGU	<u> </u>			
VTIMYRPPILIGISTDYSTGIDMM*GQVEYMGGPCKGGGUTT ATOPAAPLFTYPEDERWGGLTFYEATGREGLHFT FRILSEEAMALCAVETHE 5739 1 1222 SFORRGINWINTHLIPPHARAWAGIGRGHGS*ALLGEARAPALC FPILESPESLEPDLPALRAMGLHURAAGPGTHRAGISDLLAEV SAEVDDPVPGYLSSPQSITDTCLYIFISGTTGLEKARAISHLX LQCGFYQLCUVIGBUYIYLAPLIPHSMSGLIGUVGMGIGATV VLKSKFSAGOPWEDCQORRYTVPQYIGELCKYLVNOPPSKAERG HKWRLAVSGLRPTMERFYRRFGPLQVLETTGLIFGANTATINY GQRGAVGRASHLYKHIFPSSLIRTDYTTGFFIGLFGANTATINY GQRGAVGRASHLYKHIFPSSLIRTDYTTGFFIGLFGANTATINY TQCRGAVGRASHLYKHIFPSSLIRTDYTTGFFIGLFGANTATINY TQCRGAVGRASHLYKHIFPSSLIRTDYTTGFFIGLFGANTATINY TQCRGAVGRASHLYKHIFPSSLIRTDYTTGFFIGLFGANTATINY TQCRGAVGRASHLYKHIFPSSLIRTDYTTGFFIGLFGANTATINY TQCRGAVGRASHLYKHIFPSSLIRTDYTTGFFIGLFGANTATINY TQCRGAVGRASHLYKHIFPSSLIRTDYTGFFIGLFGANTATINY TQCRGAVGRASHLYKHIFPSSLIRTDYTGFFIGLFGANTATINY TQCRGAVGRASHLYKHIFPSSLIRTDYTGFFIGLFGANTATINY TQCRGAVGRASHLYKHIFPSSLIRTDYTGFFIGLFGANTATINY TQCRGAVGRASHLYKHIFPSSLIRTDYTGFIGLFGANTATINY TQCRGAVGRASHLYKHIFPSSLIRTDYTGFIGLFGANTATINY TQCRGAVGRASHLYKHIFPSSLIRTDYTGFIGLFGANTATINY TQCRGAVGRASHLYKHIFPSSLIRTDYTGFIGLFGANTATINY TQCRGAVGRASHLYKHIFPSSLIRTDYTTTGFIGLFGANTATINY TCFYRALIHAPPGAPQDQDYSTLPETTYSAGCPHAVAQFILV ACKEPKKK CCLADSPSPHDTQQDSGRGAGIKHIPPLKKK TCFYRALIHAPPGAPQDQDYSTLPETTYSAGCFILDAGAVITATION TGCFYRALIHAPPGAPQDQDYSTLPETTYSAGCFILDAGAVITATION TGCFYRALIHAPGAPQADGATTINTOKGGNTALMIASKEGGTETUQDLDGAG TTWIPDRAGGTYLLIGAVGGNETURATINGTATION TALWAVEKGNATWADILQCONPOTELTTICG STATUSIPPRSGTYLLIGAVGGGSSREKTREVIDAASVITATIOLEGGNNX TALWAVEKGNATWADILQCONPOTELTTICG VEYDDEMETDLATTTGPGTSGARGIKHIPPLAGTATIOLEGGNNX TALWAVEKGNATWADILQCONPOTELTTAGG VEYDDEMETDLATTTSGTLFFERRISPGCARGICTHYBGGNATHAGA TVATIPPTTTTROMTTTPALPTTVTTPLTTTTQMTTTTTLTTLQMTTT STATUSTTTSGTTTTSGTTLTTSGNSSS PQCGASDTALVERSYNGGATHAGATATION TGCRGADDGLIFTL SGRGWATHAGATATATATATATATATATATATATATATATATATA				APSPTSQGCCEGRCDAVPKHRAWRTPLCSQ
S739 1 1222 SFOREGIERMYHTIMPERAVAGIGRGUGS FALIGRARAPAC	5738	8	460	DTLSLNCTLPETLPMTPSF*LSFL*FPGLARAKSIPTKTYSNEV
1 1222 SFORRGIERWINTEHPIPRAWAGIGRGHGS*ALLGRARAPALC SFORRGIERWINTEHPIPRAWAGIGRGHGS*ALLGRARAPALC SFORRGIERWINTEHPIPRAWAGIGRGHGS*ALLGRARAPALC PPTLLEFLESLEPDLFALRAWGLHKAAQPGTHPAGISLLAW SAEVDGPVRGUSSPQSITDTCLYIFTSGTTGLPKAARISHLKI LQCGFYGLGVHGBDYTVLALLFIHMSGSILGIVGCWGIGATV VLKSKFSAQGWEDCQHRVTVRQYIGBLGXTIVMPSFARER HKWILAVASGIRPDTWERFVRRFOFLQVHETYGLFIGGRVAATINY TGGRGAVGRASHLYKHIFFFSLIRYDVTGEPIRDFQGHCMATS PGEFGLLVAPVSQGSFILGYAGGFELGGKLKDVFRCPQDFFR TRDLLVCDDQGFLRFHDRTGDPFRWKGENVATTEVABVPFALDD LQENNYUGVTV 5740 265 231 PAYWKUPTLCLESKTDLREKASHVSAQLQGBVRGLAGALMW*A VYVERVYN NISRWHALDQKRHFAGLSSSMALQLMPCLGMLMA LQSELHKLYDBETGSWVSGACGGYP TRYBREGGVARAVKANVDGEORMILABVVSYSHATNKYEVDDIDE GGKERHTLSRRRVIPLDGOKANPETDEALFÇKSQLULALIYPQT TCPYRALIHAPPQRQDDDYSVLFBDTSVAGSPPINVAQRVV ACKBYKKK*CRLADSPSPNDTGDDSGGRAGIKHIPPKKK 5742 2 362 TQSVKEILKRNPNVLTDKDGNTALMIASKGHYDLUALIYPQT TCPYRALIHAPPQRQDDDYSVLFBDTSVAGSPPINVAQRVV ACKBYKKK*CRLADSPSPNDTGDDSGGRAGIKHIPPKKK 5743 2 415 GKTPSGIDAIBEIEDLEFERSISPGEMGEEVKPLGBMYDDL KATGREISPRETTSPVIDATEGIKALLGKYADIDIRGGDNN TALWAVERGNATWURDILQCNPDTEICTKOG VRYDENETDLKTTGREGSSRFKTREVIDATEGISEPENGEE VRYDDEMETDLKTTGREGSSRFKTREVIDATEGISEPENGEE VRYDDEMETDLKTTGREGSSRFKTREVIDATEGISEPENGET ISPQS 5744 3 703 TRRTTTTSPTTRQMTTTPAALPTTVVTTPDLTTGTPLOMTTLA VPTTANTCLSITPSTIPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLITSKESVEWDLPSTSTSVARISTSDVSS PQPGASDTAVPSQNKTTKNGGMCDITMSKKNEMPISQLLMILDA VPTTANTCLSITPSTIPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLITSKESVEWDLPSTSTSVARISTSDVSS PQPGASDTAVPSQNKTTKNGGMCDITMSKKNEMPISQLKNILDA VPTTANTCLSITPSTIPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLITSKESVEWDLPSTSTORTPRSCNIFOT VENRLPQWLPAHDSRLILAGKKMETYCSQCHTRLDYLGDSKRVLMDV ORGREDEDGLFTL GKSPETENSKERKSKKSCRVVSKEERKETKKKEGQGRTEERMLMOQSI LGF EKSEERESKKKKKSCRDVSKEERKETKKKEGQGRTEERMLMOQSI LGF STAGGRTPFCPVCCKRFFRENSILAHLIKTHOPERPRSPAARLLLE LEERALLERALLGRARSSGGMQATPATEGGARAPGSSAFRCP YCKGKFFTSABRERHLHILHRPMKCGLCSFGSSGBEELLHHSLT ANGABERFPLAATSAAPPCOCPQPPPPGPERSVPQPEPPPRE EATPTPAPAADAEEPPPAPPERCQVCGCSFTGSWFLKGHRKKKKA PARGBERFPLAATSAAPPCOCPQPPPPDENSVPQPEP				VTLWYRPPDILLGSTDYSTQIDMW*GQVEVWQGPCGKGGGLVTT
1 1222 SFORRGIRRIVITILHEPRAWAGIGRENGS*ALLGRARAPACE PPITLEPLESLEPDLPALRAWGHLUANGCHIGHAGES SAEVDSPYDGVLSSPQSITOTCLYIPTSGTTGLPKAARISHIKI LQCQGYQLCQVHQBDVIYLALPLYHMSGSLGIVGGYGAV VLKKKYSAQGWEDCQUHRVIVPRYIGGLEKYLVNQPPSKAERG HKWALAVGSGURPDTWERVAVROPLQVLETYGLTEGHTROWATINY TQORGAVGRASHIKKHIPFSLIRTDVTTGPFIRDFOGHCMATS PGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVRRPGDVFFM TRDLLVCDDQGFLRPHDRTGDPFRWKGENVATTEVABVPFBLDF LQEWNYYGVTV 5740 265 231 PAWALKUPTLCLESKTDLREKASHVSAQLQGEVRGLAGALMM*A VYVERVYN NI SRNVHALBQKRHPAGLSSSNALQLAPFCLGMLMA LQSELHKLVDEETGSWYSGSACGGYP FYRTMRRGVHNTLLQGSANTLDLHINGKFDKRPPPLCGA PASGO YVARPGDKVAARVKANDGDGWILLAEVVSYSHATNYKYDDDIDE BGKRRTHLSRRVIPLDQWKANPBTDBELFKGKDLVLALPPQT TCPYRALIHAPPQRPQDDTSVLFEDTSYADGYSPPLWAQRYVV ACKEPKKK CRLADSSSPNDTGQDSKGRAGIKHIPPLKKK 5742 2 362 TOSVKEILKRNNVNLTDBCGNTALHIASKGHTETVQDLDGA TYWIPPRSGDTVLIGAVRGGHVSIVRALLQKYADIDIRGQDNX TALWAAVEKKANTWPDLICOMPTSILTOKEGOLVLALPPQT TCYSHAGIKKANTWPDLICOMPTSILTOKEGULVLALPQT TYSHIPPRSGDTVLIGAVRGGHVSIVRALLQKYADIDIRGQDNX TALWAAVEKKANTWPDLICOMPTSILTOKEGULVLALPQT TYSHIPPRSGDTVLIGAVRGGHVSIVRALLQKYADIDIRGQDNX TALWAAVEKKANTWPDLICOMPTSILTOKEGULVLALPQT TYSHIPPRSGDTVLIGAVRGGHVSIVRALLQKYADIDIRGQDNX TALWAAVEKKANTWPDLICOMPTSILTOKEGULVLALPQT TYSHIPPRSGDTVLIGAVRGGHVSIVRALLQKYADIDIRGQDNX TALWAAVEKKANTWPDLICOMPTSILTOKEGULVALPQT TYSHIPPRSGDTVLIGAVRGGHVSIVRALLQKYADIDIRGQDNX TALWAAVEKKANTWPTULCOMPTSILTOKEGULVALPQT TYSHIPPRSGDTVLIGAVRGGHVSIVRALLQKYADIDIRGQDNX TALWAAVEKSANTULCOMPTSILTOKEGULVALPQT TYSHIPPRSGDTVLIGAVRGGHVSIVRALLQKYADIDIRGDKNX TALWAAVEKSANTULCOMPTSILTOKEGULVALPQT TYSHIPPRSGDTLANGTHATATULCOMPTSILTOKEGULVALPGT TYSHIPPRSGDTVLIGAVRGGHVSIVRALLQKATTULDILGGSNAVLNDV VRTTANTCISLIPPSTLEERATGLLTEPSKECPILTAESETVLP SDSWSSASSTSADTVLILISKESKWUDLEPSKSWMXTSSDVLJAND VRTTANTCISLIPPSTLERKKKTYDSPQBELEDVIKVALPGTVLMANGTSULMILIAD SLIGVULPALFVULYALFSTNOSTSTTGASTNOMMTSTNOSTNOMMTSTOKANTSUNGMYSTSTOKANTSUNGMYSTOKSTNOSTNOSTNOSTNOSTNOSTNOSTNOSTNOSTNOSTNO	{			ATQPAAFLFTVPSLPRGVGCIFYEMATGRPLFPGSTVEEQLHFI
PPTILIEPLESLEPDLPARRANGHLIMAAGPGTIPPAGRARISHLIKS SAEVDGPVGVLSGPKGTDTCLYFITSGLPKARRISHLIKS LQCQGFVQLCQVHQBVTYLALPLYIMAGGSLIGIVCKAGTGATV VLKSKFSAQQFWGDCQQHRVTVFQYIGBLCRYIJVMQPPSKAERG HKVRLAVGSGURPDTWERVPRRGFLQVLETYGLTEGRVATINY TQGRGAVGRASMLYKHIFPFSLIRIPVTTGEPIRDFQGHCWAITS PGEGGLLVAPVSQQSFILGYAGGFLAGGKLIKUVFRPGDVFRN TRDLLVCDQGFLEPHDRTGDPFRWKGERVATTEVABVFEALDP LQEWNVYGTV 5740 255 231 PAYNLKVPTLCLESKTDLERKSHVSAQDQGEVKGLIAGALWM*A VVYYERVYN*NISRWHALDCKHPAGLSSSMALQLMPCLGMLMA LQSSLHKLYDEBTQSWVGGSACGGYP 9RKTMRRGVLMTLLQGSAMTLPIMIGKPGDRPPPLCGAAIPASGD VARPGDKVARVARVKANDGDEGWILABVVSYSHATNKYRVDDIDE BGKERHTLSRRRVIPLDQWKANPETDPEALPQKSQLVALALYPQT TCPYRALIHAPPQRPQDDVSVLFBTGTSKAGFTEVSPLIVANQRVVV ACKEPKKK*CRLADSPSPNDTSQDSKGRAGIKHIPPLKKK 5742 2 362 TQSVKETLKRNINVALTBGGRATALMTAGSPTLUALYPQT TCPYRALIHAPPQRPQDDVSVLFBTGTSKGGLEVKPLOGADKY ACKEPKKK*CRLADSPSPNDTSQDSKGRAGIKHIPPLKKK TGPSWETLKRNINVALTBGGRATALMTAGSTETLEVKKY ACKEPKKK*CRLADSPSPNDTSQDSKGRAGIKHIPPLKKK TGPSWETLKRNINVALTBGGRATALMTAGNTEVTLALYPGT STA43 2 415 GKTPSGTJDAIESITGDLETTERETSQDERGTEVFLOGADK KATGRETSPRETTPSVLDATEGLIKDLEETGRREISPERMEPQE VKPUDEMETDLLKTTGRGSSEKFKREVIDALTSGTEGLEVKPLGEMQTDL KATGRETSPRETTPSVLDATEGLIKDLEETGRREISPERMEPGE VKPUDEMETDLLKTTGRGSSFRKTREVIDALTSGTEGLEVKPLGEMQTDL KATGRETSPRETTPSVLDATEGLIKDLEETGRREISPERMEPGE VSPDTEMETDLLKTTGRGSSFRKTREVIDALTSGTEGLEVKPLGEMQTDL KATGRETSPRETTPSVLDATEGLIKDLEETGRREISPERMEPGES USPQG STATTTSPTTTROMTTTPAALPTTVVTTPDLTTGTFLOMTTIA VFTTANTCLSLTPSTLPEBATGLLTPPSKEGPLITAGSSTVLD GREEDBOGLFTL GKSRTVALMKHSKKTVDSPQDELEDYTKVQKARGLEPKTCFKKM KGDVLETCGVKGEVKSRFYTKMFGQMSTFMKTSGSVS SPGAGSSTAVPBQMNTTKTGGMCSI FMSKKEMPISQLLMI ILAP SLGSVLPALFVLPLLRCKKMETYCSQKHTRLDYTGRFKCHPBEGR RKSBERSKHKKKSRDDVVSKEGERKTKKKEGQGRTTSEEMLMOQSI LGF 5745 1400 559 GKSRTVALMHSKKTYDSPQDELEDYTKVQKARGLEPKTCFKW KGDVLETCGVKGEVKSRFYTKMFGGNALMTROMTYPSSCALLE LERALLREARLGRARSSGGMQATPATEGLARPOAPSSAFRCP VCKKKFRTSABGRENLHILLTRPMKCGLCSGSSQBEGLLHBLT ALGABERFLAARSASPGOGLOPGOPPOPPRSVAPOPEPPPPR EATPTPAPAADEBEPPAPPEFRCQVCGCSFTGSEMLMOGLSFTGSAGRELLHISLT ALGABERFLAARSASPGOGLOPTGGCSGRYEEPHGE EATPTPAPA	. ·		ļ	
FPTILEFILESLEPDLPARAMGEHLMAAGGGTTIPAGIBLLABY SAEVDGPVGVLSSPGSTIDTCLY FITSTGLPKAARISHLKI LQCGFVQLCGVHQBDVQYLALPLYHMSGSLLGIVCKGMIGATY VLKSKFSAQFWEDCQGHPVTVFQYIGELGXYLVNQPPSKAEKG HKWRLAVGSGLRPDTWERFVRFGPLQVLETYGLTEGNVATINY TGGRGAVGRASMLYKHIFFSLRTDVTTGEF IRDPGHCMAITS PGEGGLUVAPVSQOSFILGYAGGFLAGGKLLKOVFREGDVFRN TROLLVCDDQGFLEFHDRTGDFFRWGERVATTEVARVFEALDF LQEWNVYGTV 5740 255 231 PAYMLKVPTLCLESKTDLREKSSHVSAQLQGEVKGLAGALWHYA VYYERVAN NI SRWHALBCKRHPAGLSSMALQLWFCLGMMA LQSELHKLYDEETQSWVSGSACGGYP FRKTMRRGVLARLLQGSAMTLFLHIGKFGDFFPPLCGALMAWA LQSELHKLYDEETQSWVSGSACGGYP 5741 1 650 PRKTMRRGVLARLLQGSAMTLFLHIGKFGDRFPPLCGALMAWA LQSELHKLYDEETQSWVSGSACGGYP FRKTMRRGVLARLLQGSAMTLFLHIGKFGDRFPPLCGALMAWA LQSELHKLYDEETQSWVSGSACGGYP TCFYRALIHAPPQRQPQDDYSVLFBDTSXADQSSPFLNVAQRVVV ACKEPKKK-CRLADSSPRDTGQDSRGRAGIKHTPFLKKK TCFYRALIHAPPQRQPQDDYSVLFBDTSXADQSSPFLNVAQRVVV ACKEPKKK-CRLADSSPRDTGQDSRGRAGIKHTPFLKKK TGFYRALIHAPPQRQPQDDYSVLFBDTSXADQSSPFLNVAQRVVV ACKEPKKK-CRLADSSPRDTGQDSRGRAGIKHTPFLKKK TGFYNALIHAPPQRQPQDDYSVLFBDTSXADQSSPFLNVAQRVVV ACKEPKKK-CRLADSSPSPDTGQDSRGRAGIKHTPLYKK TALWAVERGNATWARDILQCNPDTEICTXOG 6TPSGTGJABFERTETDVIDATEELIKDLEETGRREISPERMGPEG VKPYDEMETDLLKTTGRGSSRKKTREVIDATEELIKDLEETGREISPERMGPEG VKPYDEMETDLLKTTGRGSSRKKTREVIDATEELIKDLEETGREISPERMGPEG VKPYDEMETDLLKTTGRGSSRKKTREVIDATEGTLCMTTIA SIGSVLFALFVLFALLGKKLMETYCSQKHTRLDYTGFFLCMTTIA STATTTSPTTTROPTTTROMTTTPAALPTTVVTTPDLTTGTFLCMTTIA SIGSVLFALFVLFALLGKKLMETYCSQKHTRLDYTGFSLVSS POPGASDTAVPEQNKTTKKGGMCDIFSMKMEMPISQUSMITAD QHREEDBOLGFTL GKSRFVALMHSKKTYDSPQDELEDYIKVQKARGLEPKTCFKM KGDVLEFTCGVKGEVNSFYTKFFGQMLSFSTQTFTRCFTFNFCNIFOT VENRLPQMLPAHDSRLELDSLSYCOPTROCTSEKPVLINNOQE YICGSRGVEHLWYKHFSDNSTSTHQSKRVLFBEGR RKSEERSKHKKKSGDDVSKKEERKETKKKEGGGRTEEEMLMDQSI LGF 5746 3 821 SFASGRITSSPATGGGLDLQRYSNGFAVSAMSLGMGAVSMSES LGF VKGKKFTSABRERHLHILHRPMKGLGCSSGSBEELHHSLT ANGABERFLAATSAAPPOQFQQPPPQDPEPRSPARALLLE LEBRALLREARLGRARSSGGMQATPATEGGLARPOAPSSAFRCP VKGKKFTSABRERHLHILHRPMKGLGCSSGSBEELHHSLT ANGABERFLAATSAAPPOQFQQPPPQDPEPRSVPQPEPPPR EATTPTAPAAPAEBEPPAPPEFRCQVCGSFTGSWFLKHRIKA STDHACOV D	5739	1	1222	SFQRRGIRWNVHTLHPHPRAVWAGIGRGHGS*ALLGRARAPALC
LQCGGFYQL.CGMGEDUTYLALPLYHMGGELLGTYCMGTGATY VIKKKFSAGOPMEDCQHRYTYGYI IGBCRTIVNOPP SKAEKG HKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINY TGQRGAVGRASMLYKHIFPFSLIRTDVTTGEP IRPQGHCMAT; PGBFGGLLVAPVGQGEP JEVGAGGFELAGKLLKDVFRGDVFRN TRDLLVCDDQGFLRFHDRTGDFFRWKGENVATTEVABVFEALDF LQEVMVYGVTV 5740 265 231 PAYWLKVPTLCLESKTDLREKASHVSAQLQGEVGLAGALMM*A LQSELHKLVDERTGGWSWGSAGCGGYV VYVERVYN*N NISRWHALDQKHPHAGISSSMALQLNPCLGMMA LQSELHKLVDERTGGWSWGSAGCGGYV VYRERVYN*N NISRWHALDQKHPHAGISSSMALQLNPCLGMMA LQSELHKLVDERTGGWSWGSAGCGGYV VYARPGKVAABVKAVGDEGWILAEVVSYSHATNNYRVDDIDB EGKERHTLSRRRVIPLJQWKANBPTDPEALFQKEQLULALPPOT TCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPLNVAQRYVV ACKEPKK*CTLADSPSFNDTGQDSGRGAGIKHIPPLKKK ACKEPKK*CTLADSPSFNDTGQDSGRGAGIKHIPPLKKK TVNIP IPRGGDTVLIGAVRGGHVEIVRALLQKYADDITGGONN TALVWAVEKGNATMWRDILDCURPDTEICTKDG 5743 2 415 GKTPEGIDAIBEIEIDLEETEREISPQEMGLEEVKPLGBMQTDL KATGREISPRETPEVIDATEEIDLOLDETGRREISPEENGPEE VKPVDEMETILLTTGRGSSREKTREVIDAABVIETDLEETERE 1SPQE 5744 3 703 TRRTTTTSPTTTRQMTTTPAALPTTVVTTPPLTTGTPLGMTTER SDSWSSAESTSADTVLLITSKESKWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPBGNRTTKTGQMGGIFMSMKEMPEISQLLMIIAP SIGFVLPALPVAPLIKERKLMETTGSQKSTRTLDVIGDSKVNLNDV QHGREDBDGLFTL GKRRFWLMKHSKKYDDSPQDELEDYIKVQKARGLEPKTCPKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPOT VENRLPQMLPAHDSKLRIDBISYCQFTRDCTSSKFVPLMFNQQE FICSHGVGFREVYKHFSDNTSTTHAGSHKQIHQKKKREPEEGG EKSEERSKHKRKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE LKKNKKKKSRDVVSKKEERKPTKKKKEQGGATPATEGLARPQAPSSSAFRCP YCGKFFTSABRERHLHILHFPKKCFSSSGEELHHSLT AHGAPERPLAATSAAPPDQPQPDPPDPEPSPAQRSSSAFRCP YCKKFFTSABRERHLHILHFPKCFSSSGSEELHHSLT AHGAPERPLAATSAAPPDPFFCQVCGGSFTQWFLKGHKKHA SDPHACV 1328 DRAVETLCHIFLGGSTGSTAKTGGRNWLKTGNCLYGMTCRFVHG PSPRGKYSSNYKRSPERPTODLREET,KKKQDVDTFPQKRKTE FATGTTPAPAADEEDPAPPEFFCQVCGGSFTQWFLKGHKHKA SDPHACVY PSPRGKYSSNYKRSPERPTODLREET,KKKQDVDTFPQKRKTE PSPRGKYSSNYKRSPERPTODLREET,KKKQDDVTTEPQKRKTE PSPRGKYSSNYKRSPERPTODLREET,KKKQDDVTTEPQKRKTE PSPRGKYSSNYKRSPERPTODLREET,KKKGDDVTTEPQKRKTE PSPRGKYSSNYKRSPERPTODLREET,KKKGDDVTTEPQKRKTE				FPTLLEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEV
VLKSKPSAGGPREDCQCHRVTVFQYIGELCRYLVNQPPSKAERG HKVRLAVGSGLRPDTWERFVRRFGEJCKTYGLTGENVATINY TGQRGAVGRASHLVKHIFFFSLIRYDVTTGEPIRDQGHCMATS PGBEGLLVAPVSQQSFILGYAGGFELAQGKLKAVFREDDVFR TRDLLVCDQGFLRHRNTGDFFRWGENVATTEVARVFREDDF LQEWNVYGVTV 5740 265 231 PAYWLKVFTLCLESKTDLREKASHVSAQLQGEVRGLAGALMW*A VYERVYNN NISRWHALEQKRHPAGLSSSMALQLNPCLGMLMA LQSELHKLVDEETQSWYSGSACGYP PKTWRRSQVMTLLQCSGMTLPJWIGKFGGDRPPPLCGAIPASGD YVARPGDKVAARVKAVGGBQMTLAEUVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPETDPEALGQKEQLVLLALYPQT TCFYRALHAPPQRRQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSNDTTQDSRGRAGIKHIPPLKKK 5742 2 362 TSVKEILKRNPNVALIFOKGMTALMAHSKEGHTEIVQDLDAG TYVNIPDRSGDTVLIGAVGGHVEIVRALLQKYADIDIRGQDNK TALWAVEKGNATWWRDILQCNPDTEICTXGG 6KTPEGIDAIBEIEIDLEETEREISPCRGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEFTGREISPERNGPEE VAPUDEWETDLKTTGREGSSREKTREVIDAREISPERNGPEE VAPUDEWETDLKTTGREGSSREKTREVIDAREISPERNGPEE USPQUE 5744 3 703 TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VPTTANTCLSLTFSTLPFERATGLLTFEFSKEGFILTARSETVLP SDSWSASESTSADTVLLISKESKVMDLPSTSHVSMKKTSDSVS POPGASDTAVPBGNNTKTTGYMGGTBAKEMPE 19GLIMIJAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTI SGKRPTLTGGYKGFWSRFTTRMFDQRLPSETIGTYPRSCNIFOT VENRLPQNLPAHDSRLADLSISVCGPKSTEEPETHPENTERE KLKNRKKESCEBIDLDKHKSIGRKATERETHVHSTEL VENRLPQNLPAHDSRLADLSISVCGPKSTEEPETHOLTETHROWSE SKEEBERSKIKKKKSCEBIDLDKHKSIGRKATERETHVHSTEL KLKNRKKKSCEBIDLDKHKSIGRKATERETHVHSTEL KLKNRKKKSCEBIDLDKHKSIGRKATERETHVHSTEL KLKNRKKKSCEGGLEDLORTSEEMLMOQSI LGF SFAGGLTPSSPAFDGELDLORYSNGPAVSAMSLGMGAVSWSES RAGERFFCCVCGKRFRFNSILALHLRTHQPERPSPARALLLE LEERALLREARLGRASSSGMQATPATEGLARPQAPSSSAFRCF VCKGKFTSASEREFHLHILHFPMKCALCSFGSSGEEELLHHSLT ANGADERPLAATSAAPPPOPOPOPPPPEPSPPPEPPPEPPPPEPPPPPPPPPP	1			SAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKI
VLKSKPSAGGPREDCQCHRVTVFQYIGELCRYLVNQPPSKAERG HKVRLAVGSGLRPDTWERFVRRFGEJCKTYGLTGENVATINY TGQRGAVGRASHLVKHIFFFSLIRYDVTTGEPIRDQGHCMATS PGBEGLLVAPVSQQSFILGYAGGFELAQGKLKAVFREDDVFR TRDLLVCDQGFLRHRNTGDFFRWGENVATTEVARVFREDDF LQEWNVYGVTV 5740 265 231 PAYWLKVFTLCLESKTDLREKASHVSAQLQGEVRGLAGALMW*A VYERVYNN NISRWHALEQKRHPAGLSSSMALQLNPCLGMLMA LQSELHKLVDEETQSWYSGSACGYP PKTWRRSQVMTLLQCSGMTLPJWIGKFGGDRPPPLCGAIPASGD YVARPGDKVAARVKAVGGBQMTLAEUVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPETDPEALGQKEQLVLLALYPQT TCFYRALHAPPQRRQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSNDTTQDSRGRAGIKHIPPLKKK 5742 2 362 TSVKEILKRNPNVALIFOKGMTALMAHSKEGHTEIVQDLDAG TYVNIPDRSGDTVLIGAVGGHVEIVRALLQKYADIDIRGQDNK TALWAVEKGNATWWRDILQCNPDTEICTXGG 6KTPEGIDAIBEIEIDLEETEREISPCRGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEFTGREISPERNGPEE VAPUDEWETDLKTTGREGSSREKTREVIDAREISPERNGPEE VAPUDEWETDLKTTGREGSSREKTREVIDAREISPERNGPEE USPQUE 5744 3 703 TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VPTTANTCLSLTFSTLPFERATGLLTFEFSKEGFILTARSETVLP SDSWSASESTSADTVLLISKESKVMDLPSTSHVSMKKTSDSVS POPGASDTAVPBGNNTKTTGYMGGTBAKEMPE 19GLIMIJAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTI SGKRPTLTGGYKGFWSRFTTRMFDQRLPSETIGTYPRSCNIFOT VENRLPQNLPAHDSRLADLSISVCGPKSTEEPETHPENTERE KLKNRKKESCEBIDLDKHKSIGRKATERETHVHSTEL VENRLPQNLPAHDSRLADLSISVCGPKSTEEPETHOLTETHROWSE SKEEBERSKIKKKKSCEBIDLDKHKSIGRKATERETHVHSTEL KLKNRKKKSCEBIDLDKHKSIGRKATERETHVHSTEL KLKNRKKKSCEBIDLDKHKSIGRKATERETHVHSTEL KLKNRKKKSCEGGLEDLORTSEEMLMOQSI LGF SFAGGLTPSSPAFDGELDLORYSNGPAVSAMSLGMGAVSWSES RAGERFFCCVCGKRFRFNSILALHLRTHQPERPSPARALLLE LEERALLREARLGRASSSGMQATPATEGLARPQAPSSSAFRCF VCKGKFTSASEREFHLHILHFPMKCALCSFGSSGEEELLHHSLT ANGADERPLAATSAAPPPOPOPOPPPPEPSPPPEPPPEPPPPEPPPPPPPPPP			,	LQCQGFYQLCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGATV
HKVRLANGSGLRPTWERFVERFELQVLITTGYLTTGWITTGWITTGWITTGWITTGWITTGWITTGWITTGW				VLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERG
FGEFGLLVAP VSQQSPELGYAGGPELAQGKLLKDVFRPGDVFNN TRDLLVCDDQGFLRPHDRTGDPFRWGGENVATTEVABVFEALDF LQEVNVYGVTV S740 265 231 PAYMLKUPTLCESKTDLREKASHVSAQLQGEVRGLAGALMM*A VYVERVVN*NISRWHALEQKRHPAGLSSSMALQINPCLGMLMA LQSELHKLYDEBTQSWVSGSACGGYP FRYMMRGVLMTLLQQSAMTLPLWIGKPGDRPPPLOGAIPASGD YVARPGKVARRYKAVDGBEØN LLAEVVSYSHATKKYEVDD IDE EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALJYPOT TCFYRALIHAPPQRPQDDYSVLFEDTSYAGVSPPLNVAQRYVV ACKEPKKK*CRLADSSSNDDTGGDSKGRAGIKHIPPLKKK S742 2 362 TOSVKEILKRNPWNILTDKGONTALMTASKEGHTEIVQDLLDAG TTVNIPDRSGDTVLIGAVRGGHVSALLQKYADDLDRQDDTS S743 2 415 GKTPEGIDAIEETEDLEETEREISPQENSLEVKPLGEMQTDL KATGREISPREKTPEVIDATEEILDKLEETGREISPGENGPEE VXPVDEMETDLKTTGREGSSREKTREVIDABSVIFDTDLEETERE ISPQE S744 3 703 TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTLA VFTTANTCLSLTPSTLPEEATGLLTPSPSKEGPILTASSETVLP SDSWSSASSTSADTVLLTKKSSKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMILAP SLGFVLFALFVAFILEGKLMETYCSQKTTRLDVIGDSKNVLINDV QHGREDEGGLFTL VSNRLPQMLPAHDSRIKLDSLSYCQFTRDCFSSKVPLNIPQQ VYCKSHGVENVYHTSSDNTSTHQASHKJTQTPRSCNIPQT VENRLPQMLPAHDSRIKLDSLSYCQFTRDCFSSKVPLNIPQQS ILGF EKSEERSKHRKKSCEBILDLKRIGKKTFVESTOTYPRSCNIPQT VENRLPQMLPAHDSRIKLDSLSYCQFTRDCFSSKVPLNIPQQS ILGF EKSEERSKHRKKSCEBILDKRIGKKTFVESTOTYPRSCNIPQT VENRLPQMLPAHDSRIKLDSLSYCQFTRDCFSSKVPLNIPQQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVVGKRFRSSSAGMQATPATEGLARRPQAPSSSAFRCP YCKGKFRTSABEREHHILLHRRPWKGGLCSFGSSGBEELLHHSLT AHGAPERPLAATSAAPPPQDQPQPPPPDPERRSAAPLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSABEREHHILLHRRPWKGGLCSFGSSGBEELHHSLL AHGAPERPLAATSAAPPPQDQPQPPPPDPERRSVPQPEPPPQPER EATPTPAPAPEEPPPAPPEFRCQVCGGTSSFTGSFAKHKKKA SDHACPV STHACPV]			HKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINY
FGEFGLLVAP VSQQSPELGYAGGPELAQGKLLKDVFRPGDVFNN TRDLLVCDDQGFLRPHDRTGDPFRWGGENVATTEVABVFEALDF LQEVNVYGVTV S740 265 231 PAYMLKVPTLCESKTDLREKASHVSAQLQGEVRGLAGALMM*A VYVERVVN*NISRWHALEQKRHPAGLSSSMALQINPCLGMLMA LQSELHKLYDEBTQSWVSGSACGGYP FRYMMRGVLMTLLQQSAMTLPLWIGKPGDRPPPLOGAIPASGD YVARPGKVARRYKAVDGDEWILLAEVYSYSHATKKYEVDDIDE BGKRRHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALJYPOT TCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLWAQRYVV ACKEPKKK*CRLADSSSNDDTGGDSKGRAGIGHIPPLKKK S742 2 362 TOSVKEILKRNPWNILTDKGONTALMTASKEGHTEIVQDLLDAG TTVNIPDRSGDTVLIGAVRGGHVSALLQKYADDLDRGQDTN TALYWAVEKGNATMVRDILQCNPDTEICTKDG S743 2 415 GKTPEGIDAIEEIEDLEETEREISPQENSLEVKPLGEMQTDL KATGREISPREKTPEVIDATEEILDKLEETGREISPESNEGPED VERPUGENSTALSTREVIPLOMKTISPESTEREISPESNEGPES VERPUGENSTALLSKYSKUMLPSTSHESMKWISDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFILEGKKMETYCSQKHTRLDYIGDSKNVLINDV QHGREDEGGLFTL VENRLPQMLPAHDSRIKLDSLSYCQFTRDCFSEKVPLNFQQE YTCGSHGVEHRVYKHFSSDNSTSTHQASHKJTGYPRSCNIPQT VENRLPQMLPAHDSRIKLDSLSYCQFTRDCFSEKVPLNFQQS YTCGSHGVEHRVYKHFSSDNSTSTHQASHKJIGKKTFVEFEGR YCKGKKRKSKKSCBEIDLKRIGKKTFVEFETTHVFTER KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQETTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLERHQPERPSSPARLLLE LEERALIREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSABEREHHILLHRFWKGGLCSFGSSGBEELLHHSLT AHGAPERPLAATSAAPPPQDQPQPPPPDPERRSAPAPLLE LEERALIREARLGRARSSGGMQATPATTEGLARPQAPSSSAFRCP YCKGKFRTSABEREHHILLHRFWKGGLCSFGSSGBEELHHISLT AHGAPERPLAATSAAPPPQDQPQPPPPDPERRSAPCPPPPERRE EATPTPAPAPEEPPAPPPEFRCQVCGGTSSFTGSFAKKHKKA SCHARCPV STHACPV	ŀ	1		TGQRGAVGRASWLYKHIFPFSLIRYDVTTGEPIRDPQGHCMATS
TRDILLYCDOGGFLRFHDRTGDPFRWKGENVATTEVAEVFEALDF LQEVNYYGVTV 1 LQEVNYYGVTV 5740 265 231 PAYMLKVPTLCLESKTDLREKASHVSAQLQGEVRGLAGALWM+A YVYBRVYN*MISRMHALEQKRHPAGLSSSMALQLNPCLGMLMA LQSELHKLYDEETGGWWSGBACGGV 5741 1 650 PRKTMRRGVLMTLLQQSAMTLPLWIGKPGDRPPLGGAIPASGD YVARPGGKVAARVKAVDGDEGWILAEVVSYSHATNKYBVDDIDE EGKBRHTLSRRRVIDH,DWKANBFTDPEALFQKEQLVLALYPOT TCYYRALIHAPPGRODDYSULFBDTSYADGVSPPLNVAGRYVV ACKEPKK*CCLALADSSPNDTQGDGRAGAIKHIPPLKKK 5742 2 362 TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLDAG TTVNIPDRSGDTVLIGAVRGGHVBIVRALLQKYADIDIRGGDN TALWAWKGNATMVBDILQCNPDTEICTKDG 5743 2 415 GKTPBGIDTLIGAVRGGHVBIVRALLQKYADIDIRGGDN KATGREISPREKTPEVIDATEIDKDEETGRBEISPREMDEBE VKPVDEMETDLKTTGREGSSREKTREVIDABSVIETDLEETERE ISPQE 5744 3 703 TRRTTTTSPTTTRQMTTTPAALPTTVVTTFDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPSPSKERFILTABSETVLP SDSWSSAESTSADTVLLTSKESKWMLDLPSTSHVSMNKTSDSVSS POPGASDTAVPEGNKTTKTGQMDGIPMSMKNEMPISQLIMIIAP SIGFVLPFALFVAFILLEGKLMETYCSQKHTRLDYIGDSKNVLNDV QGKBDEGGLFTL VENRLPQONLPAHDSRLEDLSSYCTPTDCFSSKPVPLNFNQG YYGGSHOPGIFRVYKHFSSINSTSTHQASHQIHQKKHPBEEG TYGGSHGPUNSRPTYRMFOQRIPSSTIQTYPRSCTIPQT VENRLPQONLPAHDSRLEDLSSYCTPTDCFSSKPVPLNFNQGE YYGGSHGPUNSRPTYRMFOQRIPSTITQTYPRSCTIPQT VENRLPQONLPAHDSRLEDLSSYCTPTDCFSSKPVPLNFNQGE YYGGSHGPUNSRPTXMFGGLGSRFSKPVPLNFNQGE YYGGSHGPUNSRFTXRFGQRFSTSTHQASHQIHQKKHPBEEGR EKSEBERSKHKKKSCEEIDLDKHKSIDKKKTVGFRFBGR EKSEBERSKHKKKKGEGERTDLDKHKSIDKAKTPUETETHVHTE LEERALLBEABLGRASSSGMQATPATEGLARPQAPSSSAFRCP YCKGKFTSABREBHLHILHRRWKGLCSFGSSGEELLHHSLT AHGAPERPLAATSAAPPPOPOPQPPPEPEPPPEPE EATPTPAPAPAEPEPPAPPEFFRQVCGSFTTGSFKKMRKKKA SPUNACPV 5747 2 1328 DRRWSTLCIHFLGFSTGSTAKTGGRNWLKTGNCLYGHTCFVHG PSPRGKGYSSNYRSPSPFTGDLGRRFLINKRODVDTEPCKNTKE	ļ.			PGEPGLLVAPVSOOSPFLGYAGGPELAQGKLLKDVFRPGDVFFN
LQEUNVIGUTY				TRDLLVCDDOGFLRFHDRTGDPFRWKGENVATTEVAEVFEALDF
S740 265 231 PAYWLKUPTLCLESKTDLREKASHVSAQLQGEVRGLAGALMM-A YVYERVIN'NISKNVEALEQKRHPAGLSSSMALQLINPCLGMLMA LQSELHKLYDEETGSWYSGSACGTP	1	1	1	l .
VYYERVIN*NISRNYHALEOKRIPAGISSSMALQLINFCLGMLMA LQSELHKLYDEETQSWYSGSACGGYP	5740	265	231	PAYWLKVPTLCLESKTDLREKASHVSAQLQGEVRGLAGALWM*A
LQSELHKLYDEETGSWVGGARCGYP	3710	1 200		YVYERVYN*NISRMVHALEQKRHPAGLSSSMALQLNPCLGMLMA
S741 1 650 PRKTMRRGVLMTLLQQSAMTLPLWIGKPGDRPPPLCGAIPASGD	Į.			
YVARPODKVAARVKAVDGDEØHILÆVVSYSHATNKYEVDDIDE EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCFYRALHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKK**CRLADSESPNDTGQDERGRAGIKHIPPLKKK 5742 2 362 TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNX TALYMAVEKGNATMVRDILQCNPDTEICTKDG 5743 2 415 GKTPEGIDAIBEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPQE 5744 3 703 TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESSTVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPBGNKTTKTGQMDGIHSMKNEMPISQLLMIIAP SLGFVLFALFVAPLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL 5745 1400 599 GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFKKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSSTICTYPRSCNIPOT VENRLPQWLPAHDSRLRLDSLSYCQPTRDCFSEKFVPLNFNQQE YICGSHGVEHRVYKHFSSNNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCERIDLDKHKSIQRKTEVEIETVHYSTE KLKNRKEKKSRDVVSKKEERKRYKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRRFRSILAHLRTHQPERPRSPAARLLLE LEERALLREARSGGMQATPATEGLARPQAPSSSAPRCP YCKGKPRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT ANGAPERPLAATSAAPPPQDQPQPPQPEPRSVPQPEPPEPQPER EATPTTAPAAAPEEPPAPPEFRCQVCGGSFTQSWFLKGHMKRHKA SFDHACPV DRHVETLCTHFLGPSTGSTAKTGGRWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERKNKRQDVDTEPQKRNTE	E741		650	
EGKERHTLSRREVI PLPØWKANPETDPEALFØKEQLVLALYPOT TCFYRALHHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSFSPNDTQQDERGRGIKHI PPLKKK 5742 2 362 TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TTVNI PDRSGDTVLIGAVRGGHVEJ VRALLQKYADIDIRGQDNK TALYMAVERGNATMYRDILQCNPDTBICTKDG 5743 2 415 GKTPEGIDAIBEIEIDLEETEREISPQENGLEEVKPLGENQTDL KATGREISPRETTPEVIDATEEIDKDLEETEREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVI DAAEVIETDLEETERE ISPQE 5744 3 703 TRRTTTTSPTTTRQMTTPAALPTTVVTTPDLTTGFPLØMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSASESTSADTVLITSKESKVMDLPSTSHVSMKKTSDSVSS PQDGASDTAVPEGNKTTKTGOMEGI PMSMKNEMPI SQLLMI IAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDY1GDSKNVLNDV OHGREDEDGLFTL 5745 1400 599 GKSRFVNLMKHSKKTYDSFOBELEDVIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWIDAHDSRIKALDSLSVCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEBERSKHKRKKKSCEBIDLKMKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKTKKKKEQGGERTEEEMLMDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDQRYSNGFAVSAWSLGMGAVSWSES RAGERRFPCPVCCKRFFFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKRFTSAERERHLHILHRPWKCGLCSFGSSGEELLHHSLT AHGAPERPLAATSAAPPPQPQPPPPPPSVPQPEPPPPPPR EATPTTAPAAPEEPPAPPEFRCQVCGSFTQSWFLKGHMKRHKA SFDHACPV DRIVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	3/41	_	1 030	YVARPGDKVAARVKAVDGDEOWILAEVVSYSHATNKYEVDDIDE
TCFYRALIHAPQRPQDDYSVLFEDTSYADGYSPINVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK 5742 2 362 TQSVKEILKRIPRWNUTMKDGNTALMLASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG 5743 2 415 GKTPEGIDAIBEIEIDLBETEREISPQENGLBEVKPLGEMQTDL KATGREISPREKTPEVIDATEIDKDLEETGRREISPERNGPBE VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPQE 5744 3 703 TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLISKESKWDLPSTSHVSMKKTEDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSKNEMPISQLLMIIAP SLGFVLFALFVAFILRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL 5745 1400 599 GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSSTIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKKKRHEBEGR EKSEERSKHKRKKSCEBIDLDKHKSIQRKKTEUEITFVHNSTE KLKNRREKKSRDVVSKKEERKRTKKKKEQGQETTEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRPPCPVCGKRFRNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKGGLCSFGSSQEEELLHHSLT AHGAPER PLAATSAAPPPQAPPOPPPRPSVPPSPEPPEPP EATPTTAPAAPAEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCEFVHG 57867 DRHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCEFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKMKRQDVDTEPQKRNTE	1			EGKERHTLSRRRVIPLPOWKANPETDPEALFQKEQLVLALYPQT
ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK 5742 2 362 TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG 5743 2 415 GKTPBGIDAIBEIEIDLBETEREISPQENGGLEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPQE 5744 3 703 TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPERATGLLTPETSKEGPILTABESTVLP SDSWSSAESTSADTVLLTSKESKWADLPSTSHVSMWKTSDSVSS PQPGASDTAVPBGNKTTKTGQMDGIPMSMKNEMPISQLMIIAP SLGFVLPALPVAFILRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL 5745 1400 599 GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCGFTRDCFSEKPVPLNFNQQE Y1CGSRGVEHRVYKHFSSDNSTSTHQASHKQIHQKKRHPEEGR EKSEERSKKHKRKSCEBIDLDKHKSIQPKKTEVEIETVHVSTE KKMRREKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLMDGSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKFRRNSILALHLRTHQPERPRSFAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSABRERHLHIIHRPWKCGLCSFGSSQEEELLHHSLT AHGAPER PLAATSAAPPPQOPQPPPPDEPRSVQPEPPEPQEE EATPTTAPAAREEFPRAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 DRHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 DRHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 2 DSHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 2 DSHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 2 DSHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 2 DSHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 2 DSHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 2 DSHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 2 DSHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 2 DSHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 2 DSHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 2 DSHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 2 DSHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 2 DSHVETLCTHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG 57867 2 DSHVETLCTHFLGPSTGSTAKTGGRNULKTGNCLYGNTCRFVHG 57867 2 DSHVETLCTHFLGPSTGSTAKTGGNULTGRVHG				TCEVPALTHAPPORPODDYSVLFEDTSYADGYSPPLNVAORYVV
TQSVKEILKRNPNVNLTDKDGMTALMIASKEGHTEIVQDLLDAG TTVN1PDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDK TALYMAVEKGNATMYRDILQCMPDTEICTKDG	1		l	ACKERKK*CPLADSPSPNDTGODSRGRAGIKHIPPLKKK
TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMYDILLQKPDTEICTKDG GKTPEGIDAIBEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEEATGLLTEEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQMKTIKTGGMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL 5745 1400 599 GKSRFVNLMKHSKKTYDSPQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYTMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEBRSKHKRKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNNRKEKKSRDVVSKKEERKRTKKKKEQQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQDQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFPHACPV DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSFERPTGDLRERIKNKRQDVDTEPQKRNTE	5343		363	TOCUKETI KENDMUNI TEKEGNTALMI ASKEGHTE I VODLLDAG
TALYWAVEKGNATMVRDILQCNPDTEICTKDG TALYWAVEKGNATMVRDILQCNPDTEICTKDG KATGREISPATEEIDDIEETERETSPQENGLEEVKPLGENQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPERATGLLTPEPSKEGFILTAESETVLP SDSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLERGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL 5745 1400 599 GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSSTIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKKKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFFRNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPPQPEPRSPQPER EATPTPAPAPAPEEPPAPPFFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	5/42		302	TVINTEDESCRITTITICAVEGRIVETVEALLOKYADIDIRGODNK
2 415 GKTPEGIDAIBEIEIDLEETEREISPQENGLEEVKPLGBMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPERGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPQE 5744 3 703 TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLEEBATGLLTEPSPKEGPILTAESETVLP SDSWSSAESTSADTVLLISKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGGMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL 5745 1400 599 GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERESKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRRNSILALHLRTHQPERPRSPAARLLLE LEERALLKEARLGRARSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPPPPPPPPPPPPPPPPPPPPPPPP				TALYWAYEKGNATMYRDILOCNPDTEICTKDG
KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPQE 5744 3 703 TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEEATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL 5745 1400 599 GKSRFVWLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLMFNQQE YICGSHGVEHRVYKHFSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCCKKFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAEREHHHILHRPWKCGLCSFGSSQEEELHHSLT AHGAPERPLAATSAAPPPQPQPQPPPPPPPPPPPPPPPPPPPPPPPPPP			415	CYTERCIDALECTRICIDERETERETSPOENGLEEVKPLGEMOTDL
VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQFGASDTAVPEQMKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFILLGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNILMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLINFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKHPBEEG EKSEEBRSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHILRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEBELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPPPPERSVPQPEPEPQPER EATPTPAPAAPEEPPAPPFFCQVCGQSFTQSWFLKGHMRKHKA SFPHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEFQKRNTE	5743	2	415	WANGER CORPUMDENT DATE TO VOIL FETCORE I SPEENG PEE
ISPQE TRETTTTSPTTTRQMTTTPAALPTTVTTPDLTTGTPLQMTTIA TRETTTTSPTTTRQMTTTPAALPTTVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGP1LTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDG1PMSMKNEMP1SQLLMI1AP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDY1GDSKNVLNDV QHGREDEDGLFTL THOO S99 GKSRFVNLMKHSKKTYDSFQDELEDY1KVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSET1QTYPRSCN1PQT VENRLPQWLPPAHDSRLRLDSLSYCQFTRDCFSEKFVVPLNFNQQE Y1CGSHGVEHRVYKHFSSDNSTSTHQASHKQ1HQKRKRHPEEGR EKSEEBRSKHKRKKSCEEIDLDKHKS1QRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKBERKRTKKKKEQGQERTEEEMLWDQS1 LGF S746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFFRNS1LALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV DRHVETLC1HFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	-			TATORETS PRESCRIPTION TO THE TENER OF THE TE
TRRTTTSPTTTRQMTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQFGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL 5745 1400 599 GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIGTYPRSCNIPQT VENRLPQWLPPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPBEER EKSEEERSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPPQPPPPPPPPPPPPPPPPPPPPPPPPPPP	1		•	i e e e e e e e e e e e e e e e e e e e
VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPPPPPPPPPPPPPPPPPPPPPPPP				TORKE TORKE
SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEGLFTL 5745 1400 599 GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPBGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	5744	3	703	TREATTTTSPTTTROUTTTEAAUFITVVITEUDITGTFUQMITTA
PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL 5745 1400 599 GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPBEGR EKSEBERSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETUHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPPPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	}	1		VETTANTUBETPSTEPERATORETPEPARECETRIARSET VEP
SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEGLFTL 5745 1400 599 GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRFTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPBEGR EKSEEBSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKBERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPPQPERSVPQPEPEPQPER EATPTPAPAPAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	1			
QHGREDEGLFTL 5745 1400 599 GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE				SDSWSSAESTSADIVEETSKESKVWDEPSISHVBIWKISDSVSS
5745 1400 599 GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEBRSKHKRKKSCEBIDLDKHKSIQRKKTEVEIBTVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGBERFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE				POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP
KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKHPBEGR EKSEEBRSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKBERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE				PQPGASDTAVPBQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFILRGKLMETYCSQKHTRLDYIGDSKNVLNDV
VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPBEGR EKSEEBRSKHKRKKSCEBIDLDKHKSIQRKKTEVEIBTVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGBERFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE				PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL
YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEBRSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	5745	1400	599	PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM
EKSEERSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	5745	1400	599	PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT
KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHILRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	5745	1400	599	POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE
KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHILRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	5745	1400	599	PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR
LGF 5746 3 821 SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	5745	1400	599	PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE
RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPPPPQPERSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	5745	1400	599	PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE
RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPPPPQPERSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE	5745	1400	599	PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFILRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEBRSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF
LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPPPPQPERRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE				PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKBERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES
YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPPPPQPERRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE				PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQPTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKBERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE
AHGAPERPLAATSAAPPPQPQPPPPQPERRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE				PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQPTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKBERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE
EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV 5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE				PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKBERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP
5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE				POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT
5747 2 1328 DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE				POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFFFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER
PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE				PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQPTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKBERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA
PSPKGKGISSNIKKSFBKFIGDDKKKIKKGDVDTBI gkddill	5746	3	821	POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPPPPPPPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV
ESSSPVRKESSRGRHREKEDIKITKERTPESEEENVEWETNRDD	5746	3	821	PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRVPQPEPEPPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG

	· - · · · · · · · · · · · · · · · · · ·		·
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	1	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
į.			SDNGDINYDYVHELSLEMKRQKIQRELMKLEQENMEKREEIIIK
ł			KEVSPEVVRSKLSPSPSLRKSSKSPKRKSSPKSSSASKKDRKTS
1	`l	Ì	AVSSPLLDQQRNSKTNQSKKKGPRTPSPPPPIPEDIALGKKYKB
1			KYKVKDRIBEKTRDGKDRGRDFERQREKRDKPRSTSPAGQHHSP
1		İ	ISSRHHSSSSQSGSSIQRHSPSPRRKRTPSPSYQRTLTPPLRRS
			ASPYPSHSLSSPQRKQSPPRHRSPMREKGRHDHERTSQSHDRRH
			ERREDTRGKRDREKDSREEREYEQDQSSSRDHRDDREPRDGRDR
	İ		RE
5748	934	473	SEGPQVFYKGLAPTLIAIFPYAGLQFSCYSSLKHLYKWAIPAEG
	1		KKNENLQNLLCGSGAGVISKTLTYPLDLFKKRLQVGGPEHARAA
1	1		FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM
1			FFSYEFFCNVFHCMNRTASQR
5749	552	1	GFPVDPRVRGSTLSLAERPKGMIRSGSFRDPTDDVHGSVLSLAS
1			SASSTYSSAEERMQSEQIRKLRRELESSQEKVATLTSQLSANAN
			LVAAFEQSLVNMTSRLRHLAETAEEKDTELLDLRETIDFLKKKN
	1		SEAQAVIQGALNASETTPKELRIKRONSSDSISSLNSITSHSSI
1	1		GSSKDADA
5750	22	866	IFISICLWNAHLCFLLLPKDCIDQVMKLONLFVDDSGRYLAIOF
			HLEWAYVFLYYYEYRKAKDQLDIAKDISQLQIDLTGALGKRTRF
1			QENYVAQLILDVRREGDVLSNCEFTPAPTPOBHLTKNLELNDDT
į.			ILNDIKLADCEQFQMPDLCAEEIAIILGICTNFQKNNPVHTLTE
İ			VELLAFTSCLLSQPKFWAIQTSALILRTKLEKGSTRRVERAMRO
			TQALADQFEDKTTSVLERLKIFYCCQVPPHWAIQRQLASLLFEL
			GCTSSALQIFEKLEMWE
5751	3	751	
3,31	,	751	SCGSALRAWRCGAAALATFPAPALPGLMYRALYAFRSAEPNALA
			FAAGETFLVLERSSAHWWLAARARSGETGYVPPAYLRRLQGLEQ
			DVLQAIDRAIBAVHNTAMRDGGKYSLEQRGVLQKLIHHRKETLS
			RRGPSASSVAVMTSSTSDHHLDAAAARQPNGVCRAGFERQHSLP
1			SSEHLGADGGLFQIPLPSSQIPPQPRRAAPTTPPPPVKRRDREA
5752		485	LMASGSGGHNTMPSGGNSVSSGSSVSSCI
3/54	3	471	GPVCGVGLSVAWAGPWRGPVHSVGGGGRAALHGAELPCLSGAAT
			VEREMELRHKNEMLRVETBARARAKAERENADIIREQIRLKASE
			HRQTVLESIRTAGTLFGEGFRAFVTDRDKVTATVNIFIKQGWQV
F753			AERQHVGASWSPRSCPCRLCTAL
5753	34	483	DDSXAIPGGVQAPFGAVRNIYTPRTGHRIRKLDQIQSGGNYVAG
	ľ		GQEAFKKLNYLDIGEIKKRPMEVVNTEVKPVIHSRINVSARFRK
			PLQEPCTIFLIANGDLINPASRLLIPRKTLNQWDHVLQMVTEKI
L			TLRSGAVHRLYTLEGRLV
5754	14	331	TLVHVVEFAGEHAEAIASREQEVLQGWKELLSACEDARLHVSST
			ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW
			WPTPATPSPLTAPFSME
5755	3	888	LGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYI
			WMEKRHRGPGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIK
			PEVELPLKKDGFTSESTTLEALLRGEGVEKKVDAREEESIQEIQ
			RVLENDENVEEGNEEEDLEEDIPKRKNRTRGRARGSAGGRRRHD
			AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAO
			DQETRSPPNHRNENHRPQKGPDGTVIPNNYCDFCLGGSNMNKKS
			GRPEELVSCADCGRSAHLGGEGRKEKEAAA
5756	3	621	SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR
1			WNRRHKMYREOMNLTSLDPPLQLRLEASWVOFHLGINRHGLYSR
			SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV
			HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI
	İ		AAFHLDRILDFRRVPPTVGRIVNVTKEIL
5757	3	473	
	٦	4/3	YKDALLLPDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ
[]			LSISQSVHVAVKVPPLIQPFEFPPASIGQLLYIPCVVSSGDMPI
	1		RITWRKDGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI
5758	— <u> </u>	474	ASNAAATVSRERQLIVRVPPRFVV
00,00	-	4:14:	FRRGAGAERGEHREGERGAAGMGEFKVHRVRFFNYVPSGTRCVA
			YNNQSNRLAVSRTDGTVEIYNLSANYFQEKFFPGHESRATEALC
L		· · · · · · · · · · · · · · · · · · ·	WAEGQRLFSAGLNGEIMEYDLQALNIKYAMDAFGGPIWSMAASP

CEO	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide		H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of.	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			SGSQLLVGCEDGSVKLFQITPDKIPV
5759		1240	GNAAFAGQGVVYETFHMSDLPSYTTNGTVHVVVNNQIGFTTDPR
5759	2	1240	
			MARSSPYPTDVARVVNAPIFHVNADDPEAVIYVCSVAAEWRNTF
	1		NKDVGADLVCYRRRGHNEMDEPMFTQPLMYKQIHRQVPVLKKYA
			DKLIAEGTVTLQEFEEEIAKYDRICEEAYGRSKDKKILHIKHWL
	i		DSPWPGFFNVDGEPKSMTCPATGIPEDMLTHIGSVASSVPLEDF
	1		KIHTGLSRILRGRADMTKNRTVDWALAEYMAFGSLLKEGIHVRL
	i		NGQDVERGTFSHRHHVLHDQEVDRRTCVPMNHLWPDQAPYTVCN
	1		SSLSEYGVLGFELGYAMASPNALVLWEAQFGDFHNTAQCIIDQF
	ł	1	ISTGOAKWVRHNGIVLLLPHGMEGMGPEHSSARPERFLQMSNDD
	ļ	ļ	SDAYPAFTKDFEVSQL
	<u> </u>		
5760	1	1221	VRDITSDSLSLSWTVPEGQFDHFLVQFKNGDGQPKAVRVPGHED
			GVTISGLEPDHKYKMNLYGFHGGQRVGPVSAVGLTAPGKDEEMA
			PASTEPPTPEPPIKPRLEELTVTDATPDSLSLSWTVPEGQFDHF
			LVQYKNGDGQPKATRVPGHEDRVTISGLEPDNKYKMNLYGFHGG
			QRVGPVSAIGVTAAEEETPTPTEPSMEAPEPPEEPLLGELTVTG
	1		SSPDSLSLSWTVPQGRFDSFTVQYKDRDGRPQVVRVGGEESEVT
İ			VGGLEPGRKYKMHLYGLHEGRRVGPVSTVGVTAPQEDVDETPSP
Į.	1		TEPGTEAPEPPEEPLLGELTVTGSSPDSLSLSWTVPQGRFDSFT
	*		VOYKORDGRPQAVRVGGQESKVTVRGLEPGRKYKMHLYGLHEGR
	1	ł	1 = -
			RLGPVSAIGVT
5761	3	1275	SCDMAEAAALVWIRGPGFGCKAVRCASGRCTVRDFIHRHCQDQN
	1	1	VPVENFFVKCNGALINTSDTVQHGAVYSLEPRLCGGKGGFGSML
	1		RALGAQIEKTTNREACRDLSGRRLRDVNHEKAMAEWVKQQAERE
ļ		1	AEKEOKRLERLORKLVEPKHCFTSPDYQQQCHEMAERLEDSVLK
l	•		GMOAASSKMVSAEISENRKRQWPTKSQTDRGASAGKRRCFWLGM
l	1	1	EGLETAEGSNSESSDDDSEEAPSTSGMGFHAPKIGSNGVEMAAK
	1		FPSGSORARVVNTDHGSPEOLQIPVTDSGRHILEDSCAELGESK
ł			
		1	EHMBSRMVTETEETQEKKAESKEPIBEEPTGAGLNKDKETEERT
		1	DGERVAEVAPEERENVAVAKLQESQPGNAVIDKETIDLLAFTSV
			AELELLGLEKLKCELMALGLKCGGTLQ
5762	2	344	GSTGQTPLHSQGGGGGGGGGRRTPRGMPKEKYEPPDPRRMYTI
ŀ		1	MSSEBAANGKKSHWABLEISGKVRSLSASLWSLTHLTALHLSDN
1]		SLSRIPSDIAKLHNLVYLDLSSNKIR
5763	+3	429	LDKDTGLIMLIARLDYELIORFTLTIIARDGGGEETTGRVRINV
1 3703		1	LDVNDNVPTFQKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ
			ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL
[1	
		<u> </u>	TVMAMDAGN
5764	19	441	VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLBEK
1		1	LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK
		1	MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE
	ł	1	TPEAORDKL
5765	3	825	OKILRLNNSHOPPTSSSNSKDCGGPASSGAGATAALADGLKFAS
] 3,03			VOASAPOGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS
			STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS
}			AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ
		1	GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA
[1		GEVSKSAPDSGLMGNSMLVKKBEEEEESHRRIKKLKTEKVDPLF
1			TVPAPPPHV
5766	1608	663	SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL
]		_	AWLSTYVADSGSNOLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE
1			PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD
1	1	İ	IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND
1			TEELAVARPEDTVGALKSKYFFGQESQMKLIYQGRLLQDPARTL
	1		RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG
			SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV
	1		FGMYGR
5767	1 2	892	NFRATPRPPTRPELRTGTEVILWYLDWRALMKRKRMKANIKLVG
1	1		SGFPLPSSDLDDSLTEEIDEKIGFRNDANFDWQNVADFRDAGGS
	1	1	LTEVKVEEEBRDPQSPBFEIEEEEEMLSSVIPDSRRENELPDFP
l	l l	ſ	I TONITATORODO DA CONTROL TORO DE MICEUTO DO COLONIO I DINCO

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	
NO:	location	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
		 	HIDEFFTLNSTPSRSAYDEPHLLVNIEKQKLELEKRRLDIEAER
1	1	İ	LQVEKERLQIEKERLRHLDMEHERLQLEKERLQIEREKLRLQIV
		Ì	NSEKPSLENELGQGEKSMLQPQDIETEKLKLERERLQLEKDRLQ
	1		
			FLKFESEKLQIEKERLQVEKDRLRIQKEGHLQ
5768	3	476	SSRSRLSVSVSPPPPGIVELGPPFAWEFCSRLGSAVTSQRAGPA
	1		AAMVAKDYPFYLTVKRANCSLELPPASGPAKDAEEPSNKRVKPL
	1		SRVTSLANLIPPVKATPLKRFSQTLQRSISFRSESRPDILAPRP
1	· ·		WSRNAAPSSTKRRDSKLWSETFDVC
5769	38	667	TKTKKGVKEKATDQSVKAFAEHCPELQYVGFMGCSVTSKGVIHL
			TKLRNLSSLDLRHITELDNETAMEIVKRCKNLISLNLCLNWIIN
1		ļ	DRCVEVIAKEGQNLKELYLVSCKITDYALIAIGRYSMTIETVDV
		l	GWCKEITDQGATLIAQSSKSLRYLGLMRCDKVNEVTVEQLVQQY
J	 	1	PHITFSTVLQDCKRTLERAYQMGWTPNMSAASS
5770	1	484	DSRRYDVKTRKWSFLLEEHSKLIAKVRCLPQVQLDPLPTTLTLA
1			FASQLKKTSLSLTPDVPEADLSBVDPKLVSNLMPFQRAGVNFAI
	1 '	l '	AKGGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVVPSSVRFT
l	1		WEQAFLRWLPSLSPDCINVVVTGKDRLTA
5771	168	741	GLLPSACLRARSWREASEGPSSRACSNGSQDTFEACYSGTSTPS
		1	FHGSHCSGSDHSSLGLEQLQDYMVTLRSKLGPLEIQQFAMLLRE
			YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRPFIPDQDIGYFEGF
			LEGVGIREGGILTDSFGRIKRSMSSTSASAVRSYDGAAQRPEAQ
1	ł		
5772	140		AFHRLLADITHDIE
5//2	148	383	EFNLALVSPSHPQIKAEDDQPLPGVLLSLSGGLFRSNLLTQDNG
	<u> </u>		ILTFSNLVTCSAIYHLPVFPEREPGCSMRDLRVA
5773	2	723	PRVRSKHNFCFMEMNTRLQVEHPVTEMITGTDLVEWQLRIAAGE
			KIPLSQEEITLQGHAFEARIYAEDPSNNFMPVAGPLVHLSTPRA
		•	DPSTRIETGVRQGDEVSVHYDPMIAKLVVWAADRQAALTKLRYS
]			LRQYNIVGLHTNIDFLLNLSGHPEFEAGNVHTDFIPOHHKOLLL
	!		SRKAAAKESLCQAALGLILKEKAMTDTFTLQAHDQFSPFSSSSG
1			RRLNISYTRNMTLKDGKNSK
5774	· 2	592	
1.	-	332	FVEEENIRVVRCGGSELNFRRAVFSADSKYIFCVSGDFVKVYST
	· .		VTEECVHILHGHRNLVTGIQLNPNNHLQLYSCSLDGTIKLWDYI
	:		DGILIKTFIVGCKLHALFTLAQAEDSVFVIVNKEKPDIFQLVSV
	·		KLPKSSSQEVEAKELSFVLDYINQSPKCIAFGNEGVYVAAVREF
<u></u>			YLSVYFFKKETTSRVTLSSS
5775	3	538	SSGCCDPAAPSSLAEAATMPVSKCPKKSESLWKGWDRKAQRNGL
1			RSQVYAVNGDYYVGEWKDNVKHGKGTQVWKKKGAIYEGDWKFGK
	l l		RDGYGTLSLPDQQTGKCRRVYSGWWKGDKKSGYGIQFFGPKEYY
	:		EGDWCGSQRSGWGRMYYSNGDIYEGQWENDKPNGEGMLRLSQNP
			RP
5776	2	484	RLPQDCVCQNLSESLGTLCPSKGLLFVPPDIDRRTVELRLGGNF
55	"	303	1
1			IIHISRQDFANMTGLVDLTLSRNTISHIQPFSFLDLESLRSLHL
			DSNRLPSLGEDTLRGLVNLQHLIVNNNQLGGIADEAFEDFLLTL
			EDLDLSYNNLHGPAVGLRGDAWVQPSTS
5777	2	949	GQDPEPGQDLFQPEREVDPSWGRGREPRLGKLRFQNDHLSVLKQ
			VKKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG
			GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV
]	ļ !		YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR
].			NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE
			1
1 1			DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP
j l			YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ
ļ			NSERRNV
5778	1	1210	QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS
] j			GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP
1 1			WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS
			LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKOACLAMLLHFLDT
			YQGLLQEEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHQLVE
1			TVELKIPEENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGSDEIF
1	-		
1. 1	i		CRVYMPDHSYVTIRSRLSASVQDILGSVTEKLQYSEEPAGREDS
L			LILVAVSSSGEKVLLQPTEDCVFTALGINSHLFACTRDSYEALV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequence	\=possible nucleotide insertion)
	sequence		PLPEEIOVSPGDTEIHRVEPEDVANHLTAFHWELFRCVHELEFV
			DYVFHGE
	122	1.671	EAVOVLIKHSADVNARDKNWOTPLHVAAANKAVKCAEVIIPLLS
5779	138	1671	
1	1		SVNVSDRGGRTALHHAALNGHVEMVNLLLAKGANINAFDKKDRR
Ì	1		ALHWAAYMGHLDVVALLINHGAEVTCKDKKGYTPLHAAASNGQI
ı			NVVKHLLNLGVEIDEINVYGNTALHIACYNGQDAVVNELIDYGA
			NVNQPNNNGFTPLHFAAASTHGALCLELLVNNGADVNIQSKDGK
1	ł		SPLHMTAVHGRFTRSQTLIQNGGEIDCVDKDGNTPLHVAARYGH
ŀ	1	ļ	ELLINTLITSGADTAKCGIHSMFPLHLAALNAHSDCCRKLLSSG
1	1	1	QKYSIVSLFSNEHVLSAGFEIDTPDKFGRTCLHAAAAGGNVECI
	ì		KLLQSSGADFHKKDKCGRTPLHYAAANCHFHCIETLVTTGANVN
1	1	1	ETDDWGRTALHYAAASDMDRNKTILGNAHDNSEELERARELKEK
	1		EATLCLEFLLQNDANPSIRDKEGYNSIHYAAAYGHRQCLELLLE
1	1]	RTNSGFEESDSGATKSPLHLAVSEMP
F 200	154	624	QFFRVITCLPFKGPDYRLYKSEPELTTVAEVDESNGEEKSEPVS
5780	154	024	EIETSVVKGSHFPVGVVPPRAKSPTPESSTIASYVTLRKTKKMM
			· ·
1		ł	DLRTERPRSAVEQLCLAESTRPRMTVEEQMERIRRHQQACLREK
	<u> </u>		KKĢLNVIGASDQSPLQSPSNLRDNP
5781	19	941	RGSLGGHPWRPPMRAASQGCLPVSFVTGPHQERAYGGRGPGGAF
1)	i	PAPPVSGTCPPDLIYAPTPEKAEGGSQKNHQPPPGERAAHRDGE
			QAPCRAGPTRKVAVAPRPPSCP*GPE\PGEEPRRPLDRSPPLGQ
İ		{	VQPHFTSQDAKSAEDEAPSRHLGKHQPRSAQVGSRLDALQGPKT
1			QHS1HTVTCKSPRQKEDRSPKPPQAPKHPEBHGRQS\QAPPPLP
1		1	VAPSRTCGGC*TWDPALLVSP/PQGDSTPELPAP\QQPTGGPSR
1		1	CROALPPOG*ROOPRORPR/PTGASRSHPAKAKGCQGPPKIRNY
1	**		NIMD
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE
1 5/82	27.0	123/	PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV
1		1	SOPEPPVSOSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP
1		}	
1	i .	1	PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT
1		1	THE A CONDUMCTORY DESCRIPTION OF THE STREET STATES OF THE STATES
1			VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA
1			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPARDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSKS
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSS/RDRRRRSSRSRSKSGGRRSVSKEKRKRSPKH
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSEEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSS/RDRRRRSSRSRSKSGGRRSVSKEKRKRSPKH RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRRRSR
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSS/RDRRRRSSRSRSKSRGRRSVSKEKRKRSPKH RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRRSR
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKORTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*RELLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSKSKS HRS\QTRSRSS/RDRRRRSSRSRSKSRGRRSVSKEKRKRSPKH RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRRSR SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSR
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKITSESRSRARKRSSKSKS HRS\QTRSRSRS/RDRRRSSRSRSKSRGRRSVSKEKRKRSPKH RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRRRS SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRS RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESTTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*ERLLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSK HRS\QTRSRSS/RDRRRRSSRSRSKSGGRRSVSKEKRKRSPKH RSKSRERKRKRSSSENDRKTVRARSRTPSRRSRSHTPSRRRSR SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRS RTPSRRSRTPSRRRSRSVVRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRAKKSSKSKS HRS\QTRSRSSRS/RDRRRSSRSRSKSGRRSVSKEKRKRSPKH RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRSRS SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESTTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*ERLLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSK HRS\QTRSRSS/RDRRRRSSRSRSKSGGRRSVSKEKRKRSPKH RSKSRERKRKRSSSENDRKTVRARSRTPSRRSRSHTPSRRRSR SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRS RTPSRRSRTPSRRRSRSVVRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRAKKSSKSKS HRS\QTRSRSSRS/RDRRRSSRSRSKSGRRSVSKEKRKRSPKH RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRSRS SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRAKRSSKSKS HRS\QTRSRSSKRSKSSEHKSRKLTSESRSRAKRSSKSKS RS\QTRSRSSKSFSRSRTPSRRSRTPSRRSRTPSRRSR SVGRRRSFSISPSRRSRTPSRRSRTPSRRSR SVGRRRSFSISPSRRSRTPSRRSR STPSRRSRTPSRRSR RTPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRSRTPSRRS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESTTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRAKRSSKSKS HRS\QTRSRSS/RDRRRRSSRSKSGGRRSVSKEKRKRSPKH RSKSRERKRKRSSSSDNRKTVRARSRTPSRRSRSHTPSRRSRS SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRS RTPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRS RTPSRRSRTPSRRSRSVVRRRSFSISPVLRRSRTPLRRFFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFFVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESTTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSSSRSKRSKSSEHKSRKLTSESRSRARKRSSKSKS SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSR SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRSRSVVRRRSFSISPVRLRRSRTPLRRFFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESTTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLININHHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSFRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSS/RDRRRRSSRSRSKSGGRRSVSKEKRKSPKH RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRRRSR SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRS RTPSRRSRTPSRRSRSVVRRRSFSISPVRLRRSRTPLRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKEBADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESTTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLININHHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSFRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSS/RDRRRRSSRSRSKSGGRRSVSKEKRKSPKH RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRRSR SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRSRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGGFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR
			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESTTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSS/RDRRRRSSRSRSKSGGRRSVSKEKRKRSPKH RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRRSR SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRRSRSVVRRRSFSISPVRLRRSRTPSRRS RTPSRRSRTPSRRRSRSVVRRSFSISPVLLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFFVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGGFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR
5783	1693	698	ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESTTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRAKKSSKSKS HRS\QTRSRSS/RDRRRRSSRSRSKSRGRRSVSKEKRKRSPKH RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRTPSRRSR SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSR SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRRSRSVVRRSFSISPVRLRRSRTPLRRRFS RSPIRKKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPPKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFFVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGGFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM
5783	1693	698	ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESTTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKITSESRSRAKKSSKSKS HRS\QTRSRSRS/RDRRRSSRSRSKSGGRRSVSKEKRKRSPKH RSKSRERKRKSSSRDNRKTVRARSRTPSRRSRTPSRRSR SVGRRSFSISPSRRSRTPSRRSTTPSRRSRTPSRRSR SVGRRSFSISPSRRSRTPSRRSTPSRRSRTPSRRSR GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGGFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ
5783	1693	698	ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESTTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRAKRSSKSKS HRS\QTRSRSS/RDRRRRSSRSKSGGRSVSKEKRKRSPKH RSKSRERKRKRSSSENDRKTVRARSRTPSRRSRTPSRRSR SVGRRRSFSISPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRRRSRSVVRRSFSISPVRLPRRRFTSRRSR RSPIRRKRSRSSEGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGGFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR PSGGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSL
5783	1693	698	ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESTTVL EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKITSESRSRAKKSSKSKS HRS\QTRSRSSKSKSKSSEHKSRKITSESRSRAKKSSKSKS SVGRRSFSISPSRRSRTPSRRSTPSRRSRTPSRRSR SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSR SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSR GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGGFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ

Deginning nucleotide location corresponding corresponding corresponding to first amino acid anino acid anino acid anino acid anino acid sequence of amino acid s	SEQ	Predicted	Predicted end	Amino agid cogment containing circol months
No: loucleotide corresponding to first amino acid residue of faist amino acid residue of anino acid sequence contemporary to first amino acid sequence contemporary to first anino acid sequence contemporary to first amino acid sequence contemporary to contemporary to compare the contemporary to contemporary to				Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid R-
Cortesponding	1			Glutamic Acid. FaPhenylalanina G-Glycina
Leleucine, M-Methionine, N-Asparagine, perioduc of instit amino acid residue of amino acid sequence along the sequence s				H=Histidine T=Tsoleucine K-Lucine
to first amino acid residue of amino acid amino acid sequence sequ		corresponding		L=Leucine, M=Methionine, N=Asparagine
### sequence and acid acid acid composed and acid sequence and acid sequence and acid sequence acid sequence (Codon, /=possible nucleotide deletion, %=possible nucleotide deletion, possi	į		amino acid	P=Proline, O=Glutamine, R=Arginine.
residue of amino acid sequence Sequence		amino acid	residue of	
Sequence Codon, /=possible nucleotide deletion,	ł	residue of	amino acid	
Sequence		amino acid	1	Codon. /=possible nucleotide deletion
LHGDIKSSNVIKEDFETIKICNGVSLDIDENNYTDPERCYT CTEPRKPKENZERSNUTTURADIFACHILMENMILST PIHILS NDDDDENTTPDSDFDDENYTALOTEPPIMBELDESYCKVIE LPSWCTNEDPKORPSAAHIVEALETDV TOODDENTTPDSDFDDENYTALOTEPPIMBELDESYCKVIE LPSWCTNEDPKORPSAAHIVEALETDV TOODDENTTPDSDFDDENYTALOTEPPIMBELDESYCKVIE LPSWCTNEDPKORPSAAHIVEALETDV TOODDENTTPDSDFDOLAYYAALOTEPPIMBELDESYCKVIE RMLTRATQY LAPLMANPEDPSVSRSTVRYPDNOTALOVQNDHVHL QDNYNLSFFFCATILLDGRITIGFKSICKLQCSSSGPTSINIPVKV GLSDAPVVVHRIQOIPNVRRTTYRYINVELOMSKITTHISAVEM VDSGCPESSKEMCENTEPVKT FLEEPOP*BROPPSSGS*LDPD PLADATYSCPTSLIFTEDOTKIALHLANGASTDDSAASKGGTL HAGLIVGILLULIVATAILUTYMYHHPTSAASIPFIERRPSK MPAMKERGSGEPANAVEVPUCKEGG IVSBCC GILSNITHAQNAAVELDPOPPVGHELBITVANGGFIFTORWINV GILSDAFVVVHRIQOIPNVRRTTYSTYGFSDSASBDLMVNTDOMEROXVIII AND PROPERVETOHNYTISRTYGFSDSASBDLMVNTDOMEROXVIII RMLTATQY LAPLMANPDPSVSRRSTVRYPDNOTALVVQNDHVHL QDNYNLGSFFFGATLLMORITFGVKSLLOVALDSTALVVQNDHVHL QDNYNLGSFFFGATLLMORITFGVKSLLOVALDSTALVVQNDHVHL QDNYNLGSFFFGATLLMORITFGVKSLLOVALDSTALVVQNDHVHL QDNYNLGSFFFGATLLMORITFGVKSLLOVALDSTALVVQNDHVHL QDNYNLGSFFFGATLLMORITFGVKSLLOVALDSTALVVQNDHVHL QDNYNLGSFFFGATLLMORITFGVKSLLOVALDSTALVVQNDHVHL QDNYNLGSFFFGATLLMORITFGVKSLLOVALDSTALVVQNDHVHL QDNYNLGSFFFGATLLMORITFGVKSLLOVALDSTALVVQNDHVHL QDNYNLGSFFFGATLTGVKSLLOVALDSTALVVQNDHVHL QDNYNLGSFFFGATLTGVKSLLOVALDSTALVVQNDHVHL QDNYNLGSFFFGATLTGVKSLLOVALDSTALVVQNSKITNISAVEM PLADATSCAPASGCSOPPTPTRRRFRAPGRTSKGHRQMYSCT- HAGLIVGILLULIVATAILVTVMYKHHPTSASIFFTERRSK APARLSGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS		sequence	1	\=possible nucleotide insertion)
GTEPHKPREAVERNOVI TOKADI FAPCILIJEMTILS PHINISE SPOKVIE BNDDDEDKTPDESD PDDEAVYALATEPP PIMBELDES YÇKVIE 1980 TRUEBYSTOHNYI STYGGTSSASRDLWWITONEKOKVKIE GILSHTHROARVALSTDE PYGHFLEETTVATGGFIYTGEVUH RILTAROYI APIMADHPPSVRINSTYYSPOSTASRDLWWITONEKOKVKIE GILSHTWOQARVALSTDE PYGHFLEETTVATGGFIYTGEVUH RILTAROYI APIMADHPPSVRINSTYYSPOSTASRDLWWITONEKOKVKIE GILSHTWOQI APIMADHPPSVRINSTYYSPOSTASRDLWWITONEKOKVKIE GILSHTVORI GILGHTUNDER I TIGVKRI PVLVIVO ISSTAHIPVKV GILSHTVORI GILGHTUNDER I TIGVKRI PVLVIVO ISSTAHIPVKV TPLPTLOPTROJPCVSSQIORNCSWCSKIGRCSGSTPRIRODM VDSGCESSKEMCRITERVENT YELEPOP *SROPP SSGS LPP BYDAVTSGPTSLPTSEDDTKI ALHLKUNGASTDOSAAKKGGTI. HAGILVOJI LILLIJ VATATAL LVTVVVWHINFDANAJ ET PERPSR MPAMKRRRGSGIPAYARVEPVGEKGG I VSSQC TRUENTHOODARVALSPPPPVGHFLES TTVATGFI YTGEVVH GILSHTHROARVALIG GIPCHVRST TYSTAMOP I YTGEVVH GILSHTHROARVALIG GIPCHVRST TYSTAMOP I YTGEVVH GILSHTHROARVALIG PROPPVGHENE TOWATGFI YTGEVH RILLATOYI APIMADHPSVRSTRISTYY PROMTALVORDHUMIL ONNY INGENEKVELH GILSHTWORI GIPCHVRST TYSTAMOP THE TOR TOWAT T				
NDDDDEDTFPESPDANIVELLETUV				
5784 2669 1388 PRVEREVENTENTY'S RIYGES DESARGLEWNIDONEKOKVKIE GILSNITHROARKNILS FOR PETUATORY STITUTES DESARGLEWNIDONEKOKVKIE GILSNITHROARKNILS FOR PETUATORY STITUTES STRIPLY RINGTHAN PETUATORY STATEMEN (LISNITHROARKNILS FOR PETUATORY STRIPLY WOMEN HE MILITARY FOR THE PETUATORY STRIPLY WOMEN HE MILITARY GILSNITHROARKNILS FOR PETUATORY STRIPLY WOMEN HE MILITARY GILSNITHROARKNILS FOR THE PETUATORY STRIPLY WOMEN HE MILITARY THE PETUATORY STRIPLY WOMEN HE MILITARY THE PETUATORY STRIPLY HE PETUATORY STRIPLY HE PETUATORY STRIPLY HE PETUATORY STRIPLY HE PETUATORY STRIPLY HE PETUATORY STRIPLY HE PETUATORY STRIPLY HE PETUATORY STRIPLY STRI		[[
GILENTHROARPULS FIDPPFGGHT.REITVATOGFITTEUR RMLTATOY I JAINAAD FIDE SUBBAST TAV FIDENGTALLY ON MONTHUSE RMLTATOY I JAINAAD FIDENS HAS TON TOWN FOR THE VIEW OF THE PROPERTY OF THE VIEW OF			į	
GILSNTHROARKNISTDPFYGHFILREITVATGGFTYTGEVER RMINTAQYIALMARPFDPSVSRINTVRYFNORTALVQMDHHVHL QDNNNIGSFTFQATLLMDGRIFGYKEIPVLVTQISSTNIPVKY GLSBAFVVVRIKQOIPVARREITYEHRVELQNSKITNISAVEM TPLETCLGPRICGECVSSGIGFNCSMCSKLQRCSSGFDRHROP VDSGCPESKEKNGENTEPVETI-LEDEPQTAELGPGPSSGS-LDP E/DAVTSGPFISLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL HAGLIVGALLULVIATAILUTVAWHHPTSAASIFFIERRPSR MPAMKERRGSGHANAEVERVEEWEGFIVSEQC PRVRPRVRTDHNYYISRITGPSDSASRDLWWIDGMEKOKVKIH GILSWTHRQAARVNLSFDFPFOHFLRSITVATGGFITTGEVW RMILTATQYIAPLMANEDSSVRNSTVRYFDNSTALVVQUNGVKIH GUNGNIGSFFTGATLIMDGRIFGYKELPVINTGISTHHPVKV GLSDAFVVVIRLQGIPNVRRTITTETHRVSLIMSKITNISAVEM TPLPTCLGFRIGGECVSSGIGFNCSCKLQRCSSGFDRHRQDW VDSGCPESSKEKNGENTEPVETI\FLEPPGOY-ERQPSSGS-LDV SGCPESSKEKNGENTEPVETI\FLEPPGOY-ERQPSSGS-LDV VDSGCPESSKEKNGENTEPVETI\FLEPPGOY-ERQPSSGS-LDV SAMWKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSQC #PAMKERRGSGHPAAVAEVERVEKEEFTVSGCBPMSSTSGGRPAAVE #PAMKISQRSSMSRRFLSCARPR***RGGLTVAARLPTWA- #PARTISQRSSMSRRFLSCARPR***RGGLTVAARLPTWA- #PARTISQRSSMSRRFLSCARPR***RGGLTVAARLPTWA- #PARTISQRSSMSRRFLSCARPR***PROGLTVAARLPTWA- #PARTISQRSSMSRRFLSCARPR***PROGLTVAARLPTWA- #PARTISQRSSMSRRFLSCARPR***PROGLTVAARLPTWA- #PARTISQRSSMSRRFLSCARPR***PROGLTVAARLPTWA- #PARTISQRSSMSRRFLSCARPR***PROGLTVAARLPTWA- #PARTISQRSSMSRRFLSCARPR***PROGLTVAARLPTWA- #PARTISQRSSMSRRFLSCARPR***PROGLTVAARLPTWA- #PARTISGRSSMSRRFLSCARPR***PROGLTVAARLPTWA- #PARTISGRSSMSRRFLSCARPR***PROGLTVAARLPTWA- #PARTISGRSSMSRRFLSCARPR***PROGLTVAARLPTWA- #PARTISGRSSMSRRFLSCARPR***PROGLTVAARLPTWA	5784	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDOMEKDKVKIH
ODMYNIGSTFOATILIMOGRI IFGYKSI PYLIVTQISSTHIPYKY GLSDAFVVUHIQQI PNYRRIT YEYHIVEKUKINTISAVEM TPLETCLQFNRCGPCVSSQIGPNCSWCSKLQACSGG DRERRODW VDSGCPESKKKKCENTPPUET, FLEPPQP'S ALSASIFPIERROSW WDSGCPESKKKKCENTPPUET, FLEPPQP'S ALSASIFPIERROSW HAMKERGSGHDAYABVEPVGEKEGI VSEQC 5785 2669 1388 PRVEPEVERRIBNYJSTRYTQSBASSRDLWYNIDQMEKDXVLIH GLINTHRQAARVNLSPDFPFGHFLREITVATGGFITTGEVVH RMITATQTIAPLANANDPSVSNNSTVEYPNOTALUVORDHUHL QDWYNLGSTFTGATLLIMDERI IFGYKSIFVLYTQISSTHIPVKY GLSDAFVVVHRIQQIPMYRRITITSYRFONDALUVORDHUHL QDWYNLGSTFTGATLLIMDERI IFGYKSIFVLYTQISSTHIPVKY GLSDAFVVVHRIQQIPMYRRITITSYRFONDALUVORDHUHL QDWYNLGSTFTGATLLIMDERI IFGYKSIFVLYTQISSTHIPVKY GLSDAFVVVHRIQQIPMYRRITITSYRFONDALUVORDHUHL QDWYNLGSTFTGATLLIMDERI IFGYKSIFVLYTQISSTHIPVKY GLSDAFVVVHRIQQIPMYRRITITSYRFONDALUVORDHUHL QDWYNLGSTFTGATLLIMDERI IFGYKSIFVLYTQISSTHIPVKY GLSDAFVVVHRIQQIPMYRRITITSYRFONDALUKUMIN UDSGCPESKEKNCENTEPVET\FLEPQTVSAGFSTSHORARKGGTI HAGLIVGILLIVLIVATALLIVTYMYHHPPTSAASIFFIERPROR WPAMKERRGSGHAVAZBUPGVEKEGGIVSGFOPBHRQDM FFDFAMKERRGSHAVAZBUPGVEKEGGIVSGFSIPDSAALKGGTI HAGLIVGILLIVLIVATALLIVTYMYHHPPTSAASIFFIERPROR WPAMKERRGSGAPASCEGSPEKEGGSFOPBHRQDM S*H*KRNLSQRSSSMSRFPLSCARPH***RQGLVVARRPPTWAK S*PH*KRNLSQRSSSMSRFPLSCARPH***RQGLVVARRPPTWAK S*PH*KRNLSQRSSSMSRFPLSCARPH***RQGLVVARRPPTWAK S*PH*KRNLSQRSSSMSRFPLSCARPH***RQGLVVARRPPTWAK S*PH*KRNLSQRSSSMSRFPLSCARPH***RQGLVVARRPPTWAK S*PH*KRNLSQRSSSMSRFPLSCARPH***RQGLVARRPPTWAK S*PH*KRNLSQRAFSGSSFT*PEMPTS*PGTLSTV**RA GGSTATAPPKRPPERNINPMMAB 5787 2 1460 MASAANSTSLABENOP\TOTALEBOSSSKGA/HKNFCRACL T\RCGSTATAPPKRPPENNNPMMAB ERKERROQLLITOVSTRAGGGSPRAGGSRPRNOLANV VENTERLOLVSTLGGBEDVOCHGEKIYFFCEDDEMQLCVVCR EAGEHATHTMFFLEDAA\APYREQIHKKLLEGQGSILAGLOSS GCGGGTTGABAGTARGHPAGPGSVSSTGATSTTTGHQGGDO SEGGGGTTGABAGTARGHPAGPGSVSSTGATSTTTCHQGGDO SEGGGGTTGABAGTARGHPAGPGSVSSTGATSTTTCHQGGDO SEGGGGGTTGABAGTARGHPAGPGSVSSTGATSTTTCHQGGDO SEGGGGGTTGABAGTARGHPAGPGSVSSTGATSTTTCHQGGDO SEGGGGGTTGABAGTARGHPAGPGSVSSTGATSTTTCHQUKLI FICCSKEKYRQLDHTNINLHYMMLLEHLUGLPTOLURGPTSULL FICCSKEKYRQLDHTNINLHYMMLLHILLIPANSHIYMTLGUFF UKKTURTURTSPPUNDHTSNIN		1	İ	
ODMYNIGSTFOATILIMOGRI IFGYKSI PYLIVTQISSTHIPYKY GLSDAFVVUHIQQI PNYRRIT YEYHIVEKUKINTISAVEM TPLETCLQFNRCGPCVSSQIGPNCSWCSKLQACSGG DRERRODW VDSGCPESKKKKCENTPPUET, FLEPPQP'S ALSASIFPIERROSW WDSGCPESKKKKCENTPPUET, FLEPPQP'S ALSASIFPIERROSW HAMKERGSGHDAYABVEPVGEKEGI VSEQC 5785 2669 1388 PRVEPEVERRIBNYJSTRYTQSBASSRDLWYNIDQMEKDXVLIH GLINTHRQAARVNLSPDFPFGHFLREITVATGGFITTGEVVH RMITATQTIAPLANANDPSVSNNSTVEYPNOTALUVORDHUHL QDWYNLGSTFTGATLLIMDERI IFGYKSIFVLYTQISSTHIPVKY GLSDAFVVVHRIQQIPMYRRITITSYRFONDALUVORDHUHL QDWYNLGSTFTGATLLIMDERI IFGYKSIFVLYTQISSTHIPVKY GLSDAFVVVHRIQQIPMYRRITITSYRFONDALUVORDHUHL QDWYNLGSTFTGATLLIMDERI IFGYKSIFVLYTQISSTHIPVKY GLSDAFVVVHRIQQIPMYRRITITSYRFONDALUVORDHUHL QDWYNLGSTFTGATLLIMDERI IFGYKSIFVLYTQISSTHIPVKY GLSDAFVVVHRIQQIPMYRRITITSYRFONDALUVORDHUHL QDWYNLGSTFTGATLLIMDERI IFGYKSIFVLYTQISSTHIPVKY GLSDAFVVVHRIQQIPMYRRITITSYRFONDALUKUMIN UDSGCPESKEKNCENTEPVET\FLEPQTVSAGFSTSHORARKGGTI HAGLIVGILLIVLIVATALLIVTYMYHHPPTSAASIFFIERPROR WPAMKERRGSGHAVAZBUPGVEKEGGIVSGFOPBHRQDM FFDFAMKERRGSHAVAZBUPGVEKEGGIVSGFSIPDSAALKGGTI HAGLIVGILLIVLIVATALLIVTYMYHHPPTSAASIFFIERPROR WPAMKERRGSGAPASCEGSPEKEGGSFOPBHRQDM S*H*KRNLSQRSSSMSRFPLSCARPH***RQGLVVARRPPTWAK S*PH*KRNLSQRSSSMSRFPLSCARPH***RQGLVVARRPPTWAK S*PH*KRNLSQRSSSMSRFPLSCARPH***RQGLVVARRPPTWAK S*PH*KRNLSQRSSSMSRFPLSCARPH***RQGLVVARRPPTWAK S*PH*KRNLSQRSSSMSRFPLSCARPH***RQGLVVARRPPTWAK S*PH*KRNLSQRSSSMSRFPLSCARPH***RQGLVARRPPTWAK S*PH*KRNLSQRAFSGSSFT*PEMPTS*PGTLSTV**RA GGSTATAPPKRPPERNINPMMAB 5787 2 1460 MASAANSTSLABENOP\TOTALEBOSSSKGA/HKNFCRACL T\RCGSTATAPPKRPPENNNPMMAB ERKERROQLLITOVSTRAGGGSPRAGGSRPRNOLANV VENTERLOLVSTLGGBEDVOCHGEKIYFFCEDDEMQLCVVCR EAGEHATHTMFFLEDAA\APYREQIHKKLLEGQGSILAGLOSS GCGGGTTGABAGTARGHPAGPGSVSSTGATSTTTGHQGGDO SEGGGGTTGABAGTARGHPAGPGSVSSTGATSTTTCHQGGDO SEGGGGTTGABAGTARGHPAGPGSVSSTGATSTTTCHQGGDO SEGGGGGTTGABAGTARGHPAGPGSVSSTGATSTTTCHQGGDO SEGGGGGTTGABAGTARGHPAGPGSVSSTGATSTTTCHQGGDO SEGGGGGTTGABAGTARGHPAGPGSVSSTGATSTTTCHQUKLI FICCSKEKYRQLDHTNINLHYMMLLEHLUGLPTOLURGPTSULL FICCSKEKYRQLDHTNINLHYMMLLHILLIPANSHIYMTLGUFF UKKTURTURTSPPUNDHTSNIN				RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL
GLSDAFVWHRIQQIPWRRRTIYEVIRVELQASSGTPRHROW UDSGCPESKEKMCENTEPVET\FLEPPQP*SROPPSSGS*LPP E/DAVTSQPPISJPTEDTRIALHLKUNGASTAEKKGGTI. HAGIUGILILVIIVATAILVTYWYHHPPSAASIPFIERPSR MPAMKERGGSHAPA & PEWERKEKGIIVEGE 5785 2669 1388 PRVRPRVRTDHNYYISRIYGPSDASRGLWVNIDQMEKDKVKIH GLISHTHKQARVNILSPPFFYGHTLARITVATGGFITTGSVNI RMLTATQTIALPLANKPDSVSKRSTVYYFDNOTALVVQMDEVHI- QDNYNLGSFTFQATLLHMGRIIFGYKSIPVLVTQISSTTHEVKV GLSDAFVVHRIQQIPWRRRTIYTYHRVELQMKKITNISAVEM TPLPTCLOFURCOPCVSSQIGTNCSWCSKLQRCSSGFDRHROW VDSSCCPESKEKKCENTEPVET\FLEPPQP*SRGSSLLPP E/DAVTSQPPTSLPTEDDTKIALHLKNORGSTDDSAABEKKGGTI. HAGLIVGILLULVIAVATILVTYWHHPPSAAFIPFIERPSR WPAMKERGSGHPAYABVEPVGEKEGIVSGC 5786 2532 1674 SYKLPABERRASSGOPPTFERERPRPAFGETSRGHRPQW*SGTF APPPARASTVSPASLELPFRRRFAFGHTSGHRPQW*SGTF APPPARASTVSPASLELPFRRRFAFGHTSGHRPQW*SGTF APPPARASTVSPASLELPFRRRFAFGHTSGHRPQW*SGTF APPPARASTVSPASLELPFRRRFAFGHTSGHRPQW*SGTF APPPARASTVSPASLELPFRRRFAFGHTSGHRPQW*SGTF APPPARASTVSPASLELPFRRRFAFGHTSGHRPQW*SGTF APPPARASTVSPASLELPFRRRFAFGHTSGHRPQW*SGTF APPPARASTVSTABSELSSSMERPRPTP*PRRSGGRSTV*RT GGSTATAPEKRPPRRNNPMMAB SLAPSSRIPERGRPCCVMIPSRWPASFRRNPNDFMAB SLAPSSRIPERGRPCCVMIPSRWPASFRRSGGSTFRFCALT*TYSGGT GRAMMTCTFRWTATTWSARASSRENMPTP*WRSGGSTTV*RT TGGSTATAPEKRPPRRNNPMMAB CRAMMTCTTRWTATTWSARASSRENMPTP*WRSGGSTTV*RT GGSTATAPEKRPPRRNNPMABA SPELACSFCQAAOKSQSLSSGRSTR*PERRSGGSTTV*RT GGSTATAPEKRPPRRNNPMABA SPELACSFCQAAOKSQSLSSGRSTR*PERRSGGSTTV*RT TGGSTATAPEKRPPRRNNPMABA SPELACSFCQAAOKSQSLSSGRTR*PERRSGGSTTV*RT GGSTATAPEKRPPRRNNPMABA SPELACSFCQAAOKSQSLSSGRAFT*PERRSGGSTTV*RT TGGSTATAPEKRPPRRNNPMABA SPELACSFCQAAOKSQSLSSGRAFT*PERRSGGSTTV*RT GGSTATAPEKRPPRRNNPMABA SPELACSFCQAAOKSQSLSGGATG*PRRSGGSTTV*RT TGGSTATAPEKRPPRRNPMTMABA SPELACSFCQAAOKSQSLSGGATG*PRRSGGSTTV*RT TGGSTATAPEKRPPRRNPMTMABA SPELACSFCQAAOKSQSLSGGATG*PRRSGGSTTV*TT*RQGGTGATAPEKRPTQGSTLLAQLES QDGDILRQRBPDLLVAGGTGSTALLLEEQGSTLLAQLES DQGATLAGATAPEKRPTATATATTTTTATATTTTTTTTTTTTTTTTTTTTTTT	1			
DISSCRESKENCENTEPVET\FLEPOQ**ERQPPSSSS-LPP B/DAVTSQFPSLPTEDDTKLAHLKUNGASTDSAAEKKGTL HAGLIVGILILVLIVATAILVTYYMYHPPSAASIPPIERRPSR MPAMKERGGSCHPAYAEVEVEVEKEGITVSGTS MPAMKERGGSCHPAYAEVEVEVEKEGITVSGTS MPAMKERGGSCHPAYAEVEVEVEKEGITVSGTS MPAMKERGGSCHPAYAEVEVEVEKEGITVSGTS GILSNTHRQAARVALSPOPPFYGHFLREITVATGGPITYTGEVH RMITATQTITAPLAMMPDSSVRNSTVEYPINGTALVVQMDEVHL QDMYNLGSFTCATLLIMGRITGYKRIFVLYTQISSTHPVEV GLSDAFVVHIGQIFBVRRGTITYSHTWELDGMSKITNISAVEM TPLPTCLOFURGOPCVSSQIGENCSWGSKLQRCSSGFDRRQDW VDSSCPESKEKKCENTEPVET\FLEPPQP**ERQPPSSGS*LUP B/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAABKKGTI. HAGLIVGILLIVLIVATAILVTYMYHPHPSAASIFFIERRPSR WPAMKERROSCHPAYAEVEPVCEKEGITVSGC \$786 2532 1674 SYKLPABERRASSGQPPTFTERRFPAFFGRTSGHRPQW*SGTF APRPARASTVSPASLLPYPAGRCGSSRPSAACSTEPRC*SILM* S*H*KRNISQRSSMSRPBLSCAPRH***ROGLTVARRPPT**AK S*PLACSTCOAAOKSGSLSSGSTR*PERRSFRCHRPQM*SGTF APRPARASTVSPASLLFYPAGRCGSSRPSAACSTEPRC*SILM* S*PLACSTCOAAOKSGSLSSGSTR*PERRSPRCHPDGM*SGTF APRPARASTVSPASLLFYPAGRCGSSRPSACSTFRPC*SILM* S*PLACSTCOAAOKSGSLSSGSTR*PERRSPRCHPDGM*SGTF APRPARASTVSPASLTAPPERPRNNPMAB* 5787 2 1460 MASAASVTSLADEVNEY**COGTLIKEAGSLSNGGT/KHNFCRACL T\RYCGIS\TATAPPERPRNNPMAB* SH*KRNISQLSTUTOSTRRQOVICHGEKITYFTGEDDEMOLCVVCR EAGEHATHTWRIFLEDAA\APYREQIHKCLKCLIKERESIQSIGS RENKRMOVILITOVSTKRQOVICHGEKITYFTGEDDEMOLCVVCR EAGEHATHTWRIFLEDAA\APYREQIHKCLKCLIKERESIQSIGS RENKRMOVILITOVSTKRQOVICHGEKITYFTGEDDEMOLCVVCR EAGEHATHTWRIFLEDAA\APYREQIHKCLKCLIKERESIQSIGS GCGGILRQRDEPDLLVAGEICEFSALIEELEEKMERPARABLITD IRSTLIRCETRIKCRPUAVSPELGQRITOPPQOALPLCRBEMKWP LEKLCFELDVBPAHISLDPQTSHPKLLLEEDHORAOPSVKNOS PDDVQRKGELALPREGVWAVRLAMOFVSALGSFP\TXILLEEDG GCGSTLSKVWINGVSTYNOVALLANGGSCSTVGVVS SKNRSSALAEVHLAVWRLISVFYNSCTKGSGSSSSISSSSISS APAVALASSGQATTQSKSSTKKSKKREKEKCGGTSGSQEDQ LCTALVNQUMKFANGELLQFILGCHESKLYFTGLRASVTA SPOSALQYDTLISIMENIKACAETAAQRTINGQFPCIRADSVIJ FILLOVSFLVOBERSPVLUCHILSIKOTHVSKLIPUKRLEPQII IKRSSKSOGGELLDLIMMSSIPPLAYGKKAAGGNSSAS SSPAPVAASSGQATTQSKSSTKKSKKREKEKCGGTSGSQEDQ LCTALVNQUMKFANGELLQFILGELSIKSUTSTTTGLOVKLII IKRNSKSOGGELLLDLIMMSSIPPCILLESIKSUTSTTTGOVKLII GSSTISKVTVKIGGLKERE				
### PARTY SOR PTSLIP TEDDIK TALHLIKDNGASTIDDSARKKGSTI. HAGLIVGLILVLIVATA LUTVYMYHHIPTSAASIFFIERPSE WPAMKERGSGHPAYAEVEPVGEKEGFIVSEQC PRVERERGENTYYTSTYGTYSDSASRDLWVNIDQMEKDKVKIH GILSNTHRQAARVALSP PPFFYGHERET TVATGSFITTGSVH RMLTATQYLA PLANAED PSPSYGHERET TVATGSFITTGSVH RMLTATQYLA PLANAED PSPSYGHERET TVATGSFITTGSVH RMLTATQYLA PLANAED PSPSYGHERET TVATGSFITTGSVH RMLTATQYLA PLANAED PSPSYGHERET TVATGSFITTGSVH RMLTATQYLA PLANAED PSPSYGHERET TVATGSFITTGSVH RMLTATQYLA PLANAED PSPSYGHERET TVATGSFITAVVKY GLSBAFVVVHRIQQI SIVVERRIT TYSHRVELQMSKITHISAVEM TPLPTCLOFINGGGVCYSGIGFINGSGCGSGFORHOOM VDSGCPESSKEKMENTE PVET FLEPPGP PERQPSGSS 1 LPP E / DAVTSGFPTSLPTEDDIKTALHLENDASTDSAAEKKGGTL HAGLIVGLILLVLLIVATALLUTVYWHHPTSAASIFFIERPSE WPAMKERRGSGHPAXAEVEPVGSEGGFIVANASTDDSAAEKKGGTL HAGLIVGLILLVLLIVATALLUTVYWHHPTSAASIFFIERPSE WPAMKERRGSGHPAXAEVEPVGSEGGFIVASSTSTABHREQM*SSTP APPPARATTYSPASFLPKPRAGKGSRFRSACSTFFGFS SLAMM S*H*KENLSGRSSMSRESHEGGRHPAPAGFTSRGHREQM*SSTP APPPARATTYSPASFLPKPRAGKGSRFRSACSTFFGFS SLAMM S*H*KENLSGRSSMSMSRESHEGARPH**RGGLTVAARLPTWAK SPILACSFCOAACKSGLSSGSSTR**PERMSFRP, SPDENDALT SLAPSSRP, PGREPQCTHU PSRWPASFPAPTTT**PPTSSPST GRSMMTCPTRWTATWSARASSRPRWWPTP*WRPSGRLST**RR TGGSTATATPFERPFRWMPMAE 5787 2 1460 MASAASVTSLABENOFP\TCGGTTKRAGSLSNGG/KKNFCRACT TAYCSIE PGRPQTALPT**CPTCACT TAYCSIE PGRPQTATTY**CPTCACT EAGENSTTMR*FLEDALA*, DAYBGOHIKCLIKERBESIQEIQ RENKRMQVLLTQVSTKRQQVISEFAHLEKFLEEQGSILLAQLES QCGDTLIRQRBEFFILVAGEICRFSALISELEEREKREPRELLTD IRSTLIRCETEKCREVAVSPELIGGRIBOPFQQALPLQRBEMMF LEKLGFELDVSPAHALSEDPOTSIPKLLEBENGRAPFILLEDGE ROWSLSDSFALSSESSASGATAEGHPAGGSUSSTSTAISTTTCHGGGG SCGGGGTTEGDVHTSNELMWVRULLERLQCTLPCATGGLEF HTTSSFPMBAFFILLATORGHTWVSTULLERUNGQNF SCGGGGGTTEGDVHTSNELMWVRULLERUNGQNF SCGGGGGTTEGDVHTSNELMWROUNLERUNGVPATGLLEF HTTSSFPMBFFILLQVVGHAADVFEATYTGLLTEMVLRLPYQI KKITTITNSRIPPVFUNGWFTHSLIKMVRGCHKKDDSVLI FLIGSKEKKYRGLBCHTLIGS HYNGIKSKSSCRSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS				
### HAGLIVGILIUNILVATAILUTYYMYHHTESASIPFIERRESE #### PANKERRESGCHAYARUSPOCEKEGF 1950 5785 2669 1386 PRVPERVETDINYYISTYGEDSASRDLWVNIDQMEKDKVKIH GILSNITHRQAARVALSPDEPFYGHFIRBITVATGGTITYGEVYH RMLTATQYIJALMANDEDSVERNISTVAY PENGTALVVQMDIVHL QDMYNLGSFTQATLIMDGRII FRYKEI FVLVTQISTINHDVKY GLSDAFVVVHIQQI PIVMERTIYEHYHQUMSKITNISAVEM TPLPTCLQFNRCGFCVSSQIGFNCSKCSKLQRCCSSGFDRHQDW VDSGCPESSEKKMCENTE PVENT\FLEEPG ERQPESGS1 LPP E/DAVTSQPPTSLDTEDDTKIALHLKDNGASTDDSABKKGGTI. HAGLIVGILLULIVLATALUTVYMYHHPTSAASIFFIERFSR WPANKFRRGSGHPAYAEVEPVGEKEGFIVSEQC 5786 2532 1674 SYKLIPABERRASSESGPPTPTRRWPARGRCSRTRASSIFFIERFSR WPANKFRRGSGHPAYAEVEPVGEKEGFIVSEQC 5786 SYKLIPABERRASSESGPPTPTRRWPARGRCSRTRASSIFFIERFSR WPANKFRRGSGHPAYAEVEPVGEKEGFIVSEQC 5786 SYKLIPABERRASSESGPPTPTRRWPARGRCSRTRASSIFFIERFSR S*#*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVARALPTWAK S*#*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVARALPTWAK S*#*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVARALPTWAK S*#*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVARALPTWAK S*#*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVARALPTWAK S*#*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVARALPTWAK S*#*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVARALPTWAK S*#*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVARALPTWAK S*#*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVARALPTWAK S*#*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVARALPTWAK S*#*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVARALPTWAK S*#*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVARALPTWAK S*#*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVARALPTWAK SAPLARALSGRSSSMSRRPLSCARPHR**RGGLTVARALPTWARALPTATLEGTER FUNGKEKKYRGERGLTRASSVTANALPTATLARALPTATLARALPTATLARALPTATLARALPTATLARALPTATLARALPTATLARALPTATLARALPTATLARALPTATLARALPTATLARALPTATLARALPTATLARALPTATLARALPTATLARALPTATLARALPTATLARALPTATL			ļ	
S785 1388 PRWRPRYGRUNTYGRY UPGEDGASRUWNIOQMEKOKVKIH GILSNTHRQAARVALS PDPFFYGHPLRE ITVATGGFTYTGEVVH RMITATQYITAPLAANTUS PDPFFYGHPLRE ITVATGGFTYTGEVVH RMITATQYITAPLAANTUS PDPFFYGHPLRE ITVATGGFTYTGEVVH RMITATQYITAPLAANTUS PDFFFYGHPLRE ITVATGGFTYTGEVVH RMITATQYITAPLAANTUS PDFFFYGHPLRE ITVATGGFTYTGEVVH GLSDAFVVVHRIQQIFNVERRITIFYHRVELQMSKITHISAVEM TPLPTCLGPNRCGGCVSSGIGFNCSNGCSGFDRHRQDW VDSGCPESSKEKMGNTEPVET\FLEPFQP ERQPFSSGS LDP E/DAVTSGPPTSLPTEDDFXTALHLENDKASTODSAARKGGTL HAGLIVGILLIVLIVATATLUTVYWHHPTSAASIFFIERRPSR WPAMKFRRGSGHPAYAEVEPVGEKRGFIVSBQC SYKLPAARERASSGSQPPPTPTRRRWPAGRTSRGHHPQWFSGTP APRPPARSTVSPASPLPKFRAGRGSRFRSAGSTFFFS SLN*M SYH-KRNINGORSSMSRSHELGCAPPHF** RGGITVAARLPTWAK SPHLACSFCOAAOKSGLSGSGSTR** PERMSFRP\SPDRNPATS SLAPSSRP\FYRRGPRCASSTR** PERMSFRP\SPDRNPATS SLAPSSRP\FYRRGPRNNPMMAB SH*KRNINGOLITSFRHALTPTT***APTSSGST GRSMATCPTRWTATPWSARASSRRWMPTP*WRPSGRLSTV**RA TGGSTATAPFKFPRNNMPMMAB SH*KRNINGOLITSTHILGSFRNASSTRING/HKNFCRACL T\RYCEIP\QPD\LEESP\TCP\LCKEPFR\SFRPNOLANV VENIBLALUSTIGLGEBEVCOCHEGKITYFFCDDEMQLCVVCR EAGHATHTMFFLEDAA\APPRIGHKCLKCLIKEREBIQBIQS RERNEMOVILATOSTRINGOVISSFAALLEREQGSILLAQLSS QDGDILLQRDFFDLLVAGGICRFSALIEELEKNERPARBLLTD IRSTLIRCETIKKRVAVSFBLEDQGSILLAGDSSTALIEELEKNERPARBLLTD IRSTLIRCETIKKRVAVSFBLEDGGSILDSHORAQFSYKWONS PDNPGRFDRATCVLAHTGITGGHTWVVSILLAGGSCTVGVVS EDWQRKGGLERPESUVAVALAMGFVSALIEEQGSILLAGLSS DEWQRKGGLERPESUVAVALAMGFVSALIEGQGITLAGLSCMCKOV SKNIRGSSFALSS SGSSFALSS				E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL
1388 PRVPPRVRTDINYTISTIGGESDASROLWWITGGEROKWKHT GILSNITHGARRWILSPPPPYGHIFLRITATGGITYGEVUH RMLTATQYIAPLAMANFDPSVSRISTVRYFDNGTALVVQMDIVEL QDWNIGSTFQATLLMOGRIIFGYKEIFVLVTQISSTHHVKK GLSDAFVVVHIQQIPWKRTITYEHKVELQMSKITNISAVEM TPLPTCLOFNRCGFCVSSQIGFNCSSCSKLQRCSSGFDRHQDW VDSCCPESSKKMCENTEYVETYTFLEPPGRPSSGS-LPP E/DAVTSQFPTSLPTEDDTKTALHLKDNASTDDSARKKGGTL HAGILVGILLULIVATALUTYWMYHHPTSAAJIFFIRRPSR WPAMKFRRGSGHPAVAEVEPVGEKEGFTVSQC SYKLPAAERRASCSQPPTPTRRRWPAFGTSRGHRPQM-SGTF APRPARATVSPASELPKPRRGRGSGRFRASCSTFRPC-SLIMM S-1+ KRNISQRSSSMSRRPLSCARPHR-*RGGITVARALPTWAK SPPLACSTCQAAQKSGSLSSGSTR+PEMPSGCTSTFPC-SLIMM S-1+ KRNISQRSSSGSRT+PEMPSGCTSTFPC-SLIMM S-1+ KRNISQRSSSGSRT+PEMPSGTLSTV+RR SPPLACSTCQAAQKSGSLSSGSTR+PEMPSGCTSTFPC-SLIMM S-1+ KRNISQRSSSGSRT+PEMPSGTLSTV+RR TGGSTMTCTTRTATTPWSARASSPRNWPTPT-TP*PTTSSFGST GRSMMTCTTRTATTPWSARASSPRNWPTPT-TP*PTSSFGST GRSMMTCTTRTATTPWSARASSPRNWPTP-TRSGGTLSTV+RR TGGSTATAPPKRPPRMWPMAB SLAPSSRP-PLACTFTATTPWSARASSPRNWPTP-TRSGGTLSTV+RR TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMULAWA TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMULAWA TGGSTATAPPKRPPRMULAWA TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMULAWA TGGSTATAPPKRPPRMULAWA TGGSTATAPPKRPPRMULAWA TGGSTATAPPKRPPRMULAWA TGGSTATAPPKRPPRMWPMAB TGGSTATAPPKRPPRMULAWA TGGSTATAPALLSGATAPPKRPPRMULAWA TGGSTATAPALLSGATAPPKRPPRMULAWA TGGSTATAPALLSGATAPPKRPPRMULAWA TGGSTATAPALLSGATAPPKRPPRMULAWA TGGSTATAPALLSGATAPPKRPPRMULAWA TGGSTATAPALLSGATAPPKRPPRMULAWA TGGSTATAPALLSGATAPPKRPPRMULAWA TGGSTATAPALLSGATAPPKRPPRMULAWA TGGSTATAPALLSGATAPPKRPPRMULAWA TGGSTATAPALLSGATAPPKRPPRMULAWA TGGSTATAPALSGATAPPKRPPRMULAWA TGGSTATAPPKRPPRMULAWA TGGSTATAPPKRPPRMULAWA TGGS	i	1.		HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
GILSNTERQARVNLS PDPPFYGHFLRE ITVATGGF I YTGEVVH RMITATQY TIAPHANFD SSVSRNSTVRY PDNOTALVVQMORHEL QDNYNLGSSTFQATLMORGH I TGYKE I PVLVTQLSSTHIPVKV GLSDAFVVVHRI QQI PNVRRRIT I STYHRVELQMSKITHI SAVEM TPLPTCLQNRIGGFCVSSQ1GFNCGWCSKLQRCSSSFDRHQDM VDSGCPESSKEMCENTEVPT'\FLEPPQO'* ERQPPSGS\$* LPP B /DAVTSQFPTSLPTEDDTKIALHLKUNGASTDGAARKGGTL HAGLIVGILILVILVATAILVTVYWYHHPTSAASIFFIERPSR WPAMKFROSGHPAYAEVERVGEKGGT IVSBQC 5786 2532 1674 SYKLPAAGERASSGCSQPFTTRERNPARGRTSRGHRPQM*SGTP APRPPARSTVSPASFLD KPRAGRCGSRPSACSTFPC*SIN*M S*H*KRNLSQRSSMSRFRPLSCAPPH*A*** RQGITVAARLPTWAK SPPLACSFCQAAQKSQSLSSGST** PERMSFRP,SPGDNPATP SLAPSSRP,PKGRPQCTW*I PSEMPASPPTTT*APPTSSPGST GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA TGGSTATAPPKGFPRWNDMMAB 5787 2 1460 MASAASVTSLADEVNCP*ICQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LESSP\TCP*LCKEPFP\GSFRPNWGLANV VENIERLGLVSTLLGLEGEDVCQHEGER*JFECDGVILGAGLCVCC EAGEHATHTMFLEDAA\PYREQIHKCLKCLIKEREIQEIGS RENKEMOULTOVSTKRQOVISEPAHLSEEQOSILJAQLES QDGDILRQRDBFDLLVAGEICRFSALIEELEEKNERPARBLLTD IRSTLIRCETRKCKEVAVSPELGGRIRDFQQQALPLQRBMMFF LEKLCFELDFPAHAISLDPGTHHFKLHAGGSCTVGVVS EDVQRKGELRLPPESGWAVAVELAGGGTCVGVVS EDVQRKGELRLPPESGWAVAVELAGGSTCVGVVS SEDVQRKGELRLPPESGWAVAVELAGGSTCVGVVS EDVQRKGELRLPPESGWAVAVELAGGSTCPTVGLIKLEGD SGGSSFSLSS 15788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SGGSEGETETECDEVTKSALLBLALLELGTLPQLRNWGKV SKNRBSALNEVHLVVMRLLSVFMSRTKSGGNSSICESSLISS ATAAALLSGGAVYCLHVKSLLEYWSKSQONDEBPVATSGLKP HTTSSPPMSFFILRQTVKGHAADVFRATYGLKFLLVPQI KKITDTNSELPSPPFHANFYFLSEYLMIQQTPFPVRQVKKLL FICGKEKYRQLRDLHTLDS\HVGIKKLLEGQGIFLRASVVTA SPQSALQVDTLISHMHKACABIAAQRTINNQKCIKDDSVVTA SPQSALQVDTLISHMHKACABIAAQRTINNQKCIKDDSVVTA SPQSALQVDTLISHMHKACABIAAQRTINNQKCIKDDSVVTA SPQSALQVDTLISHMHKACABIAAQRTINNQKCIKDDSVVTA SPQSALQVDTLISHMHKACABIAAQRTINNQKCIKDDSVVTA SPQSALQVDTLISHMHKACABIAAQRTINNGKCIKDDSVTA LTPROTEKKLKSYSQKAVEILRTQNHILTUNTNRTNORSVVGONGTSGSGGD CCTALVALQUINFADMETLIQFLICFLISKSVKORGETSGGSGDD LCTALVALQUINFADMETLIQFLICFLISKSVKORGETSGGSGDD CCTALVALQUINFADMETLIQFLICFLISKSVKORGETSGGSGDD OGYLESSPCLUCHMPSVPFCYTKLSI INVDITYTTSGLVVEL GSHTIS				WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
RMLTATQYTAPLMANFDPSUSRNSTWY FUNDTALVOMORIVEL ODNYNLOSS FTPOATLANDREIT FGYKE I PVLVTOISSTMHPVKV GLSDAFVVVHRIQQIPNVRRRTIYEYHRVSLGMSKITHISAVEM TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHQDW VDSSCCPESKEMCEMSTEPVET\TLEPSVET REQUESTS LIPE E/DAVTSQPFTSLPTEDDTKTALHLKNDGSTDDSAABKKGGTL HAGLIVGLILULVLVATALVATUNYMPYBAASIFPTERRPSR WPAMKFRGSGHPANAVERVGEKSGFIVSGQC 5786 2532 1674 SYKLPAARRASGCGPPTPTRRWPAPGRTSRGHPQM*SGTP APRPPARSTVSPASPLD KRRAGRGSRPRSACSTRFQC*SLIMM S*H*KRNLSQRSSSMSRRPLSCARPHK**RQCTAVARLPTWAK S*H*KRNLSQRSSSMSRRPLSCARPHK**RQCTAVARLPTWAK S*PHACSFCQAAQKSGJSSGSTF*PERPSSPPSTTPTAPTSSPGST GRSMMTCPTRWTATPWSARASSRPRNWPTP*WPSGRLSTV*PA TGGSTATAPPKRPTATWWNMAB 5787 2 1460 MASSASVTSLADEVNCP\TCQGTLKEAGSLSNGG/HKNFCRACL T\RYCSIP\GPQP\LESSP\TCT\LCKEAPFPP\GSFRPWQLAVV VENIELQLVSTLGLGBEDVCQFHGEKIYFFCEDDEMQLCVVCR EAGEHATHWRFLEDAA,APYREQIHCKCLKEREEIQEIQS QCGDTLRQRBEFDLLVAGEICGFSALLEELBEKNREPARBLLTD IRSTLIRCETTRKCRKVAVSDELQGRICKLCKLKEREEIQEIQS RENKRMQVLLTQVSTKRQQVISBPAHLRKFLEEQQSILLAQLES QCGDTLRQRBEFDLLVAGEICGFSALLEELBEKNREPARBLLTD IRSTLIRCETTRKCRKVAVSDELQGRICDLAGHGSGTVGVVS EDVQRRGELRLRPEGGWAVRLANGFVSALGSFP\TRLTLEQP RQVRVSLDYZVGWAVFTNAVTREITYTFTASFTRKVIPFFGLMG SGSSFSLSS DAPPQAFDRATCVLAHIGT GTGGHTWYDLAHGAGGFYKNQGS EDVQRGGLRLRPEGGWAVRLANGFVSALGSFP\TRLTLEQP RQVRVSLDYZVGWAVFTNAVTREITYTFTASFTRKVIPFFGLMG AIFWAVILMITTDLGGDEKKGALDNILSQLLABLGMKROV SKNERSALNSVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCHVLKSLLEYWKSQONDEBVATSQLLKP HTTSSPPDMSFFFLRQYVKGRAADVFEATTQLITEMVLRIPYQI KKTIDTNSRIPPVFPHSNFFFLSTWINGOPFFVRQVKKLL FIGGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVEBGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAVAASSGQATTQSKSSTKKSKKEEKEKKDGETSGSBGD LCTALVNQLNRFADKSTLIQFTLFCFLLESNSSVWOMAHCLTTH IYRNSKSQOELLLDLMMSIMPELPAYGRKAAQPVOLLGFFSLKK TPOTEKKLKZYSGKAVELLERQOHITHMSNITYMTLSCLUFF DGYYLESDPCLVCNNPSVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGGLKRRMVRTINYYNNRTVAGIVELKENRF RWHKAKKVQLTPCGTEVKLDLPPLINYSNLMIERADPTENNYAS	5785	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH
ODNYNIGSTTFOATLLNDGRIITGKELIPULTUSSTNHEVKY GLSDAFVUVHRIQQIPWRRTITYETHVSLQMSKITHISAVEM TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW VDSGCPEBSKEKMCENTEVET\FLEPPQP*EKPPSSGS*LPP E/DAVTSGPTSLFTEDTUKTLAHLKNOGASTDDSAARKKGGTL HAGLIUGILILVILVATAILVTVMYHHPYSAASIFFIERRFSR WPAMKFRGSGHPAYABVEPVGEKEGFIVSEQC 5786 2532 1674 SYKLPAABERASGCOPPTPTERRFPAGGTSRGHRPQM*SGTP APRPPARSTVSPASFILVENPAGGCSRPRSACSTFPPC*SLN*M S*H*KRNLSQRSSSMSRRPLSCARPHS*ROGTFTV*PATSTSGST APRPPARSTVSPASFILVENPAGGTSRGSRPRSACSTFPPC*SLN*M S*H*KRNLSQRSSSMSRRPLSCARPHS*ROGTFTV*PATSSGST GRSMMTCPTRWTATPWSARASSRPNNWFT**WRPSGRLSTV*RA SPELACSFCQAAQKSGSLSSGSST**PERNSFTPSPTT*APTSSGST GRSMMTCPTRWTATPWSARASSRPNNWFT**WRPSGRLSTV*RA TOGSTATAPPRFPRFRNNMPMAM 5787 2 1460 MASASVTSLADEUNCP\TCQ*LCKEPFRP\GSFRPNWGLANV VENIERLQLVSTIGLGEEDVQCHGERIYFFCEDDEWQLCVVCR EAGEHATHTMFFLDAA\APYKEQIHKCLKCLIKEREIQEIQS RENKRWQVLLTQVSTKRQVISEFAHLEEQGSILLQLES QDGDILRQRBFPDLLVAGEICFSALIEELEEKNREPPARBLLTD IRSTLIRCGTRKCKEVDVASPLGGGTREPQQALPLQRBMMP LEKLCFELDYBBAHISLDPOTSHPKLLLSEDHQRAQPSYKHQNS PDNPQRFPATATCVLAHTGITGRRTTWVSIDLAHGGSCTVGVVS EDVQRKGGLRLRPEEGVWAVALANGEVSALGSFP\TRILIKEOP RQVRVSLDYEGWVTFTNAVTREPIYTFTASTTRVIPFFGLMG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPADPGSVSSTGAISTTTGHQEGD SGCGGGGTEGOVHTSNRTHMVRILLURLQTLPQLRNVGVR AIPHQVILMLTTDLDGDEKNKGALDNLLSQLIAELGMDKRDV SKNNERSALNSVHLVVMRLLSULTGVHKSLEYWKSQONDEBVATSQLIKP HTTSSPPDMSPFFLRQYVKGHAADVFBATTGLLFRULLRPYQI KKITDTNSIPPYPHDASFYFLSGYLMTQQTPPVRQVKELL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQTDTLISLMSHLKACABTAAQRTINNQKRCLKDDSVLY FLLQVSFLVUDGUSSPLULGLISCALCGSKVLRALAASSGSSSAS SSPAVAASSGQATTQSKSSTKKSKKEKEKEKDGTSGSGBDQ LCTALVNQLNRFADKSTLIQFLICFLICLSCLECTSSSVWOGHCTIGH IYRNSKSQOELLLDLMMSIPPELPPAGRKAAQPVDLLGTFSLUFFE DGYYLESDPCLVCNNPEVPFCYKLSSIKVDTRYTTTQQVVKLI GSSTISKVTVKIGBLKRYSDKAVELLERQDHILTHHINFNONINTYTLSCLUFF DGYYLESDPCLVCNNPEVPFCYKLSSLKVDTRYTTTQQVVKLI GSSTISKVTVKIGBLKRYMDVTILNYNNRTVGALVELKNRPA			•	
GLSDAFVVHRIQQIPNIRRITIYEHRIVELQMSKITMISAVEM TPLETICQFRINGSPCVSSQIGFNCSNSLQDCSSGPDRHQDW VDSGCPESKEKMCENTEPVET\FLEPPQP+ERQPPSSGS*LPP E/DAVTSQFPTSLPTEDDTKIALHLKUNGASTDDSAABKKGGTL HAGLIVGILILVLIVATAILVTYMYHHPTSAASIFPIERPSR WPAMKFRGSGHPAVAEVEEVGEKEGFIVEGC 5786 2532 1674 SYKLPAAERRASSGOPPTPTRENDGTSRGHRPGM*SGTP APRPPARSTVSPASPLPKPRAGRCGSRPRAGCTSFRPC*SLN*M S*H*KRNLSQRSSSMSRPLPLSCARPHR**RGGLTVAARLPTWAK S*PLACSFCQAAQKSGLISSGSTSP*PAPGTTSRGHRPGM*SGTP SLAPSSRP/PKGRPCTWIPSRMSPRPSPTAPPTT*APTSSPGST GRSMMTCPTRWTATWASRASSRPMTPP*WRPSRGTLSTV*RA TGGSTATAPPKRPPPNNNPMAE 4 TGGSTATAPPKRPPPNNNPMAE 5787 2 1460 MAGASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\CP\LCEPPR\GSFRPNMGLANV VENIELQLVSTLGIGBEDVCQEHGEKIYFFCEDDEWQLCVVCR EAGHAHTHMR:LDBADA\PAPYRRGHCKKCLILKEREIQEIGS RENKRMQVLLTQVSTLGIGBEDVCQBHGEKIYFFCEDDEWQLCVVCR EAGHAHTHMR:LDBADA\PAPYRRGHCKKCLILKEREIQEIGS RENKRMQVLLTQVSTLGIGBEDVCGHGRKIFFQQALPLQRBMKHF LEKLCFELDYBPAHISLDPGTSHPKLLISEDHQRAQPSYKWQNS PDNPQRPDATCVLAHTGITGGHTWYSIDLAGGSCTYGVVS EDVQRGGELRLPEEGWAVRLAWGFVSALSSF\TALITLEGDP RQVSVSLDYEVGWVFTINAVTREPIYTFTASFTRKVIPFFGLNG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGGSVSSSTGAISTTTGHQEGDG SEGEGETEGGVHTISNRLHWRIMLLERLLQTLPQLRNVGNF AIPYMQVILMITTDLDGEDEKKKGAIDNLLSQLIAELGMBKKDV SKINERSALNEVHLVVMRLLSVFMSRKKSSKSSICESSSLISS ATAAALLSGAVDYCLHVLKSLLEWKSQCNDEEPVATSQLLKP HTTSSPPMSFFFLRQVVKGHAADVFEAYTQLIEWHLRLPVQI KKITDTNSRIPPPVPDHSWFYFILSEVLMIQQTPPVRQVKLLL FICGSKEKYRQLVDTLISLMEHLKACABIAARGLEGGIFLARSVVTA SPGSLQVDTLISLMEHLKACABIAARGLEGGIFLARSVVTA SPGSLQVDTLISLMEHLKACABIAARGLEGGIFLARSVVTA SPGSLQVDTLISLMEHLKACABIAARGLEGGIFLARSVVTA SPGSLQVDTLISLMEHLKACABIAARGLEGGIFLARSVVTA SPGSLQVDTLISLMEHLKACABIAARGLEGGIFLARSVVTA SPGSLQVDTLISLMEHLKACABIAARGLEGGIFLARSVVTA SPGSLQVDTLISLMEHLKACABIAARGLEGGIFLARSVVTA SPGSLQVDTLISLMEHLKACABILARGLEBGGIFLARSVVTA SPGSLGVDTLISLMEHLKACABILARGLEBGGIFLARSVVTA SPGSLGVDTLITHHTHINPNSITYTLGSLUEF DGYYLESDPCLVCNNPEVPFCYIKLSIKVDTRYTTTQQVVKLI GSSTISKVTVKIGILKRYKTINLYNNTHINPNSITYTTLGSLUEF DGYYLESDPCLVCNNPEVPFCYIKLDSILVNTMITEPDNTYTNTQASUFENNYAS	1			
TPLPTCLQFNRGPCVSSQ1GFNCSKGXCQCSSGPDRIRQDM VDSCCPESSKERKGENTEPVET\ TLEDPQP+SRQPSSGS*LDP E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL HAGLIVGILILVLIVATAILUTVYMYHHPTSAASIFFIERFSR WPAMKFRGSGBPAFAEVEVEVGEKGGFIVSAGC 5786 2532 1674 SYKLPAAERRASCSQPPTPTRRWPAPGRTSRGHRPQM+SGTP APRPPARSTVSPASPLPKPRAGRGSRPRRACSTFRPC*SLN*M S*H*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVAARLPTWAK SPPLACSFCQAAQKSQSLSSGRSTR*PEWRSPRPTYT*PATTSPGST GRSMMTCPTRWTATPWSARASSRPRWPTP+WRPSGRLSTV*RA TGGSTATAPPKRPPRNWNPMAE 5787 2 1460 MASAASVTSLADEVNCP\ICQGTLKESRGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEPFRY\GSFRPNWQLANV VENIERLGLVSTLGIGBEDVCQFHCKEKYFYCEDDEWAL VENIERLGLVSTLGIGBEDVCGPHGKKIYFFCEDDEWAL GEGHATHTMRFLEDAA\APYREQIHKCLKCLIKEREBIQEIQS REMKRWQVLLTQVSTKRQQVISEFAHLKRFLEGQSILLAQLES QCGDILLQRDBFDLLVAGEICRFSALIEELEEKKERFARRLLTD IRSTLTCCTTRCKKPVAVSPELGQRIRDFPGYMKOMS PDNPQRPDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRPESGWAVRLAMGFVSALGSF\TALTLIKKBQP RQVRVSLDYEVGWVTFTNAVTREPTYTTTASFTKKVLFFFGLMG RGSSFSLSS SPAVAASCASAVDATAEGHDAGDGSVSSTGAISTTTGHQEGGC SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNWKGVV AIFYMQVILMITTDLDGEDEKKKGALDNLLSGLIAELGMDKKOV SKNNERSALNEVHLVVNRLLSVYMRSTKSGKSSICSSSLISS ATAAALLSSGAVDYCLHVLKSLLEVWKSQONDEPVATSQLIKP HTTSSPPDMSPFFLRQVVKGHAADVFFAAYTQLLTEMVTRLPYQI KKITDTNSRIPPPFOHSWFYFLSSYLMIQQTFPVRRQVKKLL FIGGSKEXYRQLDTLISLBERLIKACABIAQRTINMQKPCIKDDSVLY FLLQVSFLVDBEVSPVLLQLLSCALCGSKVLRALAASSGSSSA SSPAVAASSQQATTQSKSTKKSKKBEKEKEKDGETSGSQEDQ LCTALVNOLNKFANKSVLIKTONHINPNSNIYNTLSGLUEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRYKGVRATHINPNSNIYNTLSGLUEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRYKTNILMYNINHTPLNTYNTYTSLSULEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRYKTNILMIYNINHTPLNTYNTYTSLSULEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRYKTNILMIYNINHTYNTYTLSGLUEF DGYYLESDPCLVCNNPEVPFCYIKLDSILSSSSVROAHCLITH I YRNSKSQQELLLDLMWST WPELPAYGRKAAQFVDLLGFLKKAP RWKKKKVQLTPEGTEFKKLDLEPTYLNYAMS RWHKKKKVQLTPEGTEFKKLDLEPTYLNYAMS RWHKKKKVQLTPEGTEFKKLDLEPTYLNYAMS				
VDSCCPESSEMCENTEPUET\FLEDQOP*ERQPPSSGS*LDP E/DAVTSQPPTSLDTEDDTKIALHLKONGASTDDSABKKGGTL HAGLIVGILILVLTVATAILNTYMYHHPTSAASIFFIERPER WPAMKFRGSGHPAVAEVEEVUGEKEGFIVSEQC 5786 2532 1674 SYKLPAAERRASSCSOPPTTPRRWPAGRTSRGHRPQM*SGTP APRPPARSTVSPASPLPKPRAGRCGSRPRSACSTFRPC*SLN*M S*H*KRNLSQRSSSMSRRPLSCARPHR**RGQLTVAARLPTWAK S*PLACSFCQAAQKSQSLSSGSTSF*P*PEMSFRP\SPPGMPAT GLAFSSRP/PKGRPCCTWIPSRMPASPTAPPTT*APTSSPGST GRSMMTCPTRWTATPWSARASSRPRNWPT**WRSGRLSTV*RA TGGSTATAPPKRFPRNWNPMMAE 5787 2 1460 MASSASVTSLADEVNCP\TCGGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LESSP\TCP\LCKEPPR\GSFRPNWQLANV VENIERLQLVSTLGIGBEDVCQEHGEKIYFFCEDDEMQLCVVCR EAGEHATHTMRFLEDAA\APYREQHKCLKLIKEREIQEIGS QDGDILRQRDBFDLLVAGSICGRFSALIEELEKKERPARBLITD LIFSTLIRCETRKCRKPVAVSPELGQVISFPALLEKKEREAGEILID LIFSTLIRCETRKCRKPVAVSPELGQRIROPPQQALPLQRBMKMP LEKLCFELDYBPAHISLDPQTSHPKLLLSEDHGRAGPSYKWONS PDDPQRFDRATCVLAHTGITGGRHTMVVSIDLARGGSCTVGVVS EDVQRRGGLIRLPEGWAVRLAMGVSSALSSFP\TAILTLKEOP RQVRVSLDYEVGWVFFINAVTREPIYTFTASFTRKVIPFFGLNG RGSSFSLS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGGTETGDVHTSNRLHMVRLMLIERLIGTDPQLRNVGGGVR AIPYMQVILMITTOLDGEDEKVGRADDNLLSQTLAFULKDP HTTSSFPDMSFPFLRGVVKGHAADVFBAYTGLLERWHRLPVOI KKITDTNSRIPPPVPDHSWFYFLSSYLMIQQTPPVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\TWRGKTKGDGSLEGGIFLRASVVTA SPQSALQYDTLISIMEHLKACAEIAAQRTILMCRIPGTSUKTA SPQSALQYDTLISIMEHLKACAEIAAQRTILMCRIPGTSUKTA SPSALQYDTLISIMEHLKACAEIAAQRTILMCRIPGTSGGBDD LCTALVNQLNKFADKSTLTQFRCFLESNSSVRNOAHCLITH IYNSSKSQOBLLLDLMWSIWPELPAYGRKAAGPVOLLGYFSLK TPOTEKKKKEYSQKAVSULRTONHITHPNSNIYYNTLSGLUEF DGYYLESDPCLVCNNPEVPPCVIKLSSLKVDTRYTTQQAVVKLI GSHTISKVTVKIGDLKRTRMVRTINLIYNNRTVQAIVELKNRA RWHKAKKVQLTPCGTEVKIDDLEVILVANLMIEFRAPYENNYAS				
E/DAVTSQPTSLPTEDDIKALHIKDNGASTDDSABKKGGTL HAGGIUSILILUIVATAILUTVATHAIDTSABASIFFIERRPSR WPAMKFRGSGHPAYAEVEPVGEKEGFIVSEQC 5786 2532 1674 SYKLPAAERRASSCSQPPTPTTRRWRPAEGTSRGHRPQM*SGTP APRPPARSTVYPASPLPKPRRAGCGSRPSACSTFPC*SLINM S*H*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVARALPTWAK SPPLACSFCQAAQKSQSLSSGRSTA*PERMSFRP\SPPGNPAIP SLAPSSRP/PKGRPCTWIPSRWPASPTAPPTTT*APTSSPGST GRSMMTCPTRWTATDWSARASSRPRWWFTP*WRPSGRLSTV*RA TGGSTATAPPKRPRPRWWMPMAY 5787 2 1460 MASAASYTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL T\RYCELP\GPD\DEEX\TCP\LCCKEPFRP\GSFRPNO\LANV VENIERLQLVSTLGJEBEDVCGEKKIYPFCEDDEMQLCVVCR EAGEHATHTWRFLEDAA\APVREQIHKCLKCLIKERBEIDEIQS RENKRMQVLLITOYSTROQOVISEKIYPFCEDDEMQLCVVCR EAGEHATHTWRFLEDAA\APVREQIHKCLKCLIKERBEIDEIQS GRENKRMQVLLTOYSTROQOVISEKIYPFCEDDEMQLCVVCR EAGEHATHTWRFLEDAA\APVREQIHKCLKCLIKERBEIDEIQS GRENKRMQVLLTOYSTROQOVISEKIYPFCEDDEMQLCVVCR EAGEHATHTWRFLEDAA\APVREQIHKCLKLIKERBEIDEIQS GRENKRMQVLLTOYSTROQOVISEKIYPFCEDDEMQLCVVCR EAGEHATHTWRFLEDAA\APVREQIHKCLLEGCSILLAQLES QDGDILRQRDEFDLLVAGEICRFSALIEELEEKNERPARELLTD IRSTLIRCETLYBEAHISLDPQTSHPKLLLISEDHGRAGPSYKWQNS PDMPQRFDRATCVLAHTGITGGRHTWVS IDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVSPELAQRITEPFQQALPLCHEMMAF LEKLCFELDYBEAHISLDPQTSHPKLLLSEDHGRAGPSYKWQNS PDMPQRFDRATCVLAHTGITGGRHTWVS IDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLIKEOP RQVRVSLDVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS 5788 2 6860 EHSVSGRSSYGDATAEGHPAGPGSVSSSTAISTTTGHQEGDG SKEGEGEGFTGDVHTSNRLHWVRLLLEQLIGLTEMYLELPVOI KKITDTNSRIPPVFDHSWFYFLSEYLMIQQTPFVRRQVKLLL FIGSKEKYRQLRDLHTLDS\HVWRLLSGLKLLEEGGIFLRRSVVTA SPQSALQYDTLISHENLKACAEAAGRTINMCKCHCHDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSA SSPAPVAASSGQATTQSKSSTKKSKKEKKEKKDETSGSQBDQ LCTALVNQLNKRADKETLIGPLRCFLLESNSSVFRQAHCLTLH IYRNSSKSQOELLLDLMWSIMPELPPAGRRAAGFVDLLGYFSLK TPOTEKKLEYSGKAVEILETROHNILINHPNSNI YNTLSGLUFF DGYYLESDPCLVCNNPEVPGCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRAWATINLYYNNRTVQAIVELKNKPA RHKKAKKVQLTPGGTEVKILDLPJVASILMLEFADPYENYQAS	1			TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW
HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFPIERRPSR WPAMKFRGSGHPAYAEVEPVGEKGFIVSEQC 5786 2532 1674 SYKLPAAERRASSCSQPPTPITERRNPABGRTSRGHRPQM*SGTP APRPPARSTVSPASLIPKFRAGRCGSRPRSACSTFRPC*SLN*M S*H*KRNLSQRSSSMSRRPLSCARPH**RQGLTVAARLPTWAK SPPLACSFCQAAQKSQSLSSGRSTR*PERMSFRPTSPBPATPT SLAPSSRP/PKGRPQCTWIPSRWASPTAPTTT*APTSSPGST GRSMMTCPTRWTATPWSARASSRPNNWFD**WRPSGRLSTV*RA TGGSTATAPPKRPPRNWNPMAB 5787 2 1460 MASAASVTSLADEVNCP\\ICQSTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\\LEESP\TCP\\LCKEPFR\GSFRPNWGLANV VENIERLGLUSTIGLGEBDVCQEHGEKIYFFCEDDEMQLCVVCR EAGHATHTMFFLEDAA\APYREQIHKCLKCLIKEREEIQEIQS RENKRMQVLLITQVSTKRQQVISEFAHLEKFLEEQQSILLAQLES QDGDLLRQRBEPDLLVAGEICFFSALIEELEEKNERPARBLLTD IRSTLITCETTRKGREVAVSPSLGTRDFPQQAFLQKEMKMF LEKLCFELDYBPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDPATCVLAHTGITGGRTTWVVSIDLAHGGSCTVGVVS EDVQRRGELRLRPESGWAVRLAMGFVSALGSFP\TRLTLKKOP RQSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDWTSNBLHWVRLMLLERLIQTLPQLRWGGWR AIPYMQVILMLTDLDGEDEBKOKGALDNLISQLIABLGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQONBEEPVATSQLLKP HITSSPPDMSFFFLRQVYKGHAADVFEATYGLLTEWVLELPVQI KKITDINSRIPPPVFDHSWFYFLSEYLMIQQTFFVRQWKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAETAAQRTINMQKFCIKDDSVLY FLLQVSFLVDEGVSFVLLGLSCALGSKVLRALAASSGSSAS SSPAPVAASSGQATTOSKSSTKKKEEKEKERDGETSGGRDQ LCTALVNQLNKFADKETLIGFLRCFLLESNSSSVRWQAHCLTLH IYKNSSKSQOELLLDLMWSIMPELPAYGRAAQFVDLLGYFSLK TPQTEKKLEYSGRAVETLETQUNHILTNHPNSNI YNTI.SGLVFF DGYYLESDPCLVCNNPEVPPCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRIVMTIINJYNNRTVQAIVELKNKPA RWHKAKKVQLTPGGTEVKILDPLFIVASLIMMEFADFYENYQAS				
### WPAMKFRRGSGHPAYABURPUGEKEGFIVSEQC SYKLPAAERRASCSQPPTTTRRRWPAGRTSRGHRPQM*SGTP APRPPARSTYSPASFLPKERAGRGSRPRSAGSTFRPC*SLINM S*H*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVAARLETWAK SPPLACSFCQAAQKSQSLSSGRST*PEC*SLINM S*H*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVAARLETWAK SPPLACSFCQAAQKSQSLSSGRST*PERSTRPLSPDFONPAIP SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTTT*APTSSPGST GRSMMTCPTRWTATTPWSARASSRPRNWFTP*WRPSGRLSTV*RA TGGSTATAPPKEPRPRNWNPMAB 5787 2 1460 MASAASVTSLADEVNCP/ICGGTLKEAGSLSNCG/HKNFCRACL T\RYCSIP\GPD\LEESP\TCP\LCKEPFPR\GSFRPNWQLANV VENIERLQLVSTLGGEBCVCGEKEYTPFCEDDEMQLCVVCR EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKEREEIQEIQS RENKRMQVLITQVSTKRQQVISEFAHLEKHERQGSILLAQLES QCGGDILRQRDEPFDLVAGGICFSALIEELEEKREPABELITD IRSTLIRCSTRKCREVAVSPELGQRIRDFPQQALPLQREMKMF LEKLCFELDYBPAHISLDPQTSHPKLLLSEHGRAGFSYKWONS PDNPQFPDRATCVLAHTGITGGRTHWVVSIDLAHGGSCTVGVVS EDVQRKGELRLPEESGVWAVKLAWGFVSALGSFP\TRITLKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPPFGLWG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTAISTTTGHQEGGC SEGEGETETGDVHTSNRIHMVRIMLLERLLQTLPQLRNVGGVR AIPYMQV ILMLTIDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFNSRTKSGKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQONDEEPVATSQLLKP HTTSSPPDMSPFFLRQVVKGHAADVFEAYTQLLTEMVLRLEVQI KKITDTNSRIPPPVBCHSWFYFLSEVLMIQQTFFVRRQVKRLL FIGGSKEKYGLRDLHHTLDS\HVMSIKKLLEEGGIFLARSVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FILLQVSFLVDECVSFVLLQLLSCALCGSKVKRALAASSGSSSAS SSPAPVAASSGGATTQSKSSTKKREEKEKERDGETGGSGBDQ LCTALVNQLNKRADKETLIQFLCFLLESNSSVRWAAICLTH IYRNSKSQOELLDLHWISIMPELPAYGRKAAQFVULGYFSLK TPQTTEKKLKEYSGQATIGSKSTKKKKREKKEKEDGETGGSGBDQ LCTALVNQLNKRADKETLIQFLCFLLESNSSVRWAAICLTH IYRNSKSQOELLDLLWWSIMPELPAYGRKAAQFVULGYFSLK GSHTISKVTVKRIGDLKRIVWRTINLYYNNRTVQAIVELKNKPA RWHKKAKKVQLTPGGTEVKILDLPLFIVASILMLEFADFYENYQAS	ł			
S786 2532 1674 SYKLPABERRASSCSQPTTTRRWPAPGRTSRGHRPQM*SGTP APRPPARSTYSPASPLD*KPRAGRCGSGRRSAGSTRPC*SLM*M	1	_		
APRPPARSTYSPASPIPKPRAGRCGSRPRSACSTFRPC'SLN*M S*H*KRNLSQRSSMSRPISCARPHR**RQGLTVAARLPTWAK SPPLACSFCQAAQKSQSLSSTR*P PERMSRP\SPPCMPPAIP SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTTT*APTSSPGST GRSMMTCPTRWTATPWSARASSRPRMAW TGGSTATAPPKRFPRNWNPMMAE 5787 2 1460 MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL T\RYCELP\QPD\LEBSP\TCP\LCKEPFRP\GSFRPNWQLANV VENIBRLQLUSTGLGEBPVCQEHGKKIYFFCEDDEMQLCVVCR EAGEHATHTRFLEDAA\APYRRQIHKCLKCLIKEREBIQEIGS RENKRMQVLLTQVSTKRQQVISEFAHLERLEEQQSILLAQLES QDCDILRQRDBFPLLVAGBICFPSALIEELEEKNERPARELLTD IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQRBMKMF LEKLCFELDYBPAHISLDPQTSHFKLLLSCDHQRAQPSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEESVWAVRLAWGFVSALGSFP\TRLILKRQP RQVRYSLDYBEVGWVFTINAVTREPIYTFTASFTKVIPFFGLMG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGFGSVSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHWVLMLLERLLQTLPQLRRVGGWR AIPYMQVILMLTTDLDGEDEKDKGALDNLLQLIAELGMDKKDV SKKNRESALNEVHLVVWRLLSVFMSRTKGGSKSSICESSSLISS ATAAALLSSGADVYCLHVLKSLLEVMKSQONDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKTTDTNSIPPPVFDHSNFYFLSSTLMIQQTPFVRRQVRKLLL FIGSKEKVRGLRDHTTDLS,HVRGIKKLLEEGGIFLRRSVVTA SPQSALQYDTLISLMEHLKACABIAAQRTINWQKPCIKDDSVLY FILLQVSFLUDECVSBVLLQLLAGCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKERSKEKEGETSGQEBQ LCTALVNQLNKFADKETLJOFLRCFLLESNSSVVRQAHCTTLH IYRNSKSQOELLLDLMMSIWPELFAYGRKAAQFVOLLGYFSLK TPQTEKKLKEYSGKAVEILLRTONHILITHHPNSNIVTNTLSGLVEF DGYYLESDPCLVCNNPEVPCYIKLSLKKAPA RWHKAKKVQLTREQTEVKUDLPLPIVASNLMIEFADFYEIN	E706	2522	1674	
S*H*KRILSQRSSSMSRRPLSCARPHR**RQCITVARALPTMAK SPPLACSFCQAAQKSQSLSSGRSTR*PERMSFRP\SPPGNPAIP SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTTT*APTSSPGST GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA TGGSTATAPKFRPRNWNPMAP*WRPSGRLSTV*RA TGGSTATAPKFRPRNWNPMAP*WRPSGRLSTV*RA TGGSTATAPKFRPRNWNPMAP* MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEPFR\GSFRPNWQLANV VENIERLQLVSTLGIGEBUVCQERGKTYFFCEDDEMQLVVCR EAGEHATHTMFFLEDAA\APYREQIHKCLKCLIKEREBIQEIQS RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES QOGDLRQRDEFFDLLVAGEICRFSALIEELEEKKERPARBLLTD IRSTLIRCETRKCKEVAVASSELGQRIRDFPQAALPLQRBMEMF LEKLCFFLDVEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRITWVSIDLAHGGSCTVGVVS EDVQRKGELRIPEEGGWAVRLAMGFVSALGSFP\TRILTERBOP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDCDEDEKDKGALDNILSQLIAELGMDKKDV SKKNERSALMEVHLVVWRLSVFMSRTKSGKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLKP HTTSSPPDMSFFFLRQVVKGHAADVFRAYTQLLTEMVLRLPYQI KKITDTNSRTPPPVFHORYTSGSKSSICESSSLISS ATAAALLSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLKP HTTSSPPDMSFFFLRQVVKGHAADVFRAYTQLTFMVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACABIAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKEKEKKDGETSGSGEDQ LCTALVNQLNKFADKSTLKGNEKIKKKEKEKKDGETSGSGEDQ LCTALVNQLNKFADKSTLKGNEKILSIKVDTRYTTYQQVVKLI IYRNSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKSYSGKAVEILRTQNHILITNHNSNIYNTLSGLVEF DGYYLESDPCLUCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVTRINLYYNNRTVQAIVELKNKPA RWHKKKVQLTFGQTEVKIDLPPIVASNLMIEFADPYENVQAS	3/88	2532	16/4	
SPPLACSFCQAAQKSQSLSSGRSTR*PERMSFRP\SPPGNPAIP SLAPSSRP/PKGRPQCTWIPSRWBASPTAPBTTTT*APTSSPGST GRSMMTCPTRWTATPWSRARASSRPRNWPTP*WRPSGRLSTV*RA TGGSTATAPPKRPPRRNMPMMAB 5787 2 1460 MASAASVTSLADEVNCP\ICQSTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEPFR\GSRPNWQLANV VENIERLQLVSTLGLGEBDVCQEHEEKIYFFCEDDEMQLCVVCR EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKEREBIQEIQS RENKRMQVLLTQVSTKRQQVISBFAHLEKFLEEQQSILLAQLES QDGDILRQRDBFDLLVAGEICRFSALIELELEKKBRPPARBLLTD IRSTLIRCETRKCRKPVAVSPGLGQRIRDFPQQALPLQREMKMF LEKLCFELDVEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWONS PDNPQRFDRATCVLAHTGITGGRITWVVSIDLAHGSCTVGVVS EDVQRKGELRLRPEEGVWAVALAWGFVSALGSFP\TRLIKEQP RQVRVSLDYBVGWVTFTNAVTREPIYTTASFTRKVIFFGLWG RGSSFSLSS 5788 2 6860 EHSVSGRSAYGDATAEGHPAGPGSVSSTGAISTTTGHQEGDG SEGEGEGTEGDVHTSNRLHMVRIMLLERLLQTLPQLENVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIABLGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSGAVDYCLHVLKSLLEYWKSQONDEBPVATSQLIKP HTTSSPPDMSFFFLRQVVKGHAADVFERYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVKKLL FIGGSKEKYRQLBDHTLDS\HVRGIKKLLEEQGIFRASVVTA SPQSALQYDTLISLMEHLKACABIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSA SSPAPVAASSGQATTGSKSSTKKSKKEEKKEKDGETSGSQBDQ LCTALNVQLNKFADKSTKKSKSTKKSKKEKEKEKDGETSGSQBDQ LCTALNVQLNKFADKSTKKSKSKSKKKKEKEKEKDGETSGSQBDQ LCTALNVQLNKFADKSTLIKTQNHILTNHNSNIYNTLSGLVEF DGYYLESDPCLUCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVTRINLYYNNRTVQAIVELKNKPA RWHKKKKVQLTPGQTFEVKIDLPLPIVASNLMIEFADPYENVQAS				
SLAPSSRP/PKGRPQCTWIPSRWASPTAPPTTT*APTSSPGST GRSMMTCPTRWTATPWSARASSRPNWPTP*WRPSGRLSTV*RA TGGSTATAPPKRPPRNNMPMAE 5787 2 1460 MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRPNWQLANV VENIERLQLVSTLIGLBEBP\TCP\LCKEPFRP\GSFRPNWQLANV VENIERLQLVSTLIGLBEBP\TCP\LCKEPFRP\GSFRPNWQLANV VENIERLQLVSTLIGLBEBP\TCP\LCKEPFRP\GSFRPNWQLANV VENIERLQLVSTLIGQBEBCCHGEKIKFPCEDGWGLCVVCR EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKEREEIQEIQS RENKRMQVLLTQVSTKRQQVISBFAHLRKFLEEQQSILLAQLES QDCGDILRQNBFFDLLVAGC EGFSALIEBLEKNERPARELLTD IRSTLIRCETRKCKKPVAVSPELGQRIRDFFQQALPLQREMKMF LEKLCFELDVEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWONS PDNPQRPDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGWAVKLAMGFVSALGSFF\TRILLKOP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNRESALMEVHLVVVMKLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSFFFLRQVVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRTIPPVFDHSVFLSVYLNGQTFFVRRQVFKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FILLQVSFLVBGGVSPVLSCALCAGSKVLRALAASSGSSAS SSPAPVAASSGQATTQSKSSTKKSKKEKEKEKDGETSGQEDQ LCTALVNQLNKFADKSTLIGFLRCALCSCKVLRALAASSGSSAS SSPAPVAASSGQATTQSKSSTKKSKKREKEKEKDGTSGQEDQ LCTALVNQLNKFADKSTLIGFLRCALCARAQFVDLLGYFSLK TPQTEKKLKEYSGKAVEILRTQNHILITNHNSNIYNTLSGLVEF DGYYLESDPCLUCNNPEVPFCYIKLSSIKVDTRTYTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKKKKVQLTPGQTEVKRUPTINLYYNNRTVQAIVELKNKPA RWHKKKVQLTPGQTEVKRUPLPIVASNLMIEFADPYENVQAS				-
GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA TGGSTATAPPRRFPRNWNPMMS 1460 MASAASVTSLADEVNCP\TCGGTLKEAGSLSNCG/HKNFCRCL T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRPNWQLANV VENIERLQLVSTLGIGBEDVCGHGEKIYFFCEDDEMQLCVVCR EAGHATHTMRFLEDAA\APYREQIHKCLKCLIKEREEIQEIQS RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQGSILLAQLES QCGDILRQRDBFDLLVAGEICRFSALIEBLEEKNERPARBLLTD IRSTLIRCETRKCRKPVAVSPELGQRIRDFFQQALPLQREMMF LEKLCFELDYBPAHISLDPQTSHPKLLLSEDHORAQFSYKWONS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEGGWAVRLAWGFVSALGSFP\TTLILKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS 5788 2 6860 EHSVGRSSAVGDATAEGHPAGPGSVSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHLWRLRLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSGGAVDYCLHVLKSLLEWKSQQNDEEPVATSQLLKP HTTSSPPDMSFFFLRGVKHAADVFBATYQLLFUMVLRIPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\JWVGIKKLDEEGGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FILQVSFLVDEGVSPVLUQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATQSKSSTKKSKKEEKEKEDGETSGSQBDQ LCTALVNQLNKKFADKETLIQFLERCFLLESNSSSVRWAHCLITLH IYNNSKSQQELLDLHMSIWPELPAYGRKRAAQFVDLLGYPSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRYWVTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGGTEVKIDLPLPIVASNLMIEFADFYENYQAS				, ,
TGGSTATAPPKEPPRWNPMMAE 5787 2 1460 MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LCKEPPR\GSFRPNWQLANV VENIERLQLVSTLGLGEEDVCQEHGEKIYFFCEDDEMQLCVVCR EAGEHATHTMR:FLDAA\APYREQIHKCLKCLIKEREEIQEIQS RENKRMQVLLTQVSTRRQQVISEFAHLRKFLEEQQSILLAQLES QDGDILRQRDBFDLLVAGEICRFSALIEELBEKNERPARBLLTD IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQREMKMF LEKLCFELDYBPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRITWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLANGFVSALGSFP\TRLTLKEQP RQVRVSLDYSUGWVFFTNAVTREPIYTFTASFTRKVIPFFGLWG SGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETECDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTFDLDGEDEKDKGALDNLLSQLIAELGMNKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSSSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQVVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVPDHSMFYFLSEYLMIQQTPFVRRQVKRLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLERQGIPLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKPCIKDDSVLY FILLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEKDGETSGSQBDQ LCTALVNQLNKFADKETLICPIRCFLLESNSSVRWOAHCLTLH IYRNSSKSQOELLDLMSIMPBLPAYGKAAQFVDLLGFYSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPSGTEVKIDLLPLIVSNLMIEFADFYENYQAS				
TARCEIP\GPP\LESP\TCP\LCKEPFRP\GSFRPWQLANV VENIERLQLVSTIGLGEDVCQEHGEKIYFFCEDDEMQLCVVCR EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKEREIQEIQS RENKRMQVLLTQVSTRQQVISEFAHLRKFLEEQQSILLAQLES QDGDILRQRDBFDLLVAGEICRFSALIEELEKNEREPARELLTD IRSTLIRCETRKCRKPVAVSPELGGRIRDFPQQALPLQREMMF LEKLCFELDYBPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRTTWVVSIDLAHGGSCTVGVVS EDVQKKGELRLRPEGGVAVAVRLAWGFVSALGSFP\TRITLKEQP RQWRVSLDYEVGWVFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS 5788	1		•	
T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRPNWQLANV VENIERIQLUSTIGLGEBDVCQEHGEKIYFFCEDDEMQLCVVCR EAGGHATHTMR FILEDAA\APYREQIHKCLKCLIKEREIQEIQS RENKRMQVILTQVSTKRQQVISEFAHLRKFLEEQQSILLQLES QDGDILRQRDEFDLLVAGEICFSALIEELEEKNERPARBLLTD IRSTLIRCETRKCRKPVAVSPELGQRIRDFFQQALPLQREMKMF LEKLCFELDYEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGWAVARLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYFVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SECGEGEGTEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIABLGMDKKDV SKKNERSALNEVHLVVWRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSGAVDYCLHVLKSLLEVWKSQONDEEFVATSQLLKP HTTSSPPDMSFPFLRQVVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFPHSWFFFLSQVIKLLEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FILGVSFLVDEGVSPVLLQLLSCALGGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKSTTKLSGKKEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKSTTKLSGKKEKEKEKDGETSGSGEDQ LCTALVNQLNKFADKSTTLIOFLRCFILESNSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAGFVDLLGYFSIK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPIPVASNLMIEFADFYENYQAS	5787	2	1460	
VENTERLQLVSTIGLGBEDVCQEHGEKIYFFCEDDEMQLCVVCR EAGEHATHTMRFLEDAA_APYREQIHKCLKCLIKEREEIQEIQS RENKRMQVLLTVQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES QDGDILRQRDBFDLLVAGEICRFSALIEELEEKNERPARBLLTD IRSTLIRCETRKCRKPVAVSPELGQRIRDFFQQALPLQREMKMF LEKLCFELDYBPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS SEGEGEGTEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIABLGMDKKDV SKKNERSALNEVHLVVWRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSGAVDYCLHVLKSLLEYWKSQNDEBPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLLPYQI KKITDTMSRIPPPVFHSWFYFLSEYLMIQQTPFVRRQVKKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SSPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKENDGETSGSQBDQ LCTALVNQLNKFADKETLIQPIRCFLLESNSSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKINKPA RWHKAKKVQLTPGQTEVKIDLPIPVASNLMIEFADFYENYQAS		_	, 1100	T\RYCEIP\GPD\LEESP\TCP\LCKEDEPD\GSEPDNMOLANN
EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKEREEIQEIQS RENKRMQVULTQVSTKRQQVISEFAHLRKFLEEQSILLAQLES QDGDILRQRDEFDLLVAGEICRFSALIEELEEKNERPARELTD IRSTLIRCETRKCKKPVAVSPELGQRIRDFPQQALPLQRBMKMF LEKLCFELDYBPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRILLERLLQTLPQLRRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVWRLLSVFWSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFBAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FILQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSGKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRYKWRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPIVASNLMIEFADFYENYQAS				
RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES QDGDILRQRDBFDLLVAGEICRFSALIEELBEKNERPARBELLTD IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQREMKMF LEKLCFELDYBPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVWRLLSVFMSRTKKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYIMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTTH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS	1	,	•	
QDGDILRQRDEFDLLVAGEICRFSALIEELEEKNERPARELLTD IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQREMKMF LEKLCFELDYEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDVEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIABLGMDKKDV SKKNERSALNEVHLVVWRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVKKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKEEKEKDGETSGSQEDQ LCTALVNQLNKFADKETLTQFLRCFLLESNSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNSTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS	1	1		
IRSTLIRCETRKCRKPVAVSPELGQRIRDFFQQALPLQREMKMF LEKLCFELDVEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLPPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDVEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SECEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVWRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKVRQLRDLHTLDS\HVGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKEEKEKEDGETSGSQBDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH IVRNSSKSQQELLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNRPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS			1	
LEKLCFELDYBPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNILSQLIABLGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVUKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWGFCIKDDSVLY FILLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKREKEKEKEGGETSGSQBDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS		·		
PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSFFFLRQYVKGHAADVFEAYTOLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKEEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS	<u> </u>	•		LEKLCFELDYBPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS
EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSTGAISTTTGHQEGDG SEGEGEGTETGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGDEKDKGALDNLLSQLIABLGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRIPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FILQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKEKEKEKKDGETSGSQBDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS		·	•	PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS
RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS 5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FILQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKEEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLITH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS				EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP
5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEKDGETSGSQBDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSVRWQAHCLTLH IYRNSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS				
SEGEGETEGDVHTSNRLHMVRLMLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIABLGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFFLESNSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS				
AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEKGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSVRWQAHCLTLH IYRNSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS	5788	2	6860	· · · · · · · · · · · · · · · · · · ·
SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEUGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFFLESNSSVRWQAHCLTLH IYRNSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS				
ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKENGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS				
HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKPCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEDGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS		J		
KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFFLESNSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS				
FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS				
SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEKDGETSGSQBDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS		ł	<i>'</i>	
FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEKDGETSGSQBDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS				
SSPAPVAASSGQATTQSKSSTKKSKKEEKEKDGETSGSQBDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS	,		i	- · · · · · · · · · · · · · · · · · · ·
LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS				
IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS		i		· · · · · · · · · · · · · · · · · · ·
TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS		1	ļ	-
DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS] [Į	l	
GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS		1		
RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS]	ŀ	ļ	
]	ŀ		· · · · · · · · · · · · · · · · · · ·
1 ET LQCPRCSASVPANPGVCGNCGENVYQCHKCRSINYDEKDPF] [[
	LJ			151 DCCFKCSASVPANFGVCGNCGENVYQCHKCRSINYDEKDPF

0.00	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, S=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l			Codon, /=possible nucleotide deletion,
	amino acid	sequence	Codon, /=possible nucleotide defector,
	sequence		\=possible nucleotide insertion)
			LCNACGFCKYARFDFMLYAKPCCAVDPIENEEDRKKAVSNINTL
1	ļ	Į	LDKADRVYHQLMGHRPQLENLLCKVNEAAPEKPQDDSGTAGGIS
l	ì		STSASVNRYILQLAQEYCGDCKNSFDELSKIIQKVFASRKELLE
l			YDLQQREAATKSSRTSVQPTFTASQYRALSVLGCGHTSSTKCYG
ļ			
ŀ	1	1	CASAVTEHCITLLRALATNPALRHILVSQGLIRELFDYNLRRGA
1	1		AAMREEVROLMCLLTRDNPEATQQMNDLIIGKVSTALKGHWANP
ĺ	1	1	DLASSLQYEMLLLTDSISKEDSCWELRLRCALSLFLMAVNIKTP
]	j	1	VVVENITLMCLRILQKLIKPPAPTSKKNKDVPVEALTTVKPYCN
	l		EIHAQAQLWLKRDPKASYDAWKKCLPIRGIDGNGKAPSKSELRH
ŀ	Į.	1	TAX SECTION OF CONCUENCE DI VI CUNIUI DOVI ETDAT
1		,	LYLTEKYVWRWKQFLSRRGKRTSPLDLKLGHNNWLRQVLFTPAT
l	1		QAARQAACTIVEALATIPSRKQQVLDLLTSYLDELSIAGECAAE
1		I	YLALYQKLITSAHWKVYLAARGVLPYVGNLITKEIARLLALEEA
ļ	1		TLSTDLQQGYALKSLTGLLSSFVEVESIKRHFKSRLVGTVLNGY
ł		1	LCLRKLVVQRTKLIDETQDMLLEMLEDMTTGTESETKAFMAVCI
[BTAKRYNLDDYRTPVFIFERLCSIIYPEBNEVTEFFVTLEKDPQ
1			PIRKLINDDIKITYETE BRUCOTTIEBBROY IBEEVILBROPQ
	ļ		QEDFLQGRMPGNPYSSNEPGIGPLMRDIKNKICQDCDLVALLED
l	1		DSGMELLVNNKIISLDLPVAEVYKKVWCTTNEGEPMRIVYRMRG
			LLGDATEEFIESLDSTTDEEEDEEEVYKMAGVMAQCGGLECMLN
١,			RLAGIRDFKQGRHLLTVLLKLFSYCVKVKVNRQQLVKLEMNTLN
}			VMLGTLNLALVAEQESKDSGGAAVAEQVLSIMEI\IQAEPNVEP
	ļ		LSEDKGNLLLTGDKDQLVMLLDQINSTFVRSNPSVLQGLLRIIP
1		ļ	YLSFGEVEKMQILVERFKPYCNFDKYDEDHSGDDKVFL\DCFCK
ł	1		AP24GEAEKWOIPAEKŁKAJCUŁDKIDEDW2GDDKAŁP/DCŁCK
l .		1	IAAGIK\NNSNGHQL\KDL\ILQKGITQNALD\YMKKHIP/SAA
1	1	li .	RIWDADI\WKSFCLRPALPFILRLLRGLAIQHPGTQVLIGTDSI
1	ł		PNLHKLEQVS\SDEGIGTLA\ENL\LESLREHPDVNKKIDA\AR
1		}	RETRAEKKRMAMAMRQKALGTLG\MTTNEKGQVVD/TRTALLEA
1	1		DWEELIEEP\GLTCCICREGYKFQPTKVLGIYTFTKRVVLGGVW
1		1	
	ì	,	ENKPRETSRATSTVSHFNIVHYDC\HLA\AVSLARGREEWESAA
			LQNANTKCNGLLPVWGPHVPESAFATCLARHNTYLQECTGQREP
1		İ	TYQLNIHDIKLLFLRFAMEQSFSADTGGGGRESNIHLIPYIIHT
Į.			GLYVLNTTRATSREEKNLQGFLEQPKEKWVESAFEVDGPYYFTV
Ī	<u> </u> -		LALHILPPEOWRATRVEILRRLLVTSQARAVAPGGATRLTDKAV
1	1 .	1	KDYSAYRSSLLFWALVDLIYNMFKKVPTSNTEGGWSCSLAEYIR
	1	1	
}	1	i	HNDMPIYEAADKALKTFQEEFMPVETFSEFLDVAGLLSEITDPE
1	1	1	SFLKDLLNSVP
5789	1	2407	LPLHAVEKTGRPGQPALKMPGKLRSDAGLESDTAMKKGETLRKQ
	1	1	TEEKEKKEKPKSDKTEEIAEEEETVFPKAKQVKKKAEPSEVDMN
1		1	SPKSKKAKK\KEEPSQNDISPKTKSLRKKKEPIEKKVVSSKTKK
			VTKNEEPSEEEIDAPKPKKMKKEKEMNGETREKSPKLKNGFPHP
1	1	1	
	1	1	EPDCNPSEAASBESNSEIEQEIPVEQKEG\AFSNFPISEETIKL
1			LKGRGVTFLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL
i			IEKLHG\ELQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKL
1			SVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHIQNGKLDLT
]	ļ	KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS
1		1	ATCPHWVFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH
		1	WICEUMALMANUTATION TECCHANICAL ADMINISTRATION
			WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD
1			AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD
		I	LVIOSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ
	1	i	
			VEOKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK
			VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM
			VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF
			VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ
			VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRFFRGQREGSRGPRGQRSGGGNKSNRSQNK
			VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ
5790	3786	1585	VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ
5790	3786	1585	VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ ARRORDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY
5790	3786	1585	VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD
5790	3786	1585	VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEEESESEDSEDSGGEEE
5790	3786	1585	VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRFFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKBEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEEESESEDSBDSGGEEE DAEEEEEEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI
5790	3786	1585	VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRFFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEEESESEDSBDSGEEE DAEEEEEEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGQESSE
5790	3786	1585	VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRFFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEESESEDSEDSGGEEE DAEEEEEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGQESSEE GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN
5790	3786	1585	VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRFFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEEESESEDSBDSGEEE DAEEEEEEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGQESSE

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Clutamia haid E Phonelalania & Clutamia
10.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	Papioline, Qaducamine, Raarginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ļ.	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
	Bequence		\=possible nucleotide insertion)
ĺ			PVLQQINTVDVLTTMGAIPAGFRPSTLSQLLEEGNQFRANYFLQ
			PELMPSQLAFRDLMWDATEGTIRSRPSRISLILTLWSCKMIPLP
			GMSIQVLSRHVRLCLFDGNKVLSNIHTVRATWQPKKPKTWTFSP
1			QVTRILPCLLDGDCFIRSNSASPDLGILFELGISYIRNSTGERG
	i		ELSCGWVFLKLFDASGVPIPAKTYELFLNGGTPYEKGIEVDPSI
Ì			SRRAHGSVFYQIMTMRRQPQLLVKLRSLNRRSRNVLSLLPETLI
1	•	ĺ	GNMCSIHLLIFYRQILGDVLLKDRMSLQSTDLISHPMLATFPML
	ļ		LEQPDVMDALRSSWAGQES\TLKRSEKR\PKEFLKVPRFLLVYH
1			\GCVLPLL/HTPTRLPPFRWAEEETETARWKVITDFLKQNQENQ
5791	3	1636	GALQALLSPDGVHEPFDLSEQTYDFLGEMRKNAV
3/31	١	1030	LRVAEFAGTSR/IGAGLIQPLHRAPARDHGLLRGGAAPALSVSH
]			GN/GKQL/AMSSQGSDDEQIKRENIRSLTMSGHVGFESLPDQLV
1			NRSIQQGFCFNILCVGETGIGKSTLIDTLFNTNFEDYESSHFCP
			NVKLKAQTYELQESNVQLKLTIVNTVGFGDQINKEESYQPIVDY
Į i	,	Ţ.	IDAQFEAYLQEELKIKRSLFTYHDSRIHVCLYFISPTGHSLKTL
			DLLTMKNLDSKVYIIPVIAKADTVSKTELQKFKIKLMSELVSNG
	İ		VQIYQFPTDDDTIAKVNAAMNGQLPFAVVGSMDEVKVGNKMVKA
			RQYPWGVVQVENENHCDFVKLREMLICTNMEDLREQTHTRHYEL
			YRRCKLEEMGFTDVGPENKPVSVQETYEAKRHEFHGERQRKEEB
			MKQMFVQRVKEKEAILKEAERELQAKFEHLKRLHQEERMKLEEK
1			RRLLEEEIIAFSKKKATSEIFHSQSFLATGSNLRKDKDRKNSQF
			FVKQKVPEHRRSSSQANFIKKKLEVCFDFAVICFITSIFGEQPQ LLIFMEKYFQVQGQYISOSE
5792	2263	653	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY
3,52	2203	653	LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER
			TARREADD (RASETTTRSHLGAERNIDLVLRVEDFDVESKFER
			TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT
l i			YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL
1			NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN
			RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ
1			FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND
i		*	ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLIDEQTSLLVLVP
1 1		•	AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY
]	:		DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF
i i			IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE
1	· .		EKATRAPHTD
5793	2263	653	
		033	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER
	,	•	TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT
			YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL
1			NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN
			RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ
	1		FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND
1			ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP
]		AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY
]	i		DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV
] [f		YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF
į			IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE
	1		EKATRAPHTD
5794	1	5016	MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV
	-	2070	KGQKGERGLPGLQGVIGFPGMOGPEGPOGPPGOKGDTGEPGLPG
	1		TKGTRGPPGASGYPGNPGLPGLPGQDGPPGPPGIPGCNGTKGER
	1		
	ļ		GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLPGLPGPPGPPGPPGPPGPPGPPGPPGPPGPP
	1	Ì	FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPPGEKGQM GLSFOGPKGDKGDOGVSGDPGVCCACACACACACACACACACACACACACACACACACAC
		İ	GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG
			YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT
1 1			PGPRGEPGPKGFPGLPGQPGPPGLPVFGQAGAPGFPGERGEKGD
1			
		İ	
			RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP

		T =	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first		P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ļ	\=possible nucleotide insertion)
1			GEPGEFYFDLRLKGDKGDPGFPGQPGMPGRAGSPGRDGHPGLPG PKGSPGSVGLKGERGPPGGVGFPGSRGDTGPPGPPGYGPAGPIG
			DKGOAGFPGGPGSPGLPGPKGEPGKIVPLPGPPGAEGLPGSPGF
	1		PGPOGDRGFPGTPGR\PGL\PGEKGAVG\QPGIGFPGPPGPKGV
	ł		DGLPGDMGPPGTPGRPGFNGLPGNPGVQGQKGEPGVGLPGLKGL
l	ļ		PGLPGIPGEKGSIGVPGVPGEHGAIGPPGLQGIRGEPGPPG
1			LPGSVGSPGVPGIGPPGARGPPGGQGPPGLSGPPGIKGEKGFPG
]		,	FPGLDMPGPKGDKGAQGLPGITGQSGLPGLPGQQGAPGIPGFPG
İ	i		SKGEMGVMGTPGQPGSPGPWGAPGLPGEKGD\HGFPGSSGPRGD
1			PGLKGDKGDVGLPGKPGSMDKVYMGSMKGOKGDQGEKGQIGPIG
			EKGSRGDPGTPGVPGKDGQAGQPGQPGPKGDPGISGTPGAPGLP
			GPKGSVGGMGLPGTPGEKGVPGIPGPQGSPGLPGDKGAKGEKGQ
			AGPPGIGIPGLRGEKGDOGIAGFPGSPGEKGEKGSIGIPGMPGS
			PGLKGSPGSVGYPGSPGLPGEKGDKGLPGLDGIPGVKGEAGLPG
			TPGPTGPAGQKGEPGSDGIPGSAGEKGEPGLPGRGFPGFPGAKG
			DKGSKGEVGFPGLAGSPGIPGSKGEQGFMGPPGPQGQPGLPGSP
	I		GHATEGPKGDRGPOGOPGLPGLPGPMGPPGLPGIDGVKGDKGNP
			GWPGAPGVPGPKGDPGFOGMPGIGGSPGITGSKGDMGPPGVPGF
ļ			OGPKGLPGLOGIKGDOGDOGVPGAKGLPGPPGPPGPYDIIKGEP
			GLPGPEGPPGLKGLQGLPGPKGQQGVTGLVGIPGPPGIPGFDGA
			PGOKGEMGPAGPTGPRGFPGPPGPDGLPGSMGPPGTPSVDHGFL
1			VTRHSOTIDDPOCPSGTKILYHGYSLLYVQGNERAHGQDLGTAG
i		1	SCLRKFSTMPFLFCNINNVCNFASRNDYSYWLSTPEPMPMSMAP
Į.			ITGENIRPFISRCAVCEAPAMVMAVHSQTIQIPPCPSGWSSLWI
1			GYSFVMHTSAGAEGSGQALASPGSCLEEFRSAPFIECHGRGTCN
1			
1		1	YYANAYSFWLATIERSEMFKKPTPSTLKAGELRTHVSRCQVCMR
			YYANAYSFWLATIERSEMFKKPTPSTLKAGELRTHVSRCQVCMR RT
5795	1192	61	1
5795	1192	61	RT
5795	1192	61	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE
5795	1192	61	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL
5795	1192	61	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN
5795	1192	61	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH
5795 5796	1192	1078	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI
			RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR
			RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF
			RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE
			RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP
			RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVMMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ
			RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R
			RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG
5796	2	1078	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG
			RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG FRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE
5796	2	1078	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWDDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASFG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR
5796	2	1078	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASFG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEBANKKMQAABISLEEKDQRIGEL
5796	2	1078	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASFG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLLLEHETEMSGELTDSDKERYQQLEEAS
5796	2	1078	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG FRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKATEBANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ
5796	2	1078	RT STRSPTVEYISAHPHILFMLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKATEBANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP
5796	2	1078	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT
5796	2	1078	RT STRSPTVEYISAHPHILFMLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT
5796	2	1078	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGBLTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG
5796	2	1078	RT STRSPTVEYISAHPHILFMLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMEMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGBLTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG
5796 5797	2	1078	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGBLTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTBVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEQARLSKIHLBKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN
5796	2	1078	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTALTYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEBANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEOARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN
5796 5797	2	1078	RT STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEBANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEQARLSKIHLBKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
5796 5797	2	1078	RT STRSPTVEYISAHPHILFMLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEBANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEQARLSKIHLBKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VYYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
5796 5797	2	1078	RT STRSPTVEYISAHPHILFMLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASFG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEBANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEOARLSKIHLEKYPNYKYKPRPKR TCIVDGKKRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP
5796 5797	2	1078	RT STRSPTVEYISAHPHILFMLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGMELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASFG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEBANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEQARLSKIHLBKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN
5796 5797	2	1078	RT STRSPTVEYISAHPHILFMLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPPPERESSILAKLKRKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL
5796 5797	2	1078	RT STRSPTVEYISAHPHILFMLKGYEAPQIALRCGIMLRECIRHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGMELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASFG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEBANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEQARLSKIHLBKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	A Tavaira M Mahiarina N Barrarina
1			L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
 	 		LLDNVDPNPENFVGAGIIOTKALOVGCLLRLEPNAOAOMYRLTL
			RTSKEPVSRHLCELLAQOF
5800	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL
3800	2079	1435	
	1		TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
			DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
	ļ	1	PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP
	j]	EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN
			KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL
	İ	ł	NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFOPTEM
			AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA
1.	1	1	LLDNVDPNPENFVGAGIIQTKALOVGCLLRLEPNAQAOMYRLTL
I			RTSKEPVSRHLCELLAOOF
F655	 	ļ	
5801	3	1413	FPRLYHLIPDGEITSIKINRVDPSESLSIRLVGGSETPLVHIII
1	1		QHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQP
1	1		CQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEE
1	1]	QLGIKLVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGH
1	1		DLRYGSPESAAHLIQASERRVHLVVSRQVRQRSPDIFQEAGWNS
1		i	NGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVA
1	1	[GGASHREWDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELT
1	1		EVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNH
		1	NMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVG
1		ĺ	GYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSG
1	1		
			MIHACLARLLKELKGRITLTIVSWPGTFL
5802	3	290	CFSLYQIMERIMDLPTLLRHAFREMFSVGGLFWMFRIRIILCLM
J.	1		GAFFYLISPLDFVPEALFGILGFLDDFFVIFLLLIYISIMYREV
<u></u>	<u> </u>		ITQRLTR
5803	2234	1299	BAQFGTTAEIYAYREEQDFGIBIVKVKAIGRQRFKVLELRTQSD
1			GIQQAKVQILPECVLPSTMSAVQLESLNKCQIFPSKPVSREDQC
1			SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLRB
1	1	,	WDENLKDDSLPSNPIDFSYRVAACLPIDDVLRIQLLKIGSAIQR
1:			LRCELDIMNKCTSLCCKOCOETEITTKNEIFSLSLCGPMAAYVN
	1 :		PHGYVHETLTVYKACNLNLIGRPSTEHSWFPGYAWTVAOCKICA
	1 :		
1		•	SHIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDKVI
<u> </u>			rcr .
5804	. 2	1707	EMEKQRQEEQRKRTEEERKRRIEQDMLEKRKIQRELAKRAEQIE
1			DINNTGTESASEEGDDSLLITVVPVKSYKTSGKMKKNFEDLEKE
	1		REEKERIKYEEDKRIRYEEQRPSLKEAKCLSLVMDDEIESEAKK
[ESLSPGKLKLTFEELERQRQENRKKQAEEEARKRLEEEKRAFEE
			ARROMVNEDEENODTAKIFKGYRPGKLKLSFEEMERORREDEKR
1			KABEEARRRIEEEKKAFAEARRNMVVDDDSPEMYKTISOEFLTP
1			GKLEINFEBLLKQKMEEEKRRTEEERKHKLEMEKQEFEQLRQEM
			GEBEEENETFGLSREYEELIKLKRSGSIOAKNLKSKFEKIGOLS
1			_
1			EKEIQKKIEEERARRAIDLEIKEREAENFHEEDDVDVRPARKS
į l			EAPFTHKVNMKARFEQMAKAREEEEQRRIEEQKLLRMQFEQREI
			DAALQKKREEEEEEGSIMNGSTAEDEEQTRSGAPWFKKPLKNT
			SVVDSEPVRFTVKVTGEPKPEITWWFEGEILQDGEDYQYIERGE
			TYCLYLPETFPEDGGEYMCKAVNNKGSAASTCILTIESKN
5805	3	776	YISDTLGQVYKSKIRWWIEENGGNGNISVDDLIALLDLAEHASS
			AFKESQQQSRDREYEVKERLYPKSKRRYDTYNIAGYQGEIEVGL
			YTIQILQLIPFFDNKNELSKRYMVNFVSGSSDIPGDPNNEYKLA
1			1
			LKNYIPYLTKLKFSLKKSFDFFDEYFVLLKPRNNIKQNEEAKTR
1	J		RKVAGYFKKYVDIFCLLEESQNNTGLGSKFSEPLQVERCRRNLV
•			ALKADKFSGLLEYLIKSQEDAISTMKCIVNEYTFLLK
[:		
5806	1257	877	AVFTFHNHGRTANLYSLHSWLGITTVFLFACQRFLGFAVFLLPW
5806	1257	877	AVFTFHNHGRTANLYSLHSWLGITTVFLFACQRFLGFAVFLLPW ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT
5806	1257	877	ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT
			ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP
5806	1257	1302	ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP RFSKKTFRRPMAVDIQPACLGLYCGKTLLFKNGSTEIYGECGVC
			ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP RFSKKTFRRPMAVDIQPACLGLYCGKTLLFKNGSTEIYGECGVC PRGQRTNAQKYCQPCTESPELYDWLYLGFMAMLPLVLHWFFIEW
			ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP RFSKKTFRRPMAVDIQPACLGLYCGKTLLFKNGSTEIYGECGVC

		·	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LMMLLRPLLVKKIACGLGKSDRFKSIYAALYFFPILTVLQAVGG
l		1	GLLYYAFPYIILVLSLVTLAVYMSASBIENCYDLLVRKKRLIVL
			FSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTAKFT
			EPSRILSEGANGH
5808	2	433	SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKNGSS
			EGRITHGFQLKSAYENNLMPYTNYTFDFKGVIDYIFYSKTHMNV
			LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPPLLP
			LVNGVHLPNRR
5809	464	2422	ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCRHGG
			RCVNTHGSFECYCMDGYLPRNGPEPFHPTTDATSCTEIDCGTPP
		1	EVPDGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTW
			ESPKLHCQEINCGNPPEMRHAILVGNHSSRLGGVARYVCQEGFE
			SPGGKITSVCTEKGTWRESTLTCTEILTKINDVSLFNDTCVRWQ
			INSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTPEVC
			LALYPGTNYTVNISTAPPRRSMPAVIGFQTAEVDLLEDDGSFNI
		·	SIFNETCLKLNRRSRKVGSEHMYQFTVLGQRWYLANFSHATSFN
			FTTREQVPVVCLDLYPTTDYTVNVTLLRSPKRHSVQITIATPPA
}			VKQTISNISGFNETCLRWRSIKTADMEEMYLFHIWGQRWYQKEF
-			AQEMTFNISSSSRDPEVCLDLRPGTNYNVSLRALSSELPVVISL
			TTQITEPPLPEVEFFTVHRGPLPRLRLRKAKEKNGPISSYQVLV
· ·			LPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAKDVPDDAM
ĺ			EIPIGDRLYYGEYYNAPLKRGSDYCIILRITSEWNKVRRHSCAV
			WAQVKDSSLMLLQMAGVGLGSLAVVIILTFLSFSAV
5810	3	1641	KVFGTHKDHEVSTLDTAISAVKVQLAEFLENLQEKSLRIEAFVS
		1	BIESFFNTIEENCSKNEKRLEEQNEEMMKKVLAQYDEKAQSFEE
1			VKKKKMEFLHEQMVHFLQSMDTAKDTLETIVREAEELDEAVFLT
			SFEEINERLLSAMESTASLEKMPAAFSLFEHYDDSSARSDQMLK
			QVAVPQPPRLEPQEPNSATSTTIAVYWSMNKEDVIDSFQVYCME
*		· ·	EPQDDQEVNELVEEYRLTVKESYCIFEDLEPDRCYQVWVMAVNF
l	į		TGCSLPSERAIFRTAPSTPVIRAEDCTVCWNTATIRWRPTTPEA
Į.			TETYTLEYCRQHSPEGEGLRSFSGIKGLQLKVNLQPNDNYFFYV
l			RAINAFGTSEQSEAALISTRGTRFLLLRETAHPALHISSSGTVI
l		1 :	SFGERRRLTEIPSVLGEELPSCGQHYWETTVTDCPAYRLGICSS
i		1	SAVQAGALGQGETSWYMHCSEPQRYTFFYSGIVSDVHVTERPAR
l			VGILLDYNNQRLIFINAESEQLLFIIRHRFNEGVHPAFALEKPG
1			KCTLHLGIBPPDSVRHK
5811	1918	851	AAALADPLPEDKWSAEKRRPLKSSLGYEITFSLLNPDPKSHDVY
		1	WDIEGAVRRYVQPFLNALGAAGNFSVDSQILYYAMLGVNPRFDS
1		1	WDIEGAVRRIVQPFDNALGAAGNESVDSQIDIIANDGVNEREDS
			ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA
!			
			ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA
			ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV
			ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT
			ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE
			ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL
5812	5204	2744	ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD
5812	5204	2744	ASSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREEEVEPGTARPPPAASAMDASLEKIADPT
5812	5204	2744	ASSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ
5812	5204	2744	ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREEEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA
5812	5204	2744	ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHBEERE
5812	5204	2744	ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHEEERE GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ
5812	5204	2744	ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREEEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA YISTLDKEKLRKITTRILSDTTLWLCRIFRYENGCAYFHEEERE GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG
5812	5204	2744	ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREEEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHBEERE GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT
5812	5204	2744	ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREEEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHEEERE GLAKICRLATHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA
5812	5204	2744	ASSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHBEERE GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHACQLS
5812	5204	2744	ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHBEERE GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHACQLS QRLQESLKKVNYIKILVEDELSSPVVVFRFFQELPGSDPVFKAV
5812	5204	2744	ASSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHEEERE GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG RLPLLLVANAGTAAVGHTÖKIGRLKELCEQYGIWLHVEGVNLAT LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHACQLS QRLQESLKKVNYIKILVEDELSSPVVVFRFFQELPGSDPVFKAV PVPNMTPSGVGRERHSCDALNRWLGEQLKQLVPASGLTVMDLEA
5812	5204	2744	ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHBEERE GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHACQLS QRLQESLKKVNYIKILVEDELSSPVVVFRFFQELPGSDPVFKAV PVPNMTPSGVGRERHSCDALNRWLGBQLKQLVPASGLTVMDLEA
5812	5204	2744	ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHBEERE GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHACQLS QRLQESLKKVNYIKILVEDELSSPVVVFRFFQELPGSDPVFKAV PVPNMTPSGVGRERHSCDALNRWLGEQLKQLVPASGLTVMDLEA EGTCLRFSPLMTAAVLGTRGEDVDQLVACTESKLPVLCCTLQLR EEFKQEVEATAGLLYVDDPNWSGIGVVRYEHANDDKSSLKSYPQ
5812	5204	2744	ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHBEERE GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHACQLS QRLQESLKKVNYIKILVEDELSSPVVVPRFFFQELPGSDPVFKAV PVPNMTPSGVGRERHSCDALNRWLGBQLKQLVPASGLTVMDLEA EGTCLRFSPLMTAAVLGTRGEDVDQLVACIESKLPVLCCTLQLR EEFKQEVEATAGLLYVDDPNWSGIGVVRYEHANDDKSSLKSYPQ GENIHAGLLKKLNELESDLTFKIGPEYKSMKSCLYVGMASDNVH
5812	5204	2744	ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHBEERE GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHACQLS QRLQESLKKVNYIKILVEDELSSPVVVFRFFQELPGSDPVFKAV PVPNMTPSGVGRERHSCDALNRWLGEQLKQLVPASGLTVMDLEA EGTCLRFSPLMTAAVLGTRGEDVDQLVACTESKLPVLCCTLQLR EEFKQEVEATAGLLYVDDPNWSGIGVVRYEHANDDKSSLKSYPQ

SEQ	Predicted	Predicted end	13-4
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
[residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Coden / named and a land a land a land
İ		sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
İ			TEPIYVYKAQGAGVTLPPTPSGSRTKQRLPGQKPFKRSLRGSDA
		Į.	LSETSSVSHIEDLEKVERLSSGPEQITLEASSTEGHPGAPSPQH
ŀ		1	TDQTEAFQKGVPHPEDDHSQVEGPESLR
5813	2936	699	HRDGVSGSLERPLTDRSRTGAFAQQRGKMATAGGGSGADPGSRG
		1	
ł	i	f	LLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQI
		1	GCQSSISGDTGVIHVVEKEEDLQWVLTDGPNPPYMVLLESKHFT
1	i	ļ	RDLMEKLKGRTSRIAGLAVSLTKPSPASGFSPSVQCPNDGFGVY
ı	ŀ		SNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLEDENETKVI
ĺ		İ	KQCYQDHNLSQNGSAPTFPLCAMQLFSHMAWLSFSTAT\CMRRS
ĺ	•		SIQSTFSINPKIVCDPLSDYNVWSMLKPINTTGTLKPDDRVVVA
ŀ	1 .		ATRLDSRSFFWNV\APGAESAVASFVTQLAAAEALQKAPDVTTL
-	ŀ		DDMMETIREOGENERATIOGRAPHOTAL TARREST T
			PRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVEL
i .			GQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVP
			AVILRRPNQSQPLPPSSLQRFLRARNISGVVLADHSGAFHNKYY
	<u>.</u>		QSIYDTAENINVSYPEWLEPLKE/ETWNFG*QDTAKALADVATV
			LGRALYELAGGTNFSDTVQADPQTVTRLLYG\FLIKANNSWFQS
1			ILQGRDLRSYLG*RGLFQH\YIAV\SSPTNTIYV/VLQYALANL
			TGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLP
			RCVRSTARLARALSPAFELSQWSSTEYSTWTESRWKDIRARIFL
1 :			
			IASKELELITLTVGFGILIFSLIVTYCINAKADVLFIAPREPGA
			VSY
5814	8500	432	ALKCRPRRVLAILVGPVQPDRMAEEGAVAVCVRVRPLNSREESL
1			GETAQVYWKTHNNVIYPVDGSKSFNFDRVLHGNETPKNVYEA\I
	• 1		AAPIIDSAIQGYNGTIFA\YGQT\ASGKTYTMMGSEDHLGVIPQ
			GQFHGHFSQKI*EVFLDREFLLRVSYMEIYNETITDLLCGTQKM
			KPLIIREDVNRNVYVADLTEEVVYTSEMALKWITKGEKSRHYGE
			1
			TKMNQRSSRSHTIFRMILESREKGEPSNCEGSVKVSHLNLVDLA
1 1			GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSDGQVGGFI
1 1			NYRDSKLTRILQNSLGGNPKTRIICTITPVSFDETLTALQFAST
			AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLETRAQ
	•		AMEKDQLAQLLEEKDLLQKVQNEKIENLTRMLVTSSSLTLQQEL
	÷	i	KAKRKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL
			LREIDESVCSESDVFSNTLDTLSEIBWNPATKLLNQENIESELN
	:		SLRADYDNLVLDYEQLRTBKEEMELKLKEKNDLDEFEALERKTK
	:		KDQEMQLIHEISNLKNLVKHREVYNQDLENELSSKVELLREKED
	ļ		
			QIKKLQEYIDSQKLENIKMDLSYSLESIEDPKQMKQTLFDAETV
1 1			ALDAKRESAFLRSENLELKEKMKELATTYKQMENDIQLYQSQLE
1 1	•		AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK
1	1		ITDLQKELNKEVEENEALRBEVILLSELKSLPSEVERLRKEIQD
1	i		KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ
1 1			SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE
į i	. 1		AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE
1 1			NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL
	}		QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKOHOETINTLKS
1	1		
			KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL
1 1		İ	TADVKDNEIIEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL
			KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR
			TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINBIE
Į l	Ì		NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL
į į	,		KELQKSPETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE
]			TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEOELLP
	!		
1			NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF
į (j	QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE
]		ļ	SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG
1		ļ	LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV
j l	ĺ		AKHLETEEELKVAHCCLKEQEETINELRVNLSEKETBISTIOKO
j 1			LEAINDKLQNKIQEIYEKEEQLNIKOISEVOEKVNELKOFKEHR
]			KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA
] [ì	
			LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNBTQEKMCE
[j	1EHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD
<u> </u>			DLRSVEETLKVERDQLKENLRETITRDLEKQEELKIVHMHLKEH
			·

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
MO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
I	sequence	Bequence	\=possible nucleotide insertion)
<u> </u>	sequence		QETIDKLRGIVSEKTNEISNMQKDLEHSNDALKAQDLKIQEELR
l			IAHMHLKEQQETIDKLRGIVSEKTDKLSNMQKDLENSNAKLQEK
1			IOELKANEHOLITLKKDVNETOKKVSEMEQLKKQIKDQSLTLSK
1			LEIENLNLAQKLHENLEEMKSVMKERDNLRRVEETLKLERDQLK
ì			ESLQETKARDLEIQQELKTARMLSKEHKETVDKLREKISEKTIQ
1			ISDIOKDLDKSKDELQKKIQELQKKELQLLRVKEDVNMSHKKIN
			EMEOLKKOFEPNYLCKCEMDNFOLTKKLHESLEEIRIVAKERDE
1		1	LRRIKESLKMERDOFIATLREMIARDRONHQVKPEKRLLSDGQQ
}		†	HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFH
1			RIMKKLKYVLSYVTKIKEEQHBCINKFEMDFIDEVBKQKELLIK
1			IOHLOODCDVPSRELRDLKLNONMDLHIEEILKDFSESEFPSIK
1			TEFQQVLSNRKEMTQFLEEWLNTRFDIEKLKNGIQKENDRICQV
		}	NNFFNNRIIAIMNESTEFEERSATISKEWEQDLKSLKEKNEKLF
			KNYOTLKTSLASGAQVNPTTODNKNPHVTSRATQLTTEKIRELE
i			NSLHEAKESAMHKESKIIKMQKELEVTNDIIAKLQAKVHESNKC
		,	LEKTKETIQVLQDKVALGAKPYKEEIEDLKMKLGKIDLEKMKNA
İ	1		KEFEKEISATKATVEYOKEVIRLLRENLRRSQQAQDTSVISEHT
			DPQPSNKPLTCGGGSGIVQNTKALILKSEHIRLEKEISKLKQQN
ļ			BOLIKOKNELLSNNOHLSNEVKTWKERTLKREAHKOVTCENSPK
1		1	SPKVTGTASKKKQITPSQCKERNLQDPVPKESPKSCFFDSRSKS
			LPSPHPVRYFDNSSLGLCPEVQNAGAESVDSQP\GPWARLFQGK
ł]	DVP\ECKTQ
5815	23	1460	SELVMWTVQNRESLGLLSFPVMITMVCCAHSTNEPSNMSYVKET
3013	""		VDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTL
	į.		TMYFQQSWKDKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKK
i			SFVHGVTVKNRMIRLHPDGTVLYGLRITTTAACMMDLRRYPLDE
•		}	ONCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELPQFSIVDY
			KMVSKKVEFTTGAYPRLSLSFRLKRNIGYFILQTYMPSTLITIL
1		1	SWVSFWINYDASAARVALGITTVLTMTTISTHLRETLPKIPYVK
1	ļ		AIDIYLMGCFVFVFLALLEYAFVNYIFFGKGPQKKGASKQDQSA
1	•		NEKNKLEMNKVQVDAHGNILLSTLEIRNETSGSEVLTSVSDPKA
			TMYSYDSASIQYRKPLSSRE\A*GRAPDRHGVPSKGRIRRRAS\
1			QLKVKIPDLTDVNSIDKWSRMFFPITFSLFNVVYWLYYVH
5816	861	191	TSSRSRAAAQEGDAETPGSVERRGRRAGAEDGMSQAPGAQPSPP
1		Í	TVYHERORLELCAVHALNNVLOQQLFSQEAADEICKRLAPDSRL
ł			NPHRSLLGTGNYDVNVIMAALQGLGLAAVWWDRRRPLSQLALPQ
1	1	ľ	VLGLILNLPSPVSLGLLSLPLRRRHLRWPCARL/VTVSYYNLDS
			K\LRAPEGPGGLRTE*GPFLAAALAQGLCEVLLVVTKEVEEKG
1	1	1	SWLRTD
5817	851	118	RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCPC*PPSPPAAD
			VMSNTTVPNAPQANSDSMVGYVLGPFFLITLVGVVVAVVMYVQK
			KKRVDRLRHHLLPMYSYDPAEELHEAEQELLSDMGDPKVV\QAG
		1	RVATSTSGCHCWMSRRDLTPLPHPSEPGVLDCLGPCHLLPLLSP
1			GSPCWVLGLHFSLHPPSAASASHALTITSLPPGLLPFVGVELTA
			HPQALMGRGFPSGMAAAGRHLCFL
5818	3	3918	QALRDKLNIFLVQSFYAVRHTESWKLMSTDDQQKIQAAAFDKGD
			DRRLGKKPIFSSSQORKQVSDSGDIKIKSWRGNNKKECWSYLST
			NKKMKSDGLGASGHSSSTNRNSINKTLKQDDVKEKDGTKIASKI
			TKELKTGGKNVSGKPKTVTKSKTENGDKARLENMSPRQVVERSA
	1		TAAAAATGQKNLLNGKGVRNQEGQISGARPKVLTGNLNVQAKAK
			PLKKATGKDSPCLSIAGPSSRSTDSSMEFSISTECLDEPKENGS
			TEEEKPSGHKLSFCDSPGQMMKNSVDSVKNSTVAIKSRPVSRVT
		1	NGTSNKKSIHEQDTNVNNSVLKKVSGKGCSEPVPQAILKKRGTS
			NGCTAAQQRTKSTPSNLTKTQGSQGESPNSVKSSVSSRQSDENV
		1	AKLDHNTTTEKQAPKRKMVKQVHTALPKVNAKIVAMPKNLNQSK
			KGETLNNKDSKQKMPPGQVISKTQPSSQRPLKHETSTVQKSMFH
			DVRDNNNKDSVSEQKPHKPLINLASEISDAEALQSSCRP\DPQK
			PLNDQEKEKLALECQNISKLDKSLKHELESKQICLDKSETKFPN
			HKETDDCDAANICCHSVGSDNVNSKFYSTTALKYMVSNPNENSL
1			NSNPVCDLDSTSAGQIHLISDRENQVGRKDTNKQSSIKCVEDVS
1			LCNPERTNGTLNSAQEDKKSKVPVEGLTIPSKLSDESAMDEDKH
L			

SEO	Predicted	Thursday and	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	t .	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid		P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1	•]	ATADSDVSSKCFSGQLSEKNSPKNMETSESPESHETPETPFVGH
			WNLSTGVLHQRESPESDTGSATTSSDDIKPRSEDYDAGGSQDDD
			GSNDRGISKCGTMLCHDFLGRSSSDTSTPEELKIYDSNLRIEVK
'			MKKQSSNDLFQVNSTSDDEIPRKRPEIWSRSAIVHSRERENIPR
			GSVQFAQEIDQVSSSADETEDERSEAENVAENFSISNPAPQQFQ
1			GIINLAFEDATENECREFSANKKFKRSVLLSVDECEELGSDEGE
			VHTPFQASVDSFSPSDVFDGISHEHHGRTCYSRFSRESEDNILE
			CKQNKGNSVCKNESTVLDLSSIDSSRKNKQSVSATEKKNTIDVL
	ľ	ĺ	SSRSRQLLREDKKVNNGSNVENDIQQRSKFLDSDVKSQERPCHL
1			DLHQREPNSDIPKNSSTKSLDSFRSQVLPQEGPVKESHSTTTEK
1			ANIALSAGDIDDCDTLAQTRMYDHRPSKTLSPIYEMDVIEAFEQ
	ļ		KVESETHVTDMDF*DDQHFAKQDWTLLKQLLSEQDSNLDVTNSV PEDLSLAQYLINQTLLLARDSSKPQGITHIDTLNRWSELTSPLD
		1	SSASITMASFSSEDCSPQGEWTILELETQH
5819	1	5557	AAAGLLGALHLVMTLVVAAARAEKEAFVQSESIIEVLRFDDGGL
] 3023	-] 3337	LQTETTLGLSSYQQKSISLYRGNCRPIRFEPPMLDFHEQPVGMP
1			KMEKVYLHNPSSE*TITLVSIFATTSHFHASFFQNRKILPGGNT
			SFDVS/VFLARVVGNVENTLFINTSNHGVFTY\QVFGVGVPNPY
ļ			RLRPFLGARVTVNSSFSPIINIHNPHSEPLQVVEMYSSGGDLHL
-			ELPTGQQGGTRKLWEIPPYETKGVMRASFSSREADNHTAFIRIK
[[TNASDSTEFIILPVEVEVTTAPGIYSSTEMLDFGTLRTQDLPKV
			LNLHLLNSGTKDVPITSVRPTPQ\NDAITVHFKPITLKAS\ESK
			YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYOAEV
l		1	LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFAILIHDVL
			LPEEAKTMFKVHNFSKPVLILPNESGYIFTLLFMPSTSSMHIDN
			NILLITNASKFHLPVRVYTGFLDYFVLPPKIEERFIDFGVLSAT
	,		EASNILFAIINSNPIELAIKSWHIIGDG\LSIELVAVDRGNRTT
			IISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGIH
			DGAIQITTDYEILTIPVK\AVIAVGSLTCSPKHVVLPPSFPGKI
i i			VHQSLNIMNSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDLEPG
			KKSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKVQPGVAMQEDM
			WDADWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNIISKI
			TABLSWPSILSSPRHLKFPLTNTNCSS\EEEITLENP/SQDVPV
,			YVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQVFRN
			SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTPVHN
.			RTVSSLIIVRNNLTVMDAVMVQGQGTTENLRVAGKLPGPGSSLR
			FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGQLQIHIETIE
			ISGYSCEGYGFKVVNCQEFTLSANASRDIIILFTPDFTASRVIR
'			ELKFITTSGSBFVFILNASLPYHMLATCAEALPRPNWELALYII
			ISGIMSALFLLVIGTA\YLEAQGIWEP\FRRRLS\FEASNPPFD
			VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA
			GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAQAA
			SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQHHAHS
			PLEOHPOPPLPPPVPQPQEPQPERLSPAPLAHPSHPERASSARH
		,	SSEDSDITSLIEAMDKDFDHHDSPALEVFTEQPPSPLPKSKGKG
			KPLQRKVKPPKKQEEKEKKGKGKPQEDELKDSLADDDSSSTTTE
			TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKLLNI
			KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTSGSK
			SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEKDSP
	[PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSPTPAS
]		PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKLTKAA
			SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSLGIS
			HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNLTGE
1		}	VFSKLGLSRSCNQASQRSWNBFNSGPSYLWESPATDPSPSWPAS
	. 1		SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTTPAN TLASIGLMGTFNSDADHADSTSSDADDLCGTTVNDWDLWSDTLGD
l			TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPTIGR
5820	310	1270	RSSDPWSNSHFPHEN RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSRGPIQ
2020	210	12/0	RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSRGPIQ SSGPTIQ\VI*IDQGLPGKK*KSN*KRKRK/DSKALAEFEEKMN
ļ			ENWKKELEKHREKLLSGSESSSKKRQRKKKEKKKSW*\DSSSS\
			SSSSDSSSSSSDSEDEDKKQGKRKKKKNRSHKSSESSMSETES
			Call Since a Canton Name On Anna Canton Cant

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	_	\=possible nucleotide insertion)
			DSKDSLKKKKKSKDGTEKEKDIKGLSKKRKMYSEDKPLSSESLS
	•		ESEYIEEVRAKKKSSEEREKATEKTKKKKKKKKKKKKKKKKAA
İ			SSSPDSP*H*EKSGFPYKESAMSEEISTVKTTTYLLKCMNFLVF
1			GIIPGLFSSHSDATV
5821	179	915	KWRNQSWRWPKPGTNWMLSCSVCWRRVTWTGSVWMRKLGKHPQT
3021	1 -73		PT/IKDCSIAATGKRPSARFPHORRKKRREMDDGLAEGGPORSN
į			TYVIKLFDRSVDLAQFSENTPLYPICRAWMRNSPSVRERECSPS
1			SPLPPLPEDEEG\SEVTNSKSR*CVQACPPTHTPGGQPKNACR\
			SRIPSPLAALRMOGTP*RWSPFEPEPSPSTLIYRNMQRWKRIRQ
1		}	RWKEASHRNQLRYSESMKILREMYERQ
		1222	
5822	464	4379	QTLKEMPIVMARDLEETASSSEDEEVISQEDHPCIMWTGGCRRI
1	1	}	PVLVFHADAILTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA
1	1	1	HGFHEVHPSSTDYNLMWTGSHLKPFLLRTLSEAQKVNHFPRSYE
	1	i	LTRKDRLYKNIIRMQHTHGFKAFHILPQTFLLPAEYAEFCNSYS
1	1		KDRGPWIVKPVASSRGRG\VYLINNPNQISLEENILVSRYINNP
1	ļ		LLIDDFKFDVRLYVLVTSYDPLVIYLYEEGLARFATVRYDQGAK
			NIRNQFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLRY
1			LKQEGRDTTALMAHVEDLIIKTIISAELAIATACKTFVPHRSSC
			FELYGFDVLIDSTLKPWLLEVNLSPSLACDAPLDLKIKASMISD
1			MFTVVGFVCQDPAQRASTRPIYPTFESSRRNPFQKPQRCRPLSA
1			SDAEMKNLVGSAREKGPGKLGGSVLGLSMEEIKVLRRVKEENDR
			RGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRLFQDRMTADG
			APELKI*SLNSKAKLHAALYERKLLSLEVRKRRRRSSRLRAMRP
			KYPVITQPAEMNVKTETESEEEEEVALDNEDEBQEASQEESAGF
Ī			LRENQAKYTPSLTALVENTPKENSMKVREWNNKGGHCCKLETQE
			LEPKFNLMQILQDNGNLSKMQARIAFSAYLQHVQI\RLMKDSGG
			QTFSASWAAKEDEQMELVVRFLKRASNNLQHSLRMVLPSRRLAL
			LERTRILAHQLGDFIIVYNKETEQMAEKKSKKKVEEEEEDGVNM
			ENFQEFIRQASEAELEEVLTFYTQKNKSASVFLGTHSKISKNNN
			NYSDSGAKGDHPETIMEEVKIKPPKQQQTTEIHSDKLSRFTTSA
1			EKEAKLVYSNSSSGPTATLQKIPNTHLSSVTTSDLSPGPCHHSS
1	j		LSOIPSAIPSMPHOPTILLNTVSASASPCLHPGAQNIPSPTGLP
1			RCRSGSHTIGPFSSFQSAAHIYSQKLSRPSSAKAGSCYLNKHHS
1		•	GIAKTOKEGEDASLYSKRYNOSMVTAELORLAEKQAARQYSPSS
1		İ	HINLLTOQVTNLNLATGIINRSSASAPPTLRPIISPSGPTWSTQ
1		1	SDPOAPENHSSSPGSRSLQTGGFAWEGEVENNVYSQATGVVPQH
ļ			KYHPTAGSYQLQFALQQLEQQKLQSRQLLDQSRARHQAIFGSQT
1			LPNSNLWTMNNGAGCRISSATASGOKPTTLPQKVVPPPSSCASL
1			VPKPPPNHEQVLRRATSQKASKGSSAEGQLNGLQSSLNPAAFVP
ļ		1	ITSSTDPAHTKIMNHKHTEKQPVHHSWVHD
F000	45	2202	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF
5823	42	2293	DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP
'	1		DISESSSANEDDE VFFGPFGHRERCIAASHEHMAPVPEQPPHP TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP
			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS
1			DSPLLGPPVGEPRLLASSPALPSSGAOARLTRAPGPPHSAHALP
		j	
		1	RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK
1		•	EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGQGK
			RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA
1			CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
1	1	1	L\PAGPVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE
1	1		GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN
		1	QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
1	1	1	RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
			PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
1			GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
Ī			EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSB
		1	SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
1			ENVDSPLLKF
5824	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF
			DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP
1			TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP

SEQ	Predicted	1 8 21 3	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO.	location	i .	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Í	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS
	· '		DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP
1	1	1	RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK
1	į		EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGQGK
1		1	RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA
			CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
		1	L\PAGPVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE
			GGG\QWLNSSCAWSESSQLNKTRSIRRDSCLNSKTKVMPTPTN
			GGG (QWENSSCAWSESSQENKTKSIKKRDSCENSKTKVMPTPTN
į			QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
}		ł	RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
1		1	PL\CVPARRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
			GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
1		1	EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE
	1	1	SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
5055	<u> </u>		ENVDSPLLKF
5825	2	4210	FLQIESASPAPFSSGFLAAHPHSPGGSLATKGRSRLSAPGMLHL
	1		SAAPPAPPPEVTATARPCLCSVGRRGDGGKMAAAGALERSFVEL
ĺ	1		SGAERERPRHFREFTVCSIGTANAVAGAVKYSESAGGFYYVESG
	}		KLFSVTRNRFIHWKTSGDTLELMEESLDINLLNNAIRLKFQNCS
		•	VLPGGVYVSETQNRVIILMLTNQTVHRLLLPHPSRMYRSELVVD
1		İ	SQMQSIFTDIGKVDFTDPCNYQLIPAVPGISPNSTASTAWLSSD
			GEALFALPCASGGIFVLKLPPYDIPGMVSVVELKQSSVMQRLLT
ľ		ļ	GWMPTAIRGDQSPSDRPLSLAVHCVEHDAFIFALCQDHKLRMWS
Ī			YKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLYL
			GIF\MHAPKRGQFCIFQLVSTESNRYSLDHISSLFTSQETLIDF
1	İ		ALTSTDIWALWHDAENQTVVKYINFEHNVAGQWNPVFMQPLPEE
1	·		EIVIRDDQDPREMYLQSLFTPGQFTNEALCKALQIFCRGTERNL
i			DLSWSELKKEVTLAVENELQGSVTEYEFSQEEFRNLQQEFWCKF
]		YACCLQYQEALSHPLALHLNPHTNMVCLLKKGYLSFLIPSSLVD
İ			HLYLLPYENLLTEDETTISDDVDIARDVICLIKCLRLIEESVTV
1			DMSVIMEMSCYNLQSPEKAAEQILEDMITIDVENVMEDICSKLO
j	ļ	<u>.</u>	EIRNPIHAIGLLIREMDYETEVEMEKGFNPAQPLNIRMNLTQLY
	:		GSNTAGYIVCRGVHKIASTRFLICRDLLILQQLLMRLGDAVIWG
		•	TGQLFQAQQDLLHRTAPLLLSYYLIKWGSECLATDVPLDTLESN
		;	LQHLSVLELTDSGALMANRFVSSPQTIVELFFQEVARKHIISHL
1			FSQPKAPLSQTGLNWPEMITAITSYLLQLLWPSNPGCLFLECLM
		•	GNCQYVQLQDYIQLLHPWCQVNVGSCRFMLGRCYLVTGEGQKAL
	,		ECFCQAASEVGKEEFLDRLIRSEDGEIVSTPRLQYYDKVLRLLD
			VIGLPELVIQLATSAITEASDDW\KSQATL\RTCIFKHHL\DLG
			\HNSQAYGSL*PQIPDSSRQLDCLRQLVVVLCERSQLQDLVEFS
1			YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAG
,			TVMFEYGMRLGREVRTLRGLEKQGNCYLAALNCLRLIRPEYAWI
j			VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE
			CSLARIRLTLAQHDPSAVAVAGSSSAEEMVTLLVQAGLFDTAIS
			LCQTFKLPLTPVFEGLAFKCIKLQFGGEAAQAEAWAWLAANQLS
			SVITTKESSATDRAWRLLSTYLERYKVQNNLYHHCVINKLLSHG
			VPLPNWLINSYKKVDAAELLRLYLNYDLLDLTPYQVIRICGC
5826	3	871	KSQLLRDHSAPPPKPCTSVGAMGC*PRQ/SPKEQQRQLKKQKNR
			AAAQRSRQKHTDKADALHQQHESLEKDNLALRKEIQSLQAELAW
		•	WSRTLHVHERLCPMDCASCSAPGLLGCWDOAEGLLGPGPOGOHG
j İ			CREQLELFOTPGSCYPAOPLSPGPOPHDSPSLLOCPLPSLSLGP
[ł		AVVAEPPVQLSPSPLLFASHTGSSLQGSSSKLSALQPSLTAQTA
			PPQPLELEHPTRGKLGSSPDNPSSALGLARLQSREHKPALSAAT
			WQGLVVDPSPHPLLAFPLLSSAQVHF
5827	194	2287	GMGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYK
	1.7°	4401	
			RENEDKVNKAAKVP**HLKTLRHPCLLRFLSCTVEADGIHLVTE
			RVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHLTHNNVCL
			SSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP
[EEMSPEFTTLPECHGHARDAFSFGTLVESLLTILNEQVSADVLS
ĺ			SFQQTLHSTLLNPIPKWRPALCTLLSHDFFRNDFLEVVNFLKSL
			TLKSEEEKTEFFKFLLDRVSCLSEELIASRLVPLLLNQLVFAEP

Deginning location cortesponding cotation cortesponding cotation corresponding to first amino acid residue of amino acid residue				Amino acid segment containing signal peptide
No:	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Corresponding to first anino acid residue of anino acid residue of anino acid residue of anino acid sequence Defeution, Particular, Pa	,			
to first amino acid residue of seidu	NO:	••	₹	
to first amino acid residue of amino acid sequence Section, T-Threonine, V-Alline, Section, T-Threonine, V-Alline, Section, T-Threonine, V-Alline, Section, T-Threonine, V-Alline, Section, T-Threonine, V-Alline, Section, T-Threonine, V-Alline, Section, T-Threonine, V-Alline, Section, T-Threonine, V-Alline, Section, T-Threonine, V-Alline, Section, T-Threonine, V-Alline, Section, V-possible nucleotide deletion, Section, V-possible nucleotide insertion, Seventhernonine, V-possible nucleotide Seventhernonine, V-possible nucleotide Seventhernonine, V-possible nucleotide Seventhernonine, V-possible nucleotide Seventhernonine, V-possible nucleotide Seventhernonine, V-possible nucleotide Seventhernonine, V-possible nucleotide Seventhernonine, V-possible nucleotide Seventhernonine, V-possible nucleotide Seventhernonine, V-possible nucleotide Seventhernonine, V-possible nucleotide Seventhernonine, V-possible nucleotide Seventhernonine, V-possible nucle		location	corresponding	
amino acid residue of amino acid sequence solvery popular "Tyrposhan, "Tyrposhan, "Alunknown, "Stor Codon, /=possible nuclectide deletion, \		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
mesidue of amino acid sequence with provided and amino acid sequence control sequence control sequence control		to first	amino acid	
residue of amino acid sequence W-Tryptophan, Y-Tyrosine, X-Unknown, *-Storon amino acid sequence Vox. Popssible nucleotide deletion, Popssible nucleotide deletion, Popssible nucleotide deletion, Popssible nucleotide insertion, Vax.		amino acid	residue of	
amino acid sequence Codon, /-possible nucleotide deletion, -possible nucleotide insertion) WAYKSKLEYLIGEKKOHGOGSTPCLLSPALFOSSVIPULO EVBERNAVLISH ERVOVALISHERDEKYITIPULO DYSSIVATITHSLAULVSLLIGERVVGGERRIFERTER TKYNTUSLSEGDEFSS JKEYNIGLSUKNYLIKPOSDREYSPALF BESSKODEPSSLDTVANGGEDTKYTYTGSGEPT PUT BESSKODEPSSLDTVANGGEDTKYTYTGSGEPT PUT BESSKODEPSSLDTVANGGEDADOLEPSKYSDGSRPLKYP GLGESFTIOVKKEYVENDEROMFADHE FIRPARAPILIPE EMMPKKODVSPVMGFSSKFAARITEGERGEWEEGELANED ANGGGRENDLISS TPKPLLEVOKKEYTGSGERPLKYP INVTREDVGKALCASEFWKMKEPDIVCTEDDADWSTADSLRYT KLTDTUNGCHITUNGCHONDSTOKELLYPHILIPE EMMPKKODVSPVMGFSSKFAARITEGERGEWEEGELANED ANGGGRENDLISS TPKPLLEVOKKELTVYPHILIPE EMMPKKODVSPVMGFSSKFAARITEGERGEWEEGELANED ANGGGRENDLISS TPKPLLEVOKKELTVYPHILIPE EMMPKKODVSPVMGFSSKFAARITEGERGEWEEGELANED ANGGGRENDLISS TPKPLLEVOKKELTVYPHILIPE EMMPKKODVSPVMGFSSKFAARITEGERGEWEEGELANED ANGGGRENDLISS TPKPLLEVOKKELTVYPHILIPE EMMPKKODVSPVMGFSSKFAARITEGERGEKEGEKERGEKERGEKERGE INVTREDVIKACACHSTANGKERGEKEGEKKEKEGEKERGEKERGE ENTYTTEDVOKACACHSTANGKERGEKEGEKKEKEGEKERGEKERGE ENTYTTEDVIKACACHSTANGKERGEKERGEKKEKEGEKERGEKERGE ENTYTTEDVIKACACHSTANGKERGEKERGEKKERGEKERGEKERGE ENTYTTEDVIKACACHSTANGKERGEKERGEKKERGEKERGEKERGE ENTYTTEDVIKACACHSTANGKERGERGEKERGEKERGEKERGEKERGE ANGGADTQVILMERNITÖDELHCKITTEDLIKACHTOPTVSFSKOG ANGGADTQVILMERNITÖDELHCKITTEDLIKACHTOPTVSFSKOG ANGGADTQVILMERNITÖDELHCKITTEDLIKACHTOPTVSFSKOG ANGGADTQVILMERNITÖDELHCKITTEDLIKACHTOPTVSFSKOG ANGGADTQVILMERNITÖDELHCKITTEDLIKACHTOPTVSFSKOG ANGGADTQVILMERNITÖDELHCKITTEDLIKACHTOPTVSFSKOG ANGGADTQVILMERNITÖDELHCKITTEDLIKACHTOPTVSFSKOG ANGGADTQVILMERNITÖDELHCKITTEDLIKACHTOPTVSFSKOG ANGGADTQVILMERNITÖDELHCKITTEDLIKACHTOPTVSFSKOG ANGGADTQVILMERNITÖDELHCKITTEDLIKACHTOPTVSFSKOG ANGGADTQVILMERNITÖDELHCKITTEDLIKACHTOPTVSFSKOG ANGGADTQVILMERNITÖDELHCKITTEDLIKACHTOPTVSFSKOG ANGGADTANGKACHTOPTVSFTSTANGKACHTOPTVSFSKOG ANGGADTANGKACHTOPTVSFTSTANGKACHTOPTVSFTSTANGKACHTOPTVSFTSTANGKACHTOPTVSFTSTANGKACHTOPTVSFTSTANGKACHTOPTVSFTSTANGKACHTOPTVSFTSTANGKACHTOPTVSFTSTANGKACHTOPTVSFTSTANGKACHTOPTVSFTSTANGKACHTOPTVSFTSTANGKACHTO			amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
sequence \possible nucleotide insertion				Codon. /=possible nucleotide deletion,
VANVASTEPLILGPKNIPGCHAGGETPCLLSPALFOGRVIPULO EVEREWYMWILSH IRAYVGALSLERGOLKUVILLYOVULGA D\TSISSIVATIHSLAVUSLLARGOKUVILLYOVULGA TX\NTOLSLEGGPSQPIKFP INGEDWINGGETKI FERTAY TX\NTOLSLEGGPSQPIKFP INGEDWINGGETKI FERTAY EESMDOCEPSIJOTKVINGGETATKEVTSGEGKP IPALIS EESMPOKSGIPQKISLVQGGDADOTEPPKYSGGETJLKYPE EESMPOKSGIPQKISLVQGGDADOTEPPKYSGGETJLKYPE EESMPOKSGIPQKISLVQGGDADOTEPPKYSGGETJLKYPE EESMPOKSGIPQKISLVQGGDADOTEPPKYSGGETJLKYPE ENYKKOLVSPYMOFSSKRAARITEGERGEKEEGELINGED W AREGGSIGAVAACGELSYSCDFCPARPHTSNLTRFVKMEFQA ANGGGSRINDLTSSI FRELEPVANTELITERLERVERFFY IVVITEDVQRALGAFFMMMARDIVCIPDDADMETADSLKYI KLKIDULVISCOLITDVALHEVVDLERAYDASLAMLARKGGO EPVPGGKKKKAVPGRPTFGVDSTGRILLPANERADLGELV GSILGKHPRIRTHTOLVDAHLYCLKYIVOPIMENG\SITESI EL\IPYLV\SGCPSASSGGGTKRIMMARKGUSFRI SFY*KEANYTGTGAPY\D\ACMI FLYLVINGSGVSSASSGGGTKRIMMARKGUSFRI SFY*KEANYTGTGAPY\D\ACMI FYLVINGSGVSSASSGGGTKRIMMARKGUSFRI SFY*KEANYTGTGAPY\D\ACMI FYLTHHBERVETVIRGGTPSWINGSVGRANFVDFN GTCLABAGSDQTVKWDVXWNLLIGHTGVHSGGVSTSPHOFP TCHABAGSDQTVKWDVXWNLLIGHTGVHSGGVSTSPHOFP GTCLABAGSDQTVKWDVXWNLLIGGSR*SIGCELDLILMI LLILPGOKAVVAUSLAVATAGGTBYLLIGGSR*SIGCELDLILMI LLILPGOKAVVAUSLAVATSIGHTAVATAGGTBYLLIGGSR*SIGCELDLILMI LLILPGOKAVVAUSLAVATSIGHTAVATAGGTBYLTYSFSKGG ASGGADTOVLLHRITTSDFHILLIGLGSR*SICLELDLILMI LLILPGOKAVVAUSLAVATSIGHTAVATAGGTBYLTYSFSKGG ASGGADTOVLLHRITTSDFHATAGGSTRALLAFTURGTTSICLULDLING LLILPGOKAVVAUSLAVATSIGHTAVATAGGTBYLTYSFSKGG ASGGADTOVLLHRITTSDFHATAGGSTRALLAFTURGTTSICLULDLING LLILPGOKAVAVUSLAVATSIGHTAVATAGGTBYLTYSFSKGG ASGGADTOVLLHRITTSTGAVARDOKATSPATAGGTBYLTYSFSKGG ASGGADTOVLLHRITTSTGAVARDOKATSPATAGGTBYLTYSFSKGG GYRVAPERICLITAGGTBYLLAGGGTTATICGSTRANGTATAGGTBYLTYSFTANA TUPTGGILSMGYTLUNGCCHTLIGGTBYLTYTTLILDIFRALRTHEPOPR TOPPGGLLSMGYTLUNGCCHTLIGGTBYLTYTTLILDIFRALRTHEPOPR TOPPGGLLSMGYTLUNGCCHTLIGGTBYLTTTTLICHTARAGGTBYLTYSTANA ADGREKKKABERERKRKKEVGCOOQCALABERRERGILIGGT TODIESPKAAPPEROUTLONGCCHTLIGGTBYLTYTTLICHTARAGGTBYLTYTTLICHTARAGGTBYLTYTTLICHTARAGGTBYLTYTTLICHTARAGGTBYLTYTTLICHTARAGGTBYLTYTTLICHTARAGGTBYLTYTTLICHTARAGGTBYLTYTTLICHTAR		1	sequence	\-nossible nucleotide insertion)
EVHERHYMVLISHIRAJVISLISHEQUKKVI,IL\POVILLO'S \[Vaiths_Land_vislish_pervivogenerish_framavous_transports		sequence		VANA KERT DATA COKKOMA CGETOCTA SPALEOSPAT DVIJALE
D\TSISTYATIHISLAULUSILAIPEWUGGERTKITERITAPY TK\NTDLSLEGIPSOPITEPINGLDWITATEGEREPPISS SEENPOMSGPEQITEPINGT\(\text{TKM}\) (DIMP\REP\\) (CDVKSQCTTI\ ESSMDOMESSIDVKISIONGTAKEDSENPPISS SEENPOMSGPE\(\text{TEXPOSTOPITATEVYTSGEQEPIPLAUS\) EESMPMKSSIPQKTSIVQSGDADQTEPPKYSQSRPLKYPS GLGEPTIQVKKKPYKDPENMYRAMISEKTSVASAPILIPEIL ENVPKKDDVSPYMQFSSKPAARITEGEABGWEEGELINWED W AREGGSLGAVAACGELSYSCDFCPARPHTSWLTTFVKMEFQA MAYGGSSRMTDLTSSIPKELPVONNCHINFYLMLERVGPE IVVTTRDVQRALGAEPMMKMPDIVCLINPYLMLERVGPE IVVTTRDVQRALGAEPMMKMPDIVCLINPYLMLERVGPE IVVTTRDVQRALGAEPMMKMPDIVCLINPYLMLERVGPE IVVTTRDVQRALGAEPMMKMPDIVCLINPYLMLERVGPE EPVPGGKKKKAVPGRPTFUDSTGRILLPMANREADLGELIV GSILGKHPRIRFHTGLVDAHMYCLKYIVOPLMENG\(\text{STYPLW}\) FSGKOPSSASSGGTFKRILPMANREADLGELIV GSILGKHPRIRFHTGLVDAHMYCLKYIVOPLMENG\(\text{STYPLW}\) FSGKOPSSASSGGTFKRILPMANREADLGELIV GSILGKHPRIRFHTGLVDAHMYCLKYIVOPLMENG\(\text{STYPLW}\) FSGKOPSSASSGGTFKRILPMANREADLGELIV GSILGKHPRIRFHTGLVDAHMYCLKYIVOPLMENG\(\text{STYPLW}\) FSGKOPSSASSGGTFKRILPMANREAGLIVERY GSILGKHPRIRFHTUSLVDAHMYCLGYGVYHSGGVACIS FHPS TLYTUNGSGVAVYANDLAUNTAGGTVSTSKAGG ASGADTOVLLWKTTFDELHCKGLTKRNIKRLHFPSPPHLL LLILPGOKAVVAUCQTRVKPPVDIS*TIP CCQNVCQOPR VLTASSOVLKYVAYSILAUNTAGGTTKSTAURLHFNSPPHLUL LLILPGOKAVVAUCQTRVKPPVDIS*TIP CCQNVCQOPR ASGADTOVLLWKTTFDEHCKGLTKRNIKRLHFPSPPHLUL LLILPGOKAVVAUCQTRVKPPVDIS*TIP CCQNVCQOPR ASGADTOVLLWKTTFDEHCKGLTKRNIKRLHFPSPPHLUL LLILPGOKAVVAUCQTRVKPPVDIS*TIP CCQNVCQOPR TAGANAPERTOLTGAPEVILGOSLAVAUCQTRVLTSSKOG QXXXSAXRNIVPSPERMIRGAENIANDLAUNTAGTVSTSL LTUTENKLNOCLENQOKLTSAVQCKS GYRYSAURRYTYPTQHTTGLTSGALDAURLHFKQCSTVN GYRYSAURRYTYPTAGTTSGALTAURLHFKQCTAVTAGA ADGREKKKBERFRERFREKTACKEVYTQGTTSGALDAURLHFKAUCTSN GYRYSAURRYTYPTAGTTSGALTAURLHFKAUCTSN GYRYSAURLHFTATAGATAGATAGATAGATAGATAGATAGATAGATAGAT				
TK,WTDLS,LEGDPSOP IN PRINCESDVINTSEDSENPPSSS SERNPRORGED PLEVAR SERVENDYON, 10 THE PLEVAL PROVISCITAL BESSNDOLDESSILDTKVNRGGITATKEVTŠGEGKPI PALLS BESSNDOLDESSILDTKVNRGGITATKEVTŠGEGKPI PALLS BESSNDOLDESSILDTKVNRGGITATKEVTŠGEGKPI PALLS BESSNDOLDESSILDTKVNRGGITATKEVTŠGEGKPI PALLS BESSNDOLDESSILDTKVNRGGITATKEVTŠGEGKPI PALLS BESSNDOLDESSILDTKVNRGGITATKEVTŠGEGKPI PALLS BESSNDOLDESSILDTKVNRGGITATKEVTŠGEGKPI PALLS BESSNDOLDESSILDTKVNRGGITATKEVTŠGEGKPI PALLS BENYPKCDUVS PVMOPESSKRABRITEGEABGMEBEGELMMED W ARGGISMANDLISS I KELLEVVONCELIVYPILLEKRYGFE IVVTTEDVGRALCABEPMMKPDI VCI PDOADMGTADSLRYI KLKTVULVLSCLITATVALHKEVULERTYDALBKUKGKGI BEPVEGKKKKAVEGRPT GVDSTGKRLIKMRKGOL BEPVEGKKKKAVEGRPT GVDSTGKRLIKMRKGOL BEVEGKKKKAVEGRPT GVDSTGKRLIKMRKGOL BEVEGKKKKAVEGRPT GVDSTGKRLIKMRKGOL BELI PYLIV ARKQFSANSOGOTHKRKRGGKKKGLKSFRI SF1* KRANYTGTGATV VD, ACM SCHANKAVGKOLKSPINFSDSVGFANFVDF SF1* KRANYTGTGATV VD, ACM SCHANKAVGKOLKSPINFSDSVGFANFVDF SF1* KRANYTGTGATV VD, ACM ASGGADTVULLWRTN FDBLHCKGLTKRALIKLIPS PPHLL PRTHHERKVETVEDFTHLIKLIGUSK*SICRSLLPLIMI LLILLEQQGKPVVGLCQTRVKRVDIS*TLP*CQNVCQDFR ASGGADTVULLWRTN FDBLHCKGLTKRALIKLIPS PPHLL PRTHHERKVETVEDFTHLIKLIGUSK*SICRSLLPLIMI LLILLEQQGKPVVGLCQTRVKRVDIS*TLP*CQNVCQDFR ASGGADTVULLWRTN FDBLHCKGLTRVALENTERPPKR QK**VTSPLVKX,VS IPLAVITALBHINEQINALTQVTSILL LLILLEQQGKPVVGLCQTRVKRPVDIS*TLP*CQNVCQDFR ASGGADTVULLWRTN FDBLHCKGLTRVALTATERPPKR QK**VTSPLVKX,VS IPLAVITALBHINEQINALQTVSILL LLILLEQQGKPVGFANASCORPSVNIPPPSSPLQVATADBRITSTY POPROLLAKGYTLILLPFRTTYTLDLIFFRALRIPDKR TDPVGGIVSFMHSFEKYGGAPPYTQGTYSQALMDAKERLI LVX.HAGDHQDBSDECRITICAPSVISIATINALPRACSTNI GYRVSQALRENTYPPLAMILLDERPRKSPLTILDTPRAKACSTNI GYRVSQALRENTYPPLAMILLDERPRKSPLTILDTPRAKACSTNI GYRVSGALRENTYPPLAMILLDERPRKSPLTILDTPRAKACSTNI GYRVSGALRENTYPPLAMILLDERPRKSPLTILDTPRAKACSTNI GYRVSGALRENTYPPLAMILLDERPRKSPLTILDTPRAKACSTNI GYRVSGALRENTYPPLAMILLDERPRKSPLTILDTPRAKACSTNI GYRVSGALRENTYPPLAMILLDERPRKSPLTILDTPRAKACSTNI GYRVSGALRENTYPPLAMILLDERPRKSPLTILTPRAKACSTNI GYRVSGALRENTYPPLAMILLDERPRKSPLTILTPRAKACSTNI GYRVSGALRENTYPPLAMILLDERPRKSPLTILTPRAKACSTNI GYRVSGA				
SEENDOMOGRESLOTKVINIQGOTANKSQCTTL ESSNDOMOGRESLOTKVINIGGGTATKVINI		1		D/TSDSTVATTEMSDAVEVSBEGFEVVVGGERTRIFRRIAF (SF
EBSSNDDCEPSILDTKNIPGGGITATKPVTSGGKRIPALE BESMPKKSLDVGNISLONGGDDGIEPPRVSGGRPLKVPS GLGEFFTIQVKKPVKDPKDDDGIPPRVSSGRPLKVPS GLGEFFTIQVKKPVKDPKDDDGIPPRVSSGRPLKVPS GLGEFFTIQVKKPVKDPKDDDGIPPRVSSGRPLKVPS ARGGSLGAVAACGELSVECDFCPARPHTSHITATRVKMFDD MAVGGSSMTDLTSSIPKPLLPVONKPLIWYPLNLLERVGFE IVVTTENDVGKALCAEPKMKMKEDIVCIT DDADMSTADSINT KLKTDVLINLSCDLITDVALBEVOUTFRAYDASLAMLMRKGDC EPVEGKGKKKAVEGRDFIGVDSTGKKLLFMANEADLDESK GSILGKHPRIRFTGLUDAHLVCLKKYIVDPIMENG SITSI GSILGKHPRIRFTGLUDAHLVCLKKYIVDPIMENG SITSI ELIYPULV/RGKOFSSASSQOGTREEKEGGSKGKGLKSFRF SFY*KEANYTOTAGPY\DACMI FETPHEREKYETYBDFIHLLCLKTONFSDSVGFANFVDFS FY*KEANYTOTAGPY\DACMI SFY*KEANYTOTAGPY\DACMI FYTHPHEEKVETYBDFIHLLCLLGUGHTGPVFTVSFSKG ASGGADTOQULWRTNPBELHCKGLKKYNLKHLHFDSPPHLL PRTPHPHEEKVETYBDFIHLLCLLGUGHTGPVFTVSFSKG ASGGADTOQULWRTNPBELHCKGLKKRNLKHHFDSPPHLL PRTPHPHEEKVETYBDFIHLLCLDLGUGHTGPVFTVSFSKG ASGGADTOQULWRTNPBCHACHGCTKRLCHKHTDFSPHLL FRIPHLEKKVCLSNOGKLFSANQUSS GKY*VTSEVXK/KVSIPLAVTDALBHIMEQLAVLTQTVSILE LUTUTEDKLKDCLSNOGKLFSANQUSS GKY*ATSERALTQETSTLLLGFOLGTKLLGFTGNALHTDSPPHLL LUTUTEDKLKDCLSNOGKLFSANQUSS TOPFGGLIGWGYYLIMPFPRTYTYTILDIFFAHRENEPPRR TDPVGGIUSFMHSFEEKYGRAPEVFYCGTYSQALNDAKETLEGF NIEAAVODRINGEGGVPSVNNPPPSRFLQVITADHRITYSHLFINFDPRR TDPVGGIUSFMHSFEEKYGRAPEVFYCGTYSQALNDAKETLEGF GYRVSQALRENTYPFLAMIMLKDRRE*PVVGRLGGGDRAYLAA ADGKERKKREERSRRKKEEVOQOKLABERRRGNIQBEK LECLPPPSPPDDPSWKI IKLENDSVCERFHSGSLTVIL LYSLKSSPLEKFOIERANSPERSONDSSDLDFHRKLPDVKDD GRANGVFHANGANGTYLSSERALERSONDSSDLDFHRKLPDVKDD ARRTSHGERKSAVPFRYLLENDSNCERFHSGOLTVIL LYSLKSSPLEKFOIERANSPERSONDSSDLDFHRKLPDVKDD ARRTSHGERKSAVPFRYLLENDSSNCERFHSGOLTY LESSLKSSPLEKFOIERANSPERSONDSSDLDFHRKLPDVKDD ARRTSHGERKSAVPFRYLLENDSRVERFHSGOLTFY LYDTYSMAGSGSPKKTUPKAVRINGGSLEPPRFATVETTIA VLDTYSMAGSGSPKKTUPKAVRINGGSLEPPRFATVETTIA VLDTYSMAGSGSPKKTUPKAVRINGGSLEPPRFATVETTIA VLDTYSMAGSGSPKTUPKARENGREVERFARGMFENGER GSPLELKONGSIEINIK SPENGTONDFLANGFRYGHTY VSESKOCKTOPTHREEKKRECHTVAPHALTYRGFPSPATUETTIA VLDTYSMAGSGSPKTUTHKARDROPTHYPKYSONDFLANGFRYGHEN GSPLELKONGSIEINIK GESPSERRKSHERSIGKKLCS				TK/NTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSENFPSSSKK
EEMMPKKSLPQKISLVQRODADQIEPPKVSSQERPLKVE GLGEPFTJQVKKPVKDPBMPAMPENETKSRAPLILIPEL EMVPKKDUSPVMQFSKFAAAEITEGEAEGWEEGELNWED W AREGGSLGAVAACGELSYSCDFCPARPHTSWLTRFVKMEFQA MAVGGSSMTDLITSSIFPKLEVEVRKLIWFPLALLERFYGE IVVTTEDVQKALCAFFKMKKPELIWFPLALLERFYGE EVYTTEDVQKALCAFFKMKKPELIWFPLALLERFYGE EVYTEDVQKALCAFFKMKKPELIWFPLALLERFYSALRAFY KLKITDWLVLSCDLITDVALHEVVDLFFAYDASLAMMINKGES EFYPKGKAKKAVEQRDFICVDSTGKALLEMMARGALDEELU GSILGKHPRIRFHTGLVDAHLVCLKKYIVDFJMENGGSTSLIGEL BLIPPLVJKGKGFSASSQOGTREKEGGGSGKGLKSFRI BLIPPLVJKGKGFSASSQOGTREKEGGGSGKGLKSFRI GTCLASAGSDDTVKVWDVRVKLLCHTVQVSGGVMCTSFRIGG ASGGADTVVLWBURVWKLLCHTVQVSGGVMCTSFRIGG ASGGADTVLWBRINFDBLICKGLTKRNLKRLHFDSFPHLLI PRTHHHEBEKVETVBDFFLHLERLIQSIR SICRSLLIPLIMI LLLIPQQKPVGLCCTRVKRPDISTTLP SICRS ASGGADTVVLWDVLCCTRVKRPDISTTLP SICRS ASGGADTVVLWDVLCCTRVKRPDISTTLP SICRS ASGGADTVVLWDRIVSTLDLLERGLIVVLTQTVSILG LLTUTENKLKDCLENQKLFSAVQUSS GKMANFBERDLTQSGTFEKLLGFODLTGTBETAGCVNLQTVSILG LLTUTENKLKDCLENQKLFSAVQUSS TOPPGGIVSTHMSFBEKKGARPVFYCGTTSAGANCQGPR TOPPGGIVSTHMSFBEKKGARPVFYCGTTSALDALDRAKELI LVYLHGDDHQDSDEFCRTTLCAPEVISLINTRMLFWAGCSTN TOPPGGIVSTHMSFBEKKGARPVFYCGTTSALDALDRAKELI LVYLHGDDHQDSDEFCRTTLCAPEVISLINTRMLFWAGCSTN TOPPGGIVSTHMSFBEKKGARPVFYCGTTSALANDAKERLI LVYLHGDDHQDSDEFCRTTLCAPEVISLINTRMLFWAGCSTN TOPPGGIVSTHMSFBEKKGARPVFYCGTTSALANDAKERLI LVYLHGDDHQDSDEFCRTTLCAPEVISLINTRMLFWAGCSTN TOPPGGIVSTHMSFBEKKGARBERRNOTQUVLRQQDBATIAM ADGKERKKRBERBRRRKKEEVQOQKLABERRRRONTQUFAR ADGKERKKRBERBRRRKKEEVQOQKLABERRRONTQUFAR ADGKERKKRBERBRRRKKEEVQOQKLABERRRONTGUFAR ADGKERKKRBERBRRRKKEEVQOQKLABERRRONTGUFAR ADGKERKKRBERBRRRKKEEVQOGKLABERRRONTGUFAR ADGKERKKRBERBRRRKKEEVQOGKLABERRRONTGUFAR ADGKERKTRBERGSTICTOMBERSSICSTERRSISTICTNETIVER SCHIKKARPARAFATARATARATARATARATARATARATARATARATAR		l		
GLGEETIOVKKPUKDPEMDWFADMIPBIKPSAPAILIDE EMMYRKDDVSPVMQFSKFAAAITEGRAGEGEGELINED W AREGGSLGAVAACGELSYSCDFCPARPHTSKILTREVAMSFOM MAVGGSEMTDLTSSIPKPLLPVONKPLIWYPLMLLERVGFE IVVTTEDVGKALCAIFKMRKREDIVCIPDDADMSTADSLIY KLKTDVLVISCDLITUVALIEVVUDLFRAYDASLAMLMRKGOL GEYPVEGKKKKAVEQRDFIGVDSTGKRILFMANSADLDESK GEYVEGKKKKAVEQRDFIGVDSTGKRILFMANSADLDESK GEYVEGKKKKAVEQRDFIGVDSTGKRILFMANSADLDESK GSLIGKHPRIRFIGLIDAHLVCLKKYIVDPLMENG SITSI BL\1PYLV/RGKOFSSASSQOGTREKKEGGSKGKRGLKSFRI SFY*KEANYTOTAGPY\0\0\0\0\0\0\0\0\0\0\0\0\0\0\0\0\0\0\0			!	
S828 2 257 AREGGELGNAGOELSYSCDFCPARPHTSMLTRFVWMS ANGGGSRNTDLTSSIPKPLLPVGNKPLIWTPNLMERVGFF IVVTTRDVQKALCASPKMKKEDIVCT PDDADMSTADSIRYI KLKTDVLIVLSCDLITDVALEWVDLFAYDASLAMIMRKED EPPVEGKKKKAVPCGRPIGVDSTGKLLFAYDASLAMIMRKED EPVPGKKKKAVPCGRPIGVDSTGKLLFAYDASLAMIMRKED EPVPGKKKKAVPCGRPIGVDSTGKLLFAYDASLAMIMRKED EFVPGKKKKAVPCGRPIGVDSTGKLLFAYDASLAMIMRKED EFVPGKGKKKAVPCGRPIGVDSTGKLLFAYDASLAMIMRKED EFVPGKGKKKAVPCGRPIGVDSTGKLLFAYDASLAMIMRKED EFVPGKGKKKAVPCGRPIGVDSTGKLLFAYDASLAMIMRKED EFVPGKGKKKAVPCGRPIGVDSTGKLLFAYDASCHAFT EFT ** KEANYTGTGAPY ID ACM** SF1** KEANYTGTGAPY ID ACM** FTCLASAGSDGTVKWDWRWKLLOHQVUSGGWKGLKSFRI SF1** KEANYTGTGAPY ID ACM** FTCLASAGSDGTVKWDWRWKLLOHQVUSGGWKGLKSFRI ASGGADTQVLLMRTNFDELHCKGLTKRNLKRLHPDS PHLLL PRTHHEBEKVETVBDFFLHLERLIQSLRVLTGYTSSKGG ASGGADTQVLLMRTNFDELHCKGLTKRNLKRLHPDS PHLLL LLHPQQKPVGLCTRVKKPUDIS** TLTSPLGWTGYGGPR** ASGGADTQVLLMRTNFDELHCKGLTKRNLKRLHPDS PHLLL LLHPQQKPVGLCTRVKKPUDIS** TLTSPLGWTGYGGPR** ASGGADTQVLLMRTNFDELHCKGLTKRNLKRLHPDS PHLLL LLHPQQKPVGLCTRVKKPUDIS** TLTSPLAYTHLER ASGGADTQVLLMRTNFDELHCKGLTKRNLKRLHPDS PHLLL LLHPQQKPVGLCTRVKKPUDIS** TLTSPLAYTHLER TLTPSLKXDCLENQKLFSRAVQKS 5830 4496 3139 GGKMANFEERDLTQGGTSKLLGFODLATIBENDCCRRTTLSTVV PQPRGLLGMGYTLIMBPRFFTYTTLDIFFFALRFITEPD TDPGDIVSTHHSFBEKYGGARPVFYQCTYADARITYSTVV PQPRGLLGMGYTLIMBPRFFTYTTLDIFFFALRFITEPD TDPGDIVSTHHSFBEKYGGARPVFYQCTYADARITYSTVV PQPRGLLGMGYTLMRPFFTYTTLDIFFFALRFITEPD TDPGDIVSTHHSFBEKYGGARPVFYQCTYAPASLEGLI\QPI LLECLPPESPBDPDPSWKLIFLENDSKYRERFITSGGLTVI LFSLKSSP\EKFQIERA\NFPRR\VLQCTFSER\WNDFTGG GLSHTSVLTVQUDIDE S6811 71 2897 TDPGSLSKCCLYLPDSINSKSCTAKPGAHSQDRRAVMDSEQ GLSHTSVLTVQUDITDS GSSLSKTSVLTVGKANGGSPSKTVTVKAVPMLTYRKYSTVQRSCBYCH REALPYKNARSGSPSKTVTKAVPMLTYRKYSTVGPSTVAV VDGXSVNGCTYHREEK KREERCVTVAPASLTKKGREB KSWSTATSPAGLGKKALQUVPPRT\PVS\DADASSTSMFDOMR RANVQPHSRARQDQLQLINNQLRSEDDKWQDLARKKSRKR QDLIKKBERKKREKKELASSEQHLTTYTVGCSTVTVAFSPSSPQL VSEKSVTTSPAGLGKKALQUVPPRT\PVS\DADASSTSMFDOMR REHLEPXKNARSGSPSKTVTTKAVPMLTYRKYSTVYAFSPPSSPQL VSEKSVTTSPAGRAVATATTRTTUTTTA VLDTSMAGSGSPSKTVTTKAVPMLTYRFSTYVAFSPPSSPQL VSEKSPQKRQ	'	1		
\$828 2 257 AREGGSLGAVAACGELSYSCDFCPARPHTSMLTEFVKMEFQA MAVGGGSRMTDLTSSTPKPLLPVONKPLTWYPIALLERUGFE IVYTTEDVQKALCAEPKMKKRPDIVCI PDDABMATADSLRYI KLKTDVILVISCDLITDVALHEVVDLFPAYDASLAMLMRKGGL EPVPGQKGKKAVAVQRDFIGVDSTGRLLFMANEADLDELV GSILQKHPRI FHITGLVDAHHEVVDLFPAYDASLAMLMRKGGL EPVPGQKGKKAVAVQRDFIGVDSTGRLLFMANEADLDELV GSILQKHPRI FHITGLVDAHHIVCLKKY IVDFLMENC\SITSI BL\TPYLV/RGKQPSSASSQQOTKEKEGGSKGRGLKSFRI SFY*KERNYTGTGAPY\D\ACMI \$5629 260 1259 PDGRLVG-GSBRTIKIWDTTNKQCWNNSDSVGPANFDFN GTCLASAGSDQTVEVMDVYRKLLQHYQVHSGGWCLSFRI YLITASSDOTIKILDLLKGRLIYTLQGHTGPVFTVSFSKGG ASGGADTQVLIWRTNFDELHCKGITKRNLKRHHFDEPPHLL PRTHHPHERKVETVEDFI-HLILRILGISLK*SICCESLDFLLW LLLLPQQQKPVVGLCQTRVKRPVDIS*TLP*CHQNVCQPRR QKT*VTSPVKVK/VSILAUTADALHHMQXVLTQTVSILL LLLLPQQQKPVVGLCQTRVKRPVDIS*TLP*CHQNVCQPRR QKT*VTSPVKVK/VSILAUTADALHHMQXVLTQTVSILL LLTLTEDKLKDCLENQQKLFSAVQQKS GGKMANEEREDLTQGGTEVKLJGFQDLTGISSMDQCRHTLEON NIBASVQDRLINGGSVPSVVNPPPBSRPLQVNTADHRIYSTVV PQPRGLLGMGYYLIMLPFRFTYYTILDIPFFAHFIRPDERS TDPVGGIVSFMHSFREEXYGRAHFVFYQGTYSQALINARKGESTN GYRVSQALERTYPFLAMMLKDRRE*PVVORLEGGLI\QYE LLYLHGDDHQDSDBFCRNTICAPEVISLITNTBMLFWACSTN GYRVSQALERTYPFLAMMLKDRRE*PVVVORLEGGLI\QYE LLYLHGDDHQDSDBFCRNTICAPEVISLITNTBMLFWACSTN GYRVSQALERTYPFLAMMLKDRRE*PVVVORLEGGLI\QYE LLYLHGDDHQDSDBFCRNTICAPEVISLITNTBMLFWACSTN GYRVSQALERTYPFLAMMLKDRRE*PVVVORLEGGLI\QYE LLYLHGDDHQDSDBFCRNTICAPEVISLITNTBMLFWACSTN GYRVSQALERTYPFLAMMLKDRRE*PVVVORLEGGLI\QYE LLYLHGDDHQDSDBFCRNTICAPEVISLITNTBMLFWACSTN GYRVSQALERTYPFLAMMLKDRRE*PVVVORLEGGLI\QYE LLYLHGDDHQDSDBFCRNTICAPEVISLITNTBMLFWACSTN GRANQEBRENTYPFALINGKEBCRAFQHAGAGARAWDSERC GRESKCHARFRESTRENTSTANCHARA ADQEKBRKREBERKREBRERKREBVQOVLARGABERRRIDGEPISL GSSRKSTTSPAULPNSNCHATHENDSTANCHARA RAPSHEBERKAPPANLYNGSDBFSGSBSSDLEPHRKLDVVKDI ARRTHGERKAPPANLYNGSDBFSGSTSFNANLCSSSFDMR RANQPHSKAPTANLYBRSNCHAPPANLSTRAMMDSERC GGREKANLYBRSGAPAGTIONGLABEDRAMMDSRC GGREKANLYBRSGAPAGTIONGLABEDRAMMDSRC GGREKANLYBRSGAPAGTTUNGLAGDPSRANGDPSNQOV VSEKQQKWGENTLAURHORSSSSAPQTTAPVEPSPSQBD GGREKANLEBLASSEPQHTTTVTRAGPTAPHESPSQBD GGREKANLEBLASSEPQHTTTTTRAGALATRESTPSNGBD GGREKANLEBLAN		į.		
\$828 2 257 AREGGICANANCELLYSCOPEC PARPHYSMLTEFVUMEFOA MANOGGSRNTDLTSS I PKPLLPVGNKPL I WYTHALLERVGFE I VYTTROVÇKALCABERMEMRED I VCI PDOADMOTADBIR'I KLKTDVLVILSCDLITOVALHEVVDLERAYDASLAMLEMRIGGE EPVPGKOKKRKAVEQRDET GVDVSTGKRILDAMSTADLDEELV. GSLLQKHPPL I FHITGLVDAHLYCLKKY I VDFLMENG (SISTSI BL) TPVLV (PKGKOFS SAS SOGGTKEKRENARDALDEELV. SEY* KEANYTGTGAPY (DVACMI SPDSVGFANFVDFS GSLLQKHPPL I KTHTGLVDAHLYCLKKY I VDFLMENG (SISTSI SIY* KEANYTGTGAPY (DVACMI SPDSVGFANFVDFS GSLLQKHPPL I KTHTGLVDAHLYCLKKY I VDFLMENG (SISTSI SIY* KEANYTGTGAPY (DVACMI SPDSVGFANFVDFS GSLLQKHPPL I KTHTGLVDAHLYCLKY I VDFLMENG (SISTSI SIY* KEANYTGTGAPY (DVACMI SPDSVGFANFVDFS GSLLQKHPPL I KTHTGLVDAHLYCLKY I VDFLMENG SITTSI SY** KEANYTGTGAPY (DVACMI SPDSVGFANFVDFS ASGGADTOLVLING I VDFLMENG SITTSI SY** KEANYTGTGAPY (DVACMI SPDSVGFANFVDFS YLTTASBODTLKI LIDLLKGRI I YTLGGHTGAPY FYSTSKGGF ASGGADT (VLKTAFT SKROE ASGGADTOLVLING I VDFLMENG SITTSI SY** CHANCAGOR (STANFAR STA		Ļ		EMVPKKDDVSPVMQFSSKFAAAEITEGEAEGWEEEGELNWEDNN
MAVGGGSINTDLTSS IPKELEPVONKPLIWPINLLERGYE IVVTTRUVQKALCAEPKMRKPD IVCT DOMATIADS.RTV KLKTDVLVIS.CDLITDVALHEVVDLFRAYDASLAMLMRKGQL EPVPGGKGKKGAVEQRDFIGVDSTGRELEFANDASLDBELV GSILGKHPRI FRITGUDAHLYCLKKY 1VDFLMENG\SITSI EL\TPYLV/RGKQPSSASSQGTRKEKEGGSKGRGLKSFRI SFY*KENNYTGTGAPY\D\AGMI 5829 260 1259 PDGRLIVGCSEDKTIKIWDTTNKQCVNNTSDBVGFANTVDF GTCLASASSDCTVXVDVRVNIKLLQHYQVHSGGVNCISFPDS YLTASSDGTLKILDLIKGRLIYTLQGHGPVFFVSFSKGGS ASGADTQVLLWRRTPDELHCKGITKRNLKRLHPDSPPHLLE PRTHPHBEKVETVEDFFLHLBRIIGSLEXICSLELLLUL LLILPQQQKPVVGLCQTRVKRPVDIS*TLD*CHQNLVQQVRX QKT*VTSPLVKK/VSIPLAUTDALEHHMQVLTQTVSILE LTLTERKKDCLENQQKLFSAVQQKS 5830 4496 3139 GGKMAAPEERDLTQGGTEKLLQFQDLTGISBNDQCRHTLEQF TOPYGDIVSFHMSFERKYDVRPPPSRPLQVNTADHRTYSYVV PQPRGLLGRGYYLIMLPFRFTYYTILDIFRFALRFINDPRR TDPYGDIVSFHMSFERKYDKRAPHFYGQTAJNDAKRELL LVYLHGDDHQDSDBFCRNTLCAPBYISLINTMLPWAGSTNI GYRVSQALRENTYPFLAMIMLKDRRE*PVVGLEGLI\QPI INQLTFIMANQTTLVSERLERBERNQTVURQQQBATLAA ADGSKERKKREERERKRRKEEVQQQKLABERRRQNLQEKK LECLPPPEPSPDPDPSWSKITIKNDPSWRVPRPSQSLNQDKEKL LECLPPPEPSPDPDPSWSKITIKNDPSWRVPRPSQSLNDKRELL LFSLKSBP\EKRGITEA\MPPRR\VLPCIPSEE\WPNPPTLQ GLSKTEVLFPODLTON ARRISHGEPKSAVPPNQYLDYBRSRDSLSPPRHGRDSFDSF FOSSBKGTPSPDVULRGSSDGSGSDSSDSDLPHKKLPDVKKD ARRISHGEPKSAVPPNQYLDYBRNKTAVVPAPLAKKRARE KSWSTATSPAGLGKKALQVGFRTP\PV3-DDASSTSMFDMR RAHVQPHSRRQGDGJLLINNQLREBDKWQDLDABWSGRK RSHSTEPNLSSFLUDPKPMKYLRQGSLPPPKFTAVTTIA VLDTMSMAGGSGPSKTUPTKAVPMTTYRAVPHDFTKRYBPDSQB GGKSRKGNIELLASSEPQHTTTVARQSLPPKFTAVTTTIA VLDTMSMAGGSGPSKTUPTKAVPSGPKNSQDVLK UGKWSVNGETVHREEKERECTVAPAHSLTKEPNSQBC GSPLELKQDKNGETHREEKERECTVAPAHSLTKREPNSGBC GGKSRKGNIELLASSEPQHFTTTVTRCSPTVAFVEFSPSPQL VSEERQKKREPNGSSSSADLSFSKESDRESGTNKFT KMPERNQLIHLPNLNSQUSPSSSSADLSFKREPSPTLITPP KMPERNQLIHLPNLNSQUSPSSSSADLSFKREPSPTLITPP KMPERNGLIHLPNLNSQUSPSSSSADLSFKREPSPTLITPP KMPERNGLIHLPNLNSQUSPSSSSADLSFKREPSPTLITPP KMPERNGLIHLPNLNSQUSPSSSSADLSFKREPSPTLITPP KMPERNGLIHLPNLNSQUSPSSSSADLSFKREPSPTLITPP KMPERNGLIHLPNLNSQUSPSSSSADLSFKREPSPRESGTMK GROQDEKQDRWKKSFQGDSDLLLKTRESDRLEEKGSLTB AISGNPVSKUEBHQLLDTARA		1		W
MAVGGGSINTDLTSS IPKELEPVONKPLIWPINLLERGYE IVVTTRUVQKALCAEPKMRKPD IVCT DOMATIADS.RTV KLKTDVLVIS.CDLITDVALHEVVDLFRAYDASLAMLMRKGQL EPVPGGKGKKGAVEQRDFIGVDSTGRELEFANDASLDBELV GSILGKHPRI FRITGUDAHLYCLKKY 1VDFLMENG\SITSI EL\TPYLV/RGKQPSSASSQGTRKEKEGGSKGRGLKSFRI SFY*KENNYTGTGAPY\D\AGMI 5829 260 1259 PDGRLIVGCSEDKTIKIWDTTNKQCVNNTSDBVGFANTVDF GTCLASASSDCTVXVDVRVNIKLLQHYQVHSGGVNCISFPDS YLTASSDGTLKILDLIKGRLIYTLQGHGPVFFVSFSKGGS ASGADTQVLLWRRTPDELHCKGITKRNLKRLHPDSPPHLLE PRTHPHBEKVETVEDFFLHLBRIIGSLEXICSLELLLUL LLILPQQQKPVVGLCQTRVKRPVDIS*TLD*CHQNLVQQVRX QKT*VTSPLVKK/VSIPLAUTDALEHHMQVLTQTVSILE LTLTERKKDCLENQQKLFSAVQQKS 5830 4496 3139 GGKMAAPEERDLTQGGTEKLLQFQDLTGISBNDQCRHTLEQF TOPYGDIVSFHMSFERKYDVRPPPSRPLQVNTADHRTYSYVV PQPRGLLGRGYYLIMLPFRFTYYTILDIFRFALRFINDPRR TDPYGDIVSFHMSFERKYDKRAPHFYGQTAJNDAKRELL LVYLHGDDHQDSDBFCRNTLCAPBYISLINTMLPWAGSTNI GYRVSQALRENTYPFLAMIMLKDRRE*PVVGLEGLI\QPI INQLTFIMANQTTLVSERLERBERNQTVURQQQBATLAA ADGSKERKKREERERKRRKEEVQQQKLABERRRQNLQEKK LECLPPPEPSPDPDPSWSKITIKNDPSWRVPRPSQSLNQDKEKL LECLPPPEPSPDPDPSWSKITIKNDPSWRVPRPSQSLNDKRELL LFSLKSBP\EKRGITEA\MPPRR\VLPCIPSEE\WPNPPTLQ GLSKTEVLFPODLTON ARRISHGEPKSAVPPNQYLDYBRSRDSLSPPRHGRDSFDSF FOSSBKGTPSPDVULRGSSDGSGSDSSDSDLPHKKLPDVKKD ARRISHGEPKSAVPPNQYLDYBRNKTAVVPAPLAKKRARE KSWSTATSPAGLGKKALQVGFRTP\PV3-DDASSTSMFDMR RAHVQPHSRRQGDGJLLINNQLREBDKWQDLDABWSGRK RSHSTEPNLSSFLUDPKPMKYLRQGSLPPPKFTAVTTIA VLDTMSMAGGSGPSKTUPTKAVPMTTYRAVPHDFTKRYBPDSQB GGKSRKGNIELLASSEPQHTTTVARQSLPPKFTAVTTTIA VLDTMSMAGGSGPSKTUPTKAVPSGPKNSQDVLK UGKWSVNGETVHREEKERECTVAPAHSLTKEPNSQBC GSPLELKQDKNGETHREEKERECTVAPAHSLTKREPNSGBC GGKSRKGNIELLASSEPQHFTTTVTRCSPTVAFVEFSPSPQL VSEERQKKREPNGSSSSADLSFSKESDRESGTNKFT KMPERNQLIHLPNLNSQUSPSSSSADLSFKREPSPTLITPP KMPERNQLIHLPNLNSQUSPSSSSADLSFKREPSPTLITPP KMPERNGLIHLPNLNSQUSPSSSSADLSFKREPSPTLITPP KMPERNGLIHLPNLNSQUSPSSSSADLSFKREPSPTLITPP KMPERNGLIHLPNLNSQUSPSSSSADLSFKREPSPTLITPP KMPERNGLIHLPNLNSQUSPSSSSADLSFKREPSPTLITPP KMPERNGLIHLPNLNSQUSPSSSSADLSFKREPSPRESGTMK GROQDEKQDRWKKSFQGDSDLLLKTRESDRLEEKGSLTB AISGNPVSKUEBHQLLDTARA	5828	2	257	AREGGSLGAVAACGELSYSCDFCPARPHTSWLTRFVKMEFQAVV
TVYTTDVQKALCABFMMMKRDUVCIPDDADMSTADSIRYI KIKTDVIJVISCDLITDVALHBYVDCIPFAYSLMMMKRGDU EPYPGGKGKKAVEQRDTIGVDSTGKRLLFMANEADLDEELU GSILQKHPRIRFHTGUVDAHIYCLKKYIVDFIMMOK SITSI EL\TPYLV\GKQKPSSASSQGSTKEKEGGSKGKGLKSFIR SF*KEANYTGTGAPY\D\ACMI EL\TPYLV\GKQKPSSASSQGSTKEKEGGSKGKGLKSFIR SF*KEANYTGTGAPY\D\ACMI SF*KEANYTGTGAPY\D\ACMI SF*KEANYTGTGAPY\D\ACMI SF*KEANYTGTGAPY\D\ACMI FORGLIVEGGSKGKKGLKSFIR SF*KEANYTGTGAPY\D\ACMI FORGLIVEGGSKGKKGLKSFIR SF*KEANYTGTGAPY\D\ACMI FORGLIVEGGSKGKKGLKSFIR SF*KEANYTGTGAPY\D\ACMI FORGLIVEGGSKGKKGLKSFIR SF*KEANYTGTGAPY\D\ACMI FORGLIVEGGSKGKKGLKSFIR ASGGATQVLLWRTNTPBLHCKGLTXRNLKRLHFDSPPTQFTSKGGG ASGGATQVLLWRTNTPBLHCKGLTXRNLKRLHFDSPPTQFTSKGGG ASGGATQVLLWRTNTPBLHCKGLTXRNLKRLHFDSPPTQFTSKGGG ASGGATQVLLWRTNTPBLHLLKLIGSLK*SICCKSLLLLLMI LLILPQQGVPVGLCQTYKRVPV1S*TLP*CHQNLQQCGGAVA QKT*VTSPVKVK\VSIPLAVTDALEHIMRQLAVVLTQTVSILL LLILPQQGVPVGLCQTYKRVPV1S*TLP*CHQNLQQCGGAVA QKT*VTSPVKVK\VSIPLAVTDALEHIMRQLAVVLTQTVSILL LLILPQQGVPVGLCQTYKRVPV1S*TLP*CHQNLQQCGAVA QKT*VTSPVKVK\VSIPLAVTDALEHIMRQLAVVLTQTVSILL LLILPQQGSVPSVTPPPPPPPPTAMTHLDIFRFALRFTRPPRS TDPVGGIUSFHHSFEKYGRAPPVYQGTYSQALNDAKELL LVYLHGDDHQDSBFCKNTTLCAPEVISLINTMLFWACCSTN GYRVSQALRENTYPFLAMTMLMORRE*PVV\VGREGLI\QPERTLYQBCLIQVEGLI\QPERTLYQBCLIQVEGLI\QPERTLYQBCLIQVEGLI\QPERTLYQBCLIQVEGLI\QPERTLYQBCLIQVEGLI\QPERTLYGGTYSQALNDAKELL LECLPPEPSPDDPDVLKGSSDGGGSDSSBDSDBDFBCDFDSISS GYRSSBQCTSPDDVULKGSSDGGGSDSSBDSBDFBKNLDEEKGDFDSISS FOSSBGCTPSDVULKGSSDGGSDSSBDJBFRKLDPDVKDD LKSEBFKSTSPGDVLKGSSDGGSDSSBDJBFRKLDPDVKDD ARRTSHGEPKSAVPPNQYLDNKSNOTAVVPAPLRKKKRREBE KSWSTATSPAGLGKKALQDYGPRT\PVS\DDASSTSMFDMR EAAVQPHSRARGGCLQLINNQLREBENKMQDLARMSSRKS QDLIKKBERKKMELLAGGDGTSBRKSSIKYTRSTUGKEG RSHGKSKNIELASSBQGLIQVIERFTISAVLGERE RSHGFTKNARSGCBASGGSDSSBDJBFRKSIKYTRSTUGKEG RSHGKGTKANARSGCBASGTLQVIERFTISAVLGERE RSHGFTKNARSGCBASGGSDSSBCSDFTTSPATTTP KMPBANQLHLHPNLNSOUPSSSEKSPTTTPFKWAMPDEERG GKSRKGNIELASSBQGHTTLTVTRCGSTTAVVBPPSSSQCIMM UDSTMSAGGSPSKTUTSSSSADLLTSGAPTGTTTPFKWAMPDEERG GKSRKGNIELASSBQGFTILIPSSRKSSTAVCKGSSTDV VSEKDQKKGEREMINGKELULLFRINGUPSSSSADLCSCTMK GNCGBERGARGNIELLFRINGUPSSSSADLCS	2020	· •	1	MAVGGGSRMTDLTSSIPKPLLPVGNKPLIWYPLNLLERVGFEEV
KLKTDWLVISCDLITDVALHEVVDLFRAYDASLAMLMRKGQD EPVPGQKGKKAVEQDDFIGVDSTGKRLFMANEADLDEELV GSILQKHPRIRFHTGLVDAHLYCLKKYIVDFLMENG\SITSI EL\LPYLV/RGKGFSASSQQGTRKEKRGGSKGKRCIKSFRI SFY*KERNTTGTGRPY\D\ACMI 5829 260 1259 PDGRLIVGCSEDKTIKTMDTTINQCVNNFSDSVGFANFVDFN GTCLSARGSDQYKVWDVNKLLQHQVQVHSGGWCLISFHE YLITASDGTLKILDLLKGRLIYTLQGHTGPVFTVSFSKGG ASGADTQVLLIMRTNFPELKFKGLTKRRIKRLHFDSPHLLL LUDQQKEVVGLCQTTVKRPVDIS*TLP*CHQNVQQVPSK QKT*VTSPVKVK/VSIPLAVTDALEHRQLNVLTQTVSIL LLILPQQQKEVVGLCQTTVKRPVDIS*TLP*CHQNVQQPSK QKT*VTSPVKVK/VSIPLAVTDALEHRQLNVLTQTVSIL LTLTEDKLKDCLENQQKLFSAVQKS GKMAAPEERDLTQEQTEKLLQFPQDLTGIESMDQCRHTLEQF NIEAAVQDELINSGEGVPSVPNPPPSRPLQVNTADHRIYSYV PQPRGLLGWGYYLINLPFRFTYTTILDIFRRAFTRPPPSK TDPYGDIVSSMHSSFEKYGRRHPVFYQTYSQALNDAKREL LVYLHGDDHQDSDECRNTLCAPEVISLINTRHLFWACSTNN GYRVSQALRRNTYPPLAMIMLKDREFSVQVQKLABERRFREPPPSK GYRVSQALRRNTYPFLAMIMLKDREFSVVVVVGLEGLI\QPI INQLTFIMDANQTYLVSERLEREBRNQTQVLRQQQDEAYLAM ADQEKEKKKBERRKRKKEEVQQQKLABERRFHPSQSLTVI LFSLKESP\SKRYIERA\MFPFRRVVLPCITSSE\MFNPFTLQI GSHKSGKTPSPDDVVLRGSSDERGSDSSESDLFHRHEPVKKD ARRTSHGEPKSAVFFNQVLDRKSNQTAVYPAPLEKKKABREB SSSTATSPAGLIKKALQDVGPFTY-TVSV\DDAESTSMFDNK RAAVQPHSRRAGDQLQLINNQLREEDDKAQDLLARWSSRKN QDLIKKEERKKMEKLLAGEGGTSERSLTYRFBLYOKED RAAVQPHSRRAGDQLQLINNQLREEDDKAQDLARWSSRKN QDLIKKEERKKMEKLLAGEGGTSERSLTYRFBLYOKED SRSSTENDLSSFLNDDNDMKXLRQGSLPPKFRTVTTTIAM VLDTMSMSGSGSPSKTVTPKAVPMLTYRFYSQFKNSQDVLK VDGKVSVNGSTVUFREEKKERCPVAPAHSLTKSQMFGVAV GSPLELKQDNGSTEINKKPNSVPGATTVFTYTAMA VLDTMSMSGSGSPSKTVTPKAVPMLTYRVYSQFKNSQDVLK VDGKVSVNGSTVUFREEKKERCPVAPAHSLTKSQMFGVAV GSPLELKQDNGSTEINKKPNSVPGDSSSSSSFTTFFKFMSNGDD GKSRKONIELASSEPQHFTTTVTRCSPTVAFVEPSSQFNOK GSPLELAGDNGSTEINKKPNSVPGDSTSSSNTEGSGTMKK GNQQDEKQDRRWKKSFQGDSDLLLKYRESDPLEEKGSLTB AHSGMPVSKSVHEDHQLLDFRAGAPHCGTNGLARGSCFMKLCS PHSSEDVKRYTLPLDKSINQLISSSSNTEGSGTMK GNQQDEKQDRRWKKSFQGDSDLLLKYRESDPLEEKGSLTB AHSGMPVSKSVHEDHQLLTPLAGFTQSLAGDPGLAGDPSDAGO PTHSSEDVKRYTLPLDKSINQLISSSSSMTEGSGTMK GNQQDEKQDRRWKKSFQGDDSLLLKYRESDPLEEKGSLTB AHSGMPVSKSVHEDHQLLTPLAGFTQSLAGDPLOTAQLAQDPSDAG PHSSEDVKRYTLPLGKFGAJCTGLAGGGTTNV NGLMCTOLTYPHSTSAGGGTTNV		1	1	
EPVPGOKGKKRAVEGENPIGUDSTGKRILIFMAKBALDEEZU GSILOKHPRIRPHTGUDARILYGLKKY1VDPLMENG\SITSI EL\[1\text{PVIV/RGKQFSSASSQQTRKEKEGGSKGKRGLKSFRI} SFY*KEANNTGTGAPY\D\ACMI 5829 260 1259 PGGLIVGCSEBKTIKKMDTINKQCVNNFSDSVGFANFVDFN GTCLASAGSDQYVKWDVRVKILOHYQVGHSGGWCISFHE YLITASSDGTLKILDLLKGRLIYTLQGHTGPVFTVSFSKGG ASGADTQVLLWRTNFDELICKGLIYKRRLKRLHFDSPHLLL PRTPHPHERKVSTVDFFLHLLGKLGIXFRRLKRLHFDSPHLLL LILIPQQGRVVGLGQCHVKVRPVDIS-LTC-CHQNVCQDQC QKT*VTSPVKVK/VSIPLAVTDALBHIMEQLNVLTQTVSILE LILIPQGQKVVGLGQCKJFSVQXQK QKT*VTSPVKVK/VSIPLAVTDALBHIMEQLNVLTQTVSILE LITLTEDKLKDCLENQGKLFSRVQXK QKT*VTSPVKVK/VSIPLAVTDALBHIMEQLNVLTQTVSILE LITLTEDKLKDCLENQGKLFSRVQXK QKTAPAPERDLTQEQTEKLLOFQDLTGISMDQCRHTLEQF NIEAAVQDRINSGEGVPSVFNPPPSRPLQVNTADHRIYSYV PQPRGLLGMSYYLINUPFFTYTYILDIFRFALFFIRPDPKS TDPVGDIVSFMISFEKYGRAHPVFYOGTYSQALNDAKRELE LVYLHGDDHQDSDEFCRNTLCAPBVII LUTTMLHFWASCAL GYRVSQALRRNTYPPILAMIMLKDRRE*PVVVGRLEGLI\QPI INQLTFIMDANQTYLVSERLERBERRQTQULVQQDAYLAK ADQKEKEKKRBERREKRKKEVQQXLABERRQNLQDEKK LECLPPEPSDDDPESVKII FKLINDSRVERRFHSQSLTVII LFSLKESP\EKKPGIRANFPRR\VLPCIPSBE\WNPPFLQUIT LFSLKESP\EKKPGIRANFPRR\VLPCIPSBE\WNPPFLQUIT LFSLKESP\EKKPGIRANFYRVLPGIPSBE\WNPPFLOYDKDGDSFDSI FGSRSGCTPSPDVVLKGSSDGRSGSDESDLHRKLPDVKXD ARRTSHGBPKSAVPFNQVLPMSSMQTAYVPAPLRKKKARREI KSWSTATSPAGLGKRALQDYGPRT\PVS\DDAESTSMFDMR RAAVQPHSRRAQDGLQLINNQLRREDDK\DDLARMSSRKN QDLIKKEERKKMEKLLAGBGGTSERKSIKTYREIVQEKE RELHEAYKNARSOERAEGILQYIERFTISBAVLERLEPMK RSHSTEPNLSSFLNDPNMKXLRQGCLARMSSRKRI LADGSVBLKURQDRGSTENKKYREVQDELANTTEKTEPNS\QBL GGKSRKGNIELASSEPQHFTTTVTRCSPTVAPKFPSSQDL VSEKDQKKPENEMSGKVELVLSGKVKVEKSEPBRATLTFP KMPEANQLHLPNINSGVDPSSSEKSPVTTPFKPMSNDPEBE QSKMQQSCELLLGERYQ\KEQDK\LLKRS\REPSSSGTMK GRQQDEKQDRENKKSFQGDBSDLLLKTRSSDRLEKGSLTMK GRQDBKQDRENKKSFQGDBSDLLLKTRSSDRLEKGSLTMS GRQDBKQDRENKKSFQGDBSDLLLKTRSSDRLEKGSLTMS GRQDBKQDRENKKSFQGDBSDLLLKTRSSDRLEKGSLTMS GRQDBKQDRENKKSFQGDBSDLLLKTRSSDRLEKGSLTMS AHSGNPVSKGVHEDHQLLDTFAGAPHCGTNPQLAQDPSONCO PTHSSBDVKFKTD-PLDKSINIQIESPSSERSSIGKKLCSS PLGKGAMIIETINIYFHIQCFRCG\1CKGQLGDAVSGTDV				
GSILOKHPRIRPHTGLUDAHLYCLKKYIVDFLMENG\SITESI EL\1\PYLY\PKGKOFSASSQOGTKKKKGGKRGLKSFRI SFY*KEANYTGTGAPY\D\ACWI 5829 260 1259 PDGRLIVGCSEBKTIKUMDITHKQCVNNFSDSVGFANFUDFS GTCLASAGSDQTVKWUNDVRVKLLQRYQVHSGGWCISFHE YLITASSDGTLKILDLLKGRLIYTLQGHTGPYFVGFKGG ASGGADTQVLLMERTHFDEHLKCKLIKRANLKRLHPDSPHLLL PRTPHPHERKVETVEDFFLHLLRLIQSLR*SICESLIPLLWI LLILDPQQKRVVGLQTVRUKGVGDLTVTLGHTGPYFVGFKGG QKT*VTSPVKVK/VSIPLAVTDALEHHLMEQLNVLTQTVSIL LTLTEDKLKDCLENQQKLFSAVQQKS GGKMAADEREDLTOSGYRKLLOFDDLTTGISSMDGCRHTLGO NIEAAVQDRLNEGEGVPSVRNPPPSRPLQVTTADHRIYSYVV PQRRGLLGNGYYLINLPFRFTYYTILDIFFALRFIRPDFR TDPYGDIVSFMHSFERKGRAHPYFYQGTYSQALNDAKRELI LVYLHGDDHQDSDEFCRNTLCAPEVISLINTMHAVACSTN GYRVSQALRENTYPPLAHMIMLKDRRS*LVVGRLEGLI\QPI INQLTFIMDANQTYLVSERLERBERNQTQVLRQQQDAYLAA ADQEKERKKREBERRKRKEEVQQXLABERRGNIQBEKI LECLPFEPSFDDPSSVKIIFKLPNDSRVERFFHSQSLTVI LFSLKESP\EKRQIBA\NFPRR\VLPCIFSES\WFNPFTLQI LSHTEVLFVQDLTDE 5831 71 2897 PCSKOKCCLYLIPSINRSKSCTAKPGHSQDRHAVMDSERQ GLSHTEVLFVQDLTDE GSRSRQTPSPDVVLRGSSDGRSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAVYAPLEKKKABEN EAAVQPHSRRAGGDLQLINNGLRSEDDKODDLARMSSRKI SKWSTATSPAGLJKKALQDVGPST-VSV\DDABETSHFDNR EAAVQPHSRRAGGDLQLINNGLRSEDDKODDLARMSSRKI QDLIKKEBERKMELLAGBGDTSERKSIKTYREVQBRLE QBLKKEBERKMELLAGBGDTSERKSIKTYREVQBRLE GSSBLKQDNGSTEINLTFKVFBNSQDDLK RSHSTENNLSSFLNDDNMKKLRQGLPPFRTTVETTIA VLDTMSMASGSSPSKTVTVFRAVPMLITKPEYSQFRNSQDVLK VDGWSVNGSTVURREEEKERCPTVAPAHSILTKSQMFGVAX GSPLELKQDNGSTEINLKKPNSVPGATTVETTIANVETTIA VLDTMSMASGSSPSKTVTTFKAVPMLITKPEYSQFRNSQDVLK VDGWSVNGSTVURREEEKERCPTVAPAHSILTKSQMFEGVAX GSPLELKQDNGSTEINLKKPNSVPGATTVETTPTRFMAWDPEEE GKRMQOBGCBILLOERVQ\KEGOR\LKEE\WERAGREVEEEE YESP\$TI\DDFVYTVSSSADLGATTRKTEPNSQBD GKSRKGNIELASSEPQHFTTTVTRCSPTVFRFMAWDPEEE YESP\$TI\DDFVYDTVSSSADLGATTRKTEPNSQBD GKSRKGNIELASSEPQHSTTTVTRFAPALTTLTAT KMPERNOLHLPHINSCVDSPSSEKSPTTTPRFMAWDPEEE YESP\$TI\DDFVYDTVSSSADLGATTRKTEPNSQBD GKSRKGNIELASSEPQCHCTTTVTRGSPTLAGERGTMK GNQQDEKQDERMKESPGODDSLLLKTRSSDRLEEKGSTMK HERGRPVSKSVHEDHQLLTPLAGSPTGVLAGERGTMK GNQQDEKQDRINGTHSKSHTTLDTFHIQCFRCG\1CKGQLGDAVSGTDV NGLLKCHOOTHSSASAGGGTTIV NGLLKCHOOTHSTANG		1	1	EDVIDGOVGVKKAVEODDETGVDCTGKDI.1.FMAMFADI.DEFI.VITK
EL\TPYLV/RGKOFSSASSOGGTRKEKEGGSKGKRGLKSFRI SFY*KEANYTGTGAPY\D\ACMI 5829 260 1259 PDGRLIVSCSEDKTI KIWDTINKQCVNNFSDSVGFANFVDFN GTCLASAGSDQTVKVWDVRVNKLLQRYQVHSGGWNCISFHES ASGGADTOVLLMRTNFFDELHCKGLTKRNLKRLHFDSPHLLL PRTPHPHEBKVETVEDFFLHLLKIQSLR*SICRSLLPLLWI PRTPHPHEBKVETVEDFFLHLLKIQSLR*SICRSLLPLLWI LLILPQQQKPVVGLCQTRVGRPUDIS*TLSP*CHQNVQQPR* QKT*VTSPVKVK/VSIPLAVTDALEHIMEQLNVLTQTVSILE LLILPQQQKBVVGLCQTRVGRPUDIS*TLSP*CHQNVQQPR* QKT*VTSPVKVK/VSIPLAVTDALEHIMEQLNVLTQTVSILE LTLTEDKLKDCLENQQKLFSAVQQKK TLSPQNTALLPRFTYTTILDIFRFARFIRPDFR TDPVGDIVSFMISFBEKVGRAHPVFYQGTYSQALNDAKRELL LVYLHGDDHQDSDBECKRTTLCAPEVILNTRMLFWACSTNI GYRVQALRENTYPPLAMIMLKDRRS*PVVVGRLEGLI\QPP INQLTFIMDANQTTILVSERLERERNQTVALRQQDEXYLA ADQSKERKKBERERKRKKEEVQQKLABERRRQNLQEKK LECLPPEPSFDDDESVKIIFKLPDKOJURQQDDAYLAA ADQSKERKKRERERERKRKKEEVQQKLABERRRQNLQEKK LECLPPEPSFDDDESVKIIFKLPDKSDLYDKKDI GLSHTEVLFVQDLTDE FCSKDKCCIYLPBSINGSKSCTAKFGAHSQDRHAVMDSERQI TDDIESSKRSIDSSYDLKTGSSDGRGSDESDLPHRIPDVKKDI GLSHTEVLFVQDLTDE FCSKDKCCIYLPBSINGSKSCTAKFGAHSQDRHAVMDSERQI TDDIESSKRSIDSTGSTDSTSSSTSSSSPBENGEDDSFDSI FGSRSRGTPSPDVVLRGSSDGRGSDESDLPHRIPDVKKDI ARTSHGBPKSAVPFNQVLPKSGNCTAVPAPLKKKARREI KSWSTATSPAGLGKALQDYGPRT\PVS\DDASSTSMFDMR RAAVQPHSRRAGDGLQLLINNQLREEDDKWQDLARMSKRKKI URDSWSVNGSTVHREEBKERRKSIKTYREIVQEKE RELHEAVKNARSOERAEGILQYIERFTISERKSIKTYREIVQEKE RELHEAVKNARSOERAEGILQYIERFTISERKSIKTYREIVQEKE RELHEAVKNARSOERAEGILQYIERFTISERKSIKTYREIVQEKE GSPLELKQDMGSIEINIKKPNSVPGSLAPTTEKTEPPSSQBD GGKSRKGNIELLASSEPQHTTTVTVCSPTVARVEPSSPQDL VSEEKDQKKPENEMSGKVELVLSGKVVKPKSPEPSATLTFP KMPEANGLHLPNILNSCVDSPSSEKSPVTTPFKFWAMDPEEE GGKMQOBGCELLLGERYQ KEGDK\LLSTSSSMTEGSGTMK GMCQDEKQDRRWKSFGGDDSDLLLKTRSDSHERKSIKTME GMCQDEKGDRRMKKSFGGDDSDLLLKTRSDSHERKSICTMM GMCQDEKGDRRMKSFGGDDSLLLKTRSDSHERKSSTMME GMCQDEKGDRRMKSFGGDDSLLLKTRSDSHERKSICTMM GMCQDEKGDRRDCHTTANDFTUSSASADJSTSSSMTEGSGTMMK GMCQDEKGDRRDCHTFLINDIFFHIGCFRCG\ICKGQLGDAVSGTDV NGLLMCHOOTYMSSASAGGGTTU			1	DELA LOGUALVAMA EÑADE TOANO LOKA DELAMA ENTA A LOGUA DE DE LA LOGUA DE LA LA LOGUA DE LA LA LOGUA DE LA LA LOGUA DE LA LA LOGUA DE LA LA LOGUA DE LA LA LOGUA DE LA LOGUA DE LA LA LOGUA DE LA LA LOGUA DE LA LA LOGUA DE LA LA LOGUA DEL LA LOGUA DE LA LOGUA DE LA LOGUA DE LA LOGUA DE LA LOGUA DEL LA LOGUA DEL LA LOGUA DE LA LOGUA DEL LOGUA
SFY*KEANYTGTGAPY\D\ACMI 5829 260 1259 PDGRLIVSCSEDKTIKIWDTTNKQCVNNFSDSVGFANFVDFN GTCTASAGSDQTVKWWDVKVKLUQHYQVISGGVNCISFHEE YLITASSDGTLKILDLLKGRIJYTLQGHTGPVFVSFSKGGE ASGGADQVLLWRINFDELHCKGLTKRNLKRLHFDSPHLLL PRTPHPHEEKVETVEDFFLHLLRLIQSLR*SICRSLLPLLWI LLILPQQQKVVGLCQTRVKRPVDIS*TLP*CIQNVCQPPS QKT*VTSPVKVK/VSTPLAVTDALHHMEQLNVLTQTVSILE LTLTEDKLKDCLENQQKLFSAVQQKS 5830 4496 3139 GGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQF NIEAAVQDRLINGEGGYPSVFNPPPSRPLQVNTADHRIYSYV PQPRGLLGWGYYLIMLPFFFTYYTLDLFFRAUFFTRPDPRK TDPVGDIVSFMHSFEKYGRAHPVFYQGTYSQALINDARELL LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLPWACSTN GYRVSQALRRNTYPFLAMIMLKDRRE*PVVVGRLEGLI\QPF INQLTFIMDANQTYLVSERLEBERENQTQVLRQQDEAYLAA ADQEKERKKREBERKRRKKESVQQQKLABERRQONLQEEK LECLPPEPSPDDPSVKITKLNDSRVERRFHFSQSLTVI LFSLKESP\EKFQLEA\NFPRR\VLPCIFSEE\WFNPPTLQI GLISHTEVLFVQDLTDE GLISHTEVLFYQDLTDE FGSKKCCLYLPDED BINSKSCTAKFGAHSQDRHAVMDSERQ TDDIESPKGSIRDSGYICMDSERSDSLSPPRHGRDDSFDS) FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFRQYLDNINGTAVPAPLIKKKABREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMK RANVQPHSRARQECLQLINNOLRSAVLESAVLESAVLESAVLESAVLESAVLESAVLESAVLE				GOTTOWNER ADDRESS COOCURA CAROLINATION OF THE PROPERTY OF THE
5829 260 1259 PDGRLIVSCSEDKTIKIWDTNKQCVNNFSDSVGFANFVDFF GTCLASAGSDTVKWWDVRVKLLQHYQVHSGGNCISFNPE YLITASSDGTVKKWDVRVKLLQHYQVHSGGNCISFNPE XLITASSDGTVKKWDVRVKLLQHYQVHSGGNCISFNPE XLITASSDGTVKKWDVRVKLLQHYQVHSGGNCISFNPE ASGGADTQVLLWRTNFDELLCKGLTKRNLKRLHFDSPPHLLL LLLLPQQQKEVVGLCQTRVKRPVDIS*TLP*CKQNVCQQPR QKT*YTSPVXVK/VSIPLAVTDALEHIMEQLNVLTQTVSILE LLTLTEDKLKDCLENQKLFSAVQOKLASHDQCRHTLEQF NIEAAVQDRLINEQGGYPSVFNPPPSRFLQVNTADHRIYSYV PQFRGLISGGYTLIMPFFRFTYTTLDIFFRALRFTRPDPR TDPVGDIVSFMHSFEEKYGRAHPVFYQGTYSQALNDAKRELL LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRHLFWACSTNI GYRVSQALRRINTYPFLAMIMLKORRE*PVVQGKLEGLIQQP INQLFFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLAA ADQEKERKKREBERKRRKEERQQKLASERRRONLQEKK LECLPPPPSPDDDPSVKIIFKLPNDRSVERRFHFSQSLTVI LFSLKESP\EKFQIEA\NFPRR\VLPCIFSEE\WFNPPTLQI GUSHTEVLFVQDLITDE 5831 71 2897 FCSKGKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQ GUSHTEVLFVQDLYDG SKRSTATSPGLGKKALQDYGPRT\PVS\DDAESTSMFDMR RANTSHGEPKSAVPFNQYLDRWSGRSDSPBSDLPHRKLDDVKKD ARRTSHGEPKSAVPFNQYLDRWSGRSDSPBSDLPHKKLDPVKKD ARRTSHGEPKSAVPFNQYLDRWSDRFADSLFTISRAVLERLEMPK KSWSTATSPGLGKKALQDYGPRT\PVS\DDAESTSMFDMR EAAVQPHSRARGCQLGLINNQLREEDDKWQDDLARWKSRRR QDLIKKEEERKKMEKLLAGEDGTSERRSIKTYKETVQEKE RELHEAYKNARSOBEAGGILQOYTAAPHASIKTSQMFEDVA GSPLELKQDNGSIEINIKRPNSVPQELAATTEKTEPNSQBD GGKSRKONIELASSEPQHFTTTVTRCSPTVAPHSFPSSPQL VOEKVSVNGETVHREEEKKRECPTVAPHASIKTKSQMFEDVA GSPLELKQDNGSIEINIKRPNSVPQELAATTEKTEPNSQBD GGKSRKONIELASSEPQHFTTTVTRCSPTVAPVEFPSSPQL VSEEKDQKVPENENSGKVELVUSQKVVKPSPEPEATLTTP KMPEANOLHLENLNSQVDSPSSEKSPVTTPFKFMAMPDEEE QEKWQQEQERLLQERYQ\KEQDK\LKEE WEKAQKBVEEEE YSEEF*II\EDPVYPFTVSSSSADQLSTSSSMTEGGTMMK GRQDEKQDRRWKKSPGQDDSDLLLKTRESDRLEKKSLTER AHSGNPVSKGMHEDHOLDTSEAGHCINNPQLADPSONQO PTHSSEDVKPKTLPLDKSINHQIESPSERKSISGKKLCSS PLGKGAAMIIETLALYPHIQCFRCG\ICKGQLGDAVSGTTV NGLLKNONCYMFSRSAGQPTTU				
GTCLASAGSDQTVKWMDVRWIKLLQHYQVISIGSVNC1SFHES YLITASDGTIKILDLLKGRLIYTLQGHTGPVFTVSFSKGG ASGGADTQVLLWRINFDELHCKGITKRNLKRLHFDSFPHLL PRTPHPHEBKVETVEDFFLHLLRLIQSLR*SICRSLLPLLWI LLILPQQQKBVVGLCTRVKRPVDIS*TLP*CGNVCQOPR QKT*VTSPVKVK/VSIPLAVTDALEHIMEQLNVLTQTVSILE LLILTEDKLKDCLENQQKLFSAVQQKS 5830 4496 3139 GCKWAAPEEDLTQGTBKLLQFQDLTGIESMDQCRHTLEQF NIEAAVQDRLINEQGGVPSVFNPPPSRPLQVWTADHRIYSYVV PQPRGLLGWGYVLIMLPFRFTYYTILDIFRFALFIRPDPRS TDPYGDIVSTMHSFEEKYGRAPPVYQGTYSQALNDAKRELE LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNN GGRVSQALRENTVPFLAMMILKDREE*PVVYGLEGLI\QPI INQLTFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLAX ADQEKEKKREERERKRKKEVQQQKLABERRQGNLGEKE LECLPPEPSPDDPSVKIIFKLMDSRVERFFHFSQSLTVI LFSLKESP\EKFQLEA\NDSRVERFFHFSQSLTVI LFSLKESP\EKFQLEA\NDSRVERFFHFSQSLTVI LFSLKESP\EKFQLEA\NDSRVERFFHFSQSLTVI LFSLKESP\EKFQLEA\NDSRVERFFHFSQSLTVI TDIESPKRSIRDSGYIDCMDSERSDLSSPFRGNDDSFPH TDIESPKRSIRDSGYIDCMDSERSDLSSPFRGNDDSFPH SGSRSGTPSPDVVLRGSSDGSGSDSESDLFHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSHMDVKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSHMDVKDI REAVQPHSRARGQCLQLINNQLEEBDDKWQDLARWKSRRR QDLIKKEEERKKMEKLLAGGGTSERKSIKTYREIVOEKEI RELHEAYKNARSQEEAGGILQQYIERFTISEAVLERLEMPK SHSTEPNLSSFINDENPKYLRQGSLPPPFATATVETTIA VLDTSMSAGGGSPKTVTPKAVPMLTPRKYSQPKNSQDVLK SHSTEVNLSSFLNDENPKYLRQGSLPPPFATATVETTIA VLDTSMSAGGSPKTVTTRAPVHTRSPTYSQFRNSQDLIK SHSTEVNLSSFLNDENPKYLRQGSLPPPFATATVETTIA VLDTSMSAGGSPSKTVTTPKSQFVVKKSPEPEATLTFP KMPEANQLHLENINSQVDSPSSEKSPVTTPFKFMSWPDEEB GKKRGNIELASSECHTTTVTRSSPTVFVFFFSSCMPETVA GSPLELKQDNKPSTURMSGKVELVLSQKVVKKSPEPEATLTTP KMPEANQLHLENINSQVDSPSSEKSPVTTPFKFMSWPDEEB GKKQQBGPRLLQERYQ\KEQDK\LKEE WEKAQKEVEEEE YEEE' II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMKK GRQQBGPRUKKSPGQDDSDLLLKTRESDRLEEKSSLTE AHSGNPVSKGWIEDHOLDTEAGAPGTNPOLADOPSONQO PTHSSEDVKPKTLPLQCFRCG\ICKGQLGDAVSGTTV NGLLKNONCYMRSRSAGQPTTU			<u> </u>	
YLITASDGTLKILDLLKGRLIYTLQGHTGPVFTVSFSKGER ASGGADTQVLLWRTNFDELHCKGLTKRNLKRLHFDSPPHLLL PRIPHHEKEVETVEDFFLHLLLRIGSLR*SICRSLJELLWILL LLILPQQQKPVGLQGTRVKRPVDIS*TLP*CHQNVCQQPR QKT*VTSPVKVK/VSIPLAVTDALEHIMGQLNVLTQTVSILE LTLTEDKLKDCLENQQKLFSAVQKS QKT*VTSPVKVK/VSIPLAVTDALEHIMGQLNVLTQTVSILE LTLTEDKLKDCLENQQKLFSAVQKS GKMAPBERDLTOEQTEKLLQFQDLTGISMDQCRHTLEQF NIEAAVQDRLNEQEGVPSVTMPPPSRPLQVTTADHRIYSYVV PQPRGLLGWGYYLTMLPFRFTYTTLDIFRFALRFIRPDPRS TDPVGDIVSFMHSFERKYGRAHPVFYCGTTYSQALNDAKRELI LVYLHGDHQDDSBFCRNTLTAFUFVACSTN GYRVSQALRENTYPFLAMIMLKORRE*PVVVGRLEGLI\QPI INQLTFINDANQTTLVSERLERERRQTVLRQQDEAYLAS ADQEKERKRERERERKRKKEVEVQQXLABERRERRQNLQEKE LECLPPEPSPDDPBSVKIIFKLPNDSRVERRFHFSGSLTVI LFSLKESP\EKFQLEA\NFPRR\VLPCIPSEB\WPNPFTLQI GLSHTEVLFVQDLTDE 5831 71 2897 FCSKOKCCLYLDDSINRSKSCTAKPGAHSQDRHAVMDSERQ TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRIGRDDSFDSJ FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGBPKSAVPFNQYLDNKSNQTAVVPAPLRKKKARREI KSWSTATSPGLGKKALQDVGPRT\PVS\DDASSTSMFDMK SWSTATSPGLGKKALQDVGPRT\PVS\DDASSTSMFDMK GSPLSLKQDNGSIEINIKPNSVPQELAATTEKTEPNSQBD GSFLBLKQDNGSIEINIKPNSVPQELAATTEKTEPNSQBD GSPLBLKQDNGSIEINIKPNSVPQELAATTEKTEPNSQBD GGKSRKGNIELASSEPQHFTTTVTCSPTVAPVEFPSSPQL VDGKVSVNGETVHREEKERRECPTVAPAHSLIKSQMFECVAI GSPLBLKQDNGSIEINIKPNSVPQELAATTEKTEPNSQBD GKSRKGNIELASSEPQHFTTTVTCSPTVAPVEFPSSPQL VSEEKDQKKPENEMSGKVLLVLSGKVVKPKSPERATLITP KMPEANOLHLPNLNSQVDSPSSERSPVTTPFKWAMDPEEL QEKWQQDGERLLQERYQ\KEDGKLYKESPERATLITP KMPEANOLHLPNLNSQVDSPSSERSPVTTPFKWAMDPEEL GRCQDEKQDERRLAERSPQCDSDLLLKTRESDRLEKGSLTB ALSGPVSKGVIEDHOLDLTEAAPCKTSCSLTE ALSGPVSKGVIEDHOLDLTEAAPCKTSCSLTE ALSGPVSKGVIEDHOLDLTEAAPCKTSCSLTE ALSGPVSKGVIEDHOLDLTEAAPCKTSCSLTE ALSGPVSKGVIEDHOLDLTEAAPCKTNCLAAPDSSQRD PTHSSEDVKRYTLPLDKSINHQIESPSERKSISGKXLCSS PLGKGAAMIETLNLYFHIDCFRCG\1CKGQLGDAVSGTDV.	5829	260	1259	
ASGADTOVLLWRINFDELHCKGLTKRNLKRILHFDS PPHLLE PRTPHPHERKVETVBDFFLHLLRLIQSLR*SICRSLPPLLWI LLILPQQQKPVVGLQQPVKRPVDIS*TLP*CHQRVCQQPR* QKT*VTSPVKYK/VSIPLAVTDALEHIMEQLNVLTQTVSILE LLTLTEDKLKDCLENQQKLFSAVQQK QKT*VTSPVKYK/VSIPLAVTDALEHIMEQLNVLTQTVSILE LTLTEDKLKDCLENQQKLFSAVQQK QKT*VTSPVKYK/VSIPLAVTDALEHIMEQLNVLTQTVSILE CKYPTPLAVENDAVA GKMAAPEERDLTQEQTEKLLGFQDDLTGIESMDQCRHTLEQF NIEAAVQDRINEGEVSVNTPPPSRPLQVMTADHRIYSYV PQPRGLLGWGYYLIMLPFRFTYTTILDIFRFALRFIRPDRS TDPVGDLVSFWHSFEEKYGRAHFVFYQGTYSQALNDAKRELL LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRNLFWAGSTNI GYRVSQALRENTYPFLAMIMLKNDRE*PVVVGRLEGLI\QPI INQLTFIMDANQTYLVSERLERERRYTQVLRQQDEAYLAK ADQEKERKRERERRKKEVQQQKLABERRRQNI\QPEKAL LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHSQSLTVII LFSLKESSP\EKFQIEA\NFPRR\VLPCIFSEE\WFNPPTLQI GLSHTEVLFVQDLTDE GLSHTEVLFVQDLTDE FGSRSQTPSPDVVLRGSSDGGSDSSSDLPHRKLPDVKND ARRTSHGBEKSAVPFNQYLDNKSNQTAYVPAPLRKKARREI KSWSTATSPAGLGKKALQDYGFRT\PVS\DDAESTSMFDMR KSWSTATSPAGLGKKALQDYGFRT\PVS\DDAESTSMFDMR KSWSTATSPAGLGKKALQDYGFRT\PVS\DDAESTSMFDMR EAAVQPHSRARQEQLQLINNQLREEDKWQDLLARKKSRR: QDLIKKEEERKKMEKLLAGBOTSBERKSIKTRIEVGENG WLKEEERKKMEKLLAGBOTSBERKSIKTRIEVGENG TUDISMAGAGSSPSKTVTPKAVPMLTPKPYSQPKNSQDLIK RSHSTEPNLSSFLNDPFMKYLRQGSLPPFKFTATVETTIA VLDTSMAGAGSSPSKTVTPKAVPMLTPKPYSQPKNSQDLIK GGKSKGNIELASSPQHFTTVVTRCSFTVAFVEFPSSPQL GGKSKGNIELASSPQHFTTVVTRCSFTVAFVEFPSSPQL GGKSKGNIELASSPQHFTTVVTRCSFTVAFVEFPSSPQL GGKSKGNIELASSPQHFTTVVTRCSFTVAFVEFPSSPQL VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLENINSQVDSPSSEKSPYTTPKWANDPEBE GRKWGADGERLJOREYQ\KQOPK\LKEN\EMEAGREEERS GRCQDEKQDGRRLJOREYQ\KQOPK\LKEN\EMEAGREEERS GRCQDEKQDGRRLJOREYQ\KQOPK\LKEN\EMEAGREEERS GRCQDEKQDGRRLJOREYQ\KQOPK\LKES\FERSALTEBROEGGTMKK GRCQDEKQDGRRLJORENQOKQDLLLKTRESDRLEKKSLTE PLISKGAAMIIETLANLYFILDKSINHQIESPSERRSIGGKLCSS PLISKGAAMIIETLANLYFILDKSINHQIESPSERRSIGGKLCSS PLISKGAMAIIETLANLYFILDKSICKGGLORAVSGTDV				GTCIASAGSDQTVKVWDVRVNKLLQHYQVHSGGVNCISFHPSGN
PRTPHPHEKVETVBDFFLHLLRLIOSLR*SICRSLLPLLWI LLILPQQKPVVGLCQTRVKRYDIS*TLP*CHQNVCQQPK QKT*TTSPVKVK/VSIPLAVTDALEHIMEQLNVLTQTVSILE LTLTEBUKLKCLENQQKLFSAVQQKS S3139 GGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQF NIEAAVQRLMEGEOVPSVFNPPPSRPLQVNTADHRIYSYV PQPRGLLGWGYYLINLPFRFTYYTILDIFRFALRFIRDPRS TDPVGDIVSFMHSFEKYGRAHPVFYQGTYSQALNDAKRELF LVYLMGDDHQDSDECRNTLCAPEVISLINTRMLFWACSTNF GYRVSQALRENTYPPLAMMMLKDRE*PV\VGRLEGLI\QPT INQLIFHIMDANQTYLVSELBERERNQTQVLRQQQDEAYLAA ADQEKERKKREBERERKRKKEEVQQQKLABERRRQNLQEEKI LECLPPEPSPDDPESVKIIFKLMNDSRVERRFHFSQSLTVIF LESLKESP\EKFQIEA\NFPR\VLPCIPSEE\WPNPPTLQI GLSHTEVLFVQDLTDE FCSKDKCCLYLDDSINRSKSCTAKFGAHSQDRHAVMDSEQT TDDISSPKRSINDSGYIDCWDSERSDSLSPPRHGRDDSFDSI FGSRSQTPSPDVVLRGSSDGRGSDSESDLPHRKLDDVKKDI ARRTSHGEKSAVPFNQYLDNKSNQTAYVPAPLRKKKAEREI KSWSTATSPAGLGKKALQDYGFRT\PVS\DDASSTSMFDMR KSWSTATSPAGLGKKALQDYGFRT\PVS\DDASSTSMFDMR REANQPHSRARQEDLQLINNQLREEDDKWQDDLARWKSKKAEREI QDLIKKEEERKKMEKLLAGEDGTSERKKSIKTYREIVQEKEI RELHEAYKNARSGEEREGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFINDPNPMKYLRQQSLPPPKFTATVETTIA VLDTSMSAGSGSPSKTUTPKAVPMLTPKPYSQPKNSQDVLK VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFECVA GSPLBLKQDNGSIEINIKRRNSVPGLATTERTEPNSQED GGKSRKGNIELASSEPQHFTTTVTRCSPTVAPVEPFSSPQL VSEEKQKKPEMEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLPNINSQVDSPSSEKSPVTTPFKWADPDEEE QEKKQCGGERLLOGRVQ\KEONE\LKEE\WEKAQKBVEEEE VSEED*II\CDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDSKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTM AHSGNPVSKSVHEDHGLDTAFAGAPHCGTINPQLAQPPSQNQQ PTHSSEDVKPKTLPLDKSINHQIESPSERKSISGKKLCSS PLGKGAMMILETLINLYFHLQCFRCG\ICKGQLGDAVSGTDV NGLINNDCVTMSSSSAQCPTTL				
LLILPQQQKPVGLCQTRVKRPVDLS*TLP*CHQNVCQQPRR QKT*VTSPVKVK/VSIPLAVTDALEHIMEQLNVLTQTVSILE LTLTEDKLKDCLENQQKLFSAVQQKS 5830 4496 3139 GGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQF NIEAAVQPRIMEQEBVPSVFNPPPSRPLQVNTADHRIYSYV PQPRGLLGMGYYLINLPFRFFTYTTLDIFRFALRFIRPDPRR TDPVGDIVSFMHSFEKYGRAHPVFYQGTYSQALNDAKRELE LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNN GYRVSQALRENTYPFLAMIMLKDREE*PV\VCRLEGLI\QPI INQLTFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLAE ADQEKERKRRERERRKRKKEVQQXLAEBRRRNLQEEKI LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHF9QSLTVII LFSLKESP\EKFQIER\NFPRR\VLPCIPSEE\WPNPPTLQI GLSHTEVLFVQDLTDE FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQI TDDIESPKRSIRDSGYIDCWDSERSDLSPPRRGRDDSFDSI FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPPRKLPDVKKDI ARRTSHGBPKSAVPFNQYLDKNSQTAYVPAPLRKKKARREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMR EAAVQPHRRARQEQLQLINNQLREEDDKWQDDLARWKSRKRI QDLIKKEERKKMEKLLAGEDGTSERKSIKTTREIVGEKEI RELHEAYKNARSQERAEGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIA VLDTSMSAGSGPSKTVTPKAVPMLTPKFYSQPKNSQDVLK VDGKVSVNGETVHREEEKRRECCPTVAPAHSLTKSQMFEGVA GSPLEIKQNDGSIEINIKKPNSVPQELAATTEKTEPNSQED VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLPNLINSQVDSPSSEKSPVTTPFKFWAWDPEEE GGKSRGNIELASSEPQHTTTVTRCSPTVAFVEFFSSPQL VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLPNLINSQVDSPSSEKSPVTTPFKFWAWDPEEE QEKMQQEGGELLQERYQ\KROPKLKEE WEKAQKEVEEEE VSEEP*II\EDPVVPFTVSSSADQLSTSSSMTGGGTNNK GNCQDEKQDERMKKSFQGDDSDLLLKTRESDRLEEKGSLTEB AHSGNPVSKGVHEDHQLDTFAGAPHCSTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINHQIESPSERRKSIGKKLCSS PLGKGAMMIETLINLYFHIQCFRCG\ICKGQLGDAVSGTDV NGLINCNDCYMSSSAGQPTTL				ASGGADTQVLLWRTNFDELHCKGLTKRNLKRLHFDSPPHLLDIY
LLILPQQQKPVGLCQTRVKRPVDLS*TLP*CHQNVCQQPRR QKT*VTSPVKVK/VSIPLAVTDALEHIMEQLNVLTQTVSILE LTLTEDKLKDCLENQQKLFSAVQQKS 5830 4496 3139 GGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQF NIEAAVQPRIMEQEBVPSVFNPPPSRPLQVNTADHRIYSYV PQPRGLLGMGYYLINLPFRFFTYTTLDIFRFALRFIRPDPRR TDPVGDIVSFMHSFEKYGRAHPVFYQGTYSQALNDAKRELE LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNN GYRVSQALRENTYPFLAMIMLKDREE*PV\VCRLEGLI\QPI INQLTFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLAE ADQEKERKRRERERRKRKKEVQQXLAEBRRRNLQEEKI LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHF9QSLTVII LFSLKESP\EKFQIER\NFPRR\VLPCIPSEE\WPNPPTLQI GLSHTEVLFVQDLTDE FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQI TDDIESPKRSIRDSGYIDCWDSERSDLSPPRRGRDDSFDSI FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPPRKLPDVKKDI ARRTSHGBPKSAVPFNQYLDKNSQTAYVPAPLRKKKARREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMR EAAVQPHRRARQEQLQLINNQLREEDDKWQDDLARWKSRKRI QDLIKKEERKKMEKLLAGEDGTSERKSIKTTREIVGEKEI RELHEAYKNARSQERAEGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIA VLDTSMSAGSGPSKTVTPKAVPMLTPKFYSQPKNSQDVLK VDGKVSVNGETVHREEEKRRECCPTVAPAHSLTKSQMFEGVA GSPLEIKQNDGSIEINIKKPNSVPQELAATTEKTEPNSQED VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLPNLINSQVDSPSSEKSPVTTPFKFWAWDPEEE GGKSRGNIELASSEPQHTTTVTRCSPTVAFVEFFSSPQL VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLPNLINSQVDSPSSEKSPVTTPFKFWAWDPEEE QEKMQQEGGELLQERYQ\KROPKLKEE WEKAQKEVEEEE VSEEP*II\EDPVVPFTVSSSADQLSTSSSMTGGGTNNK GNCQDEKQDERMKKSFQGDDSDLLLKTRESDRLEEKGSLTEB AHSGNPVSKGVHEDHQLDTFAGAPHCSTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINHQIESPSERRKSIGKKLCSS PLGKGAMMIETLINLYFHIQCFRCG\ICKGQLGDAVSGTDV NGLINCNDCYMSSSAGQPTTL				PRTPHPHEEKVETVEDFFLHLLRLIQSLR*SICRSLLPLLWISF
OKT*TTSPVKWK/VSIPLAVTDALEHIMEQLNVLTQTVSILE LTLTEDKLKDCLENQQKLFSAVQKS GGKMAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQF NIEAAVQDRLNEQEGVPSVFNPPPSRPLQVNTADHRIYSYVV PQPRGLLGWGYYLINLPFRFTYYTLDIFRFALRFIREPPRF TDPVGDIVSFMISFEEKYGRAHPVFYQGTYSQALDAKRELF LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNF GYRVSQALRENTYPPLAMMMLKDREFPVVCGTLSGLI\QPI INQLTFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLAA ADQEKERKKRERERRKRKKEEVQQKLABERRRQNLQEEKI LECLPPEPSPDDPESVKIIFKLJPNDSVERRFHFSQSLTVII LFSLKESP\EKFQIEA\NFPRR\VDLFYESSEM\PPPPTLQG GLSHTEVLFVQDLTDE TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSI FGSRSQTTSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLJPNKSNQTAYVPAPLRKKKARREI KSWSTATSPAGLGKKALQDYGPTT\PVS\DDAESTSMFDMK; QDLIKKEEERKMEKLLAGEDGTSERKSIKTYREIVQEKEI REHHAYKNARSQEEREGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFLNDDNYMKYLRQQSLPPPKFTATVETTIA VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK VDCKVSVNGETVHREEEKERECPTVAPAHSLTKSGMFECVAI GSPLELKQDNGSIEINIKERNSVQGLAJATTEKTEPNSQBD GGKSKKGNIELASSEPQHFTTTVTRCSPTVAFVEFFSSPQL VSEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTTP KMPEANQLHLPNLNSQVDSPSSKSPVTTPFKWAMDPEEE QEKWQQGCRLLQERYQ\KEQDK\LEEE\WEKAQKEVEEEE VSEEP\I\QDPVVPFTVSSSSADOLSTSSSMTEGSGTNNK GNCQDEKQDREKQDRRWKKSFQGDDSDLLLKTRESDRLEKKGSLTB AHSGNPVSKGVHEDHOLDTEAGAPHGCTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINHQLESPSERKSIGKKLCSS PLGKGAMMIIETLINLYFHIQCFRCG\ICKGQLGDAVSGTDV NGLIANCNDCYMGSRSAGQPTTL				LLILPOOOKPVVGLCQTRVKRPVDIS*TLP*CHQNVCQQPRKRK
5830 4496 3139 GCKMANPEERDLTOGOTEKLLOFODLTGIESMDQCRHTLEQF NIEAAVODRLNEGGGVPSVFNPPPSRPLQVMTADHRIYSYV PQPRGLLGWGYYLIMLPFRFTYYTILDIFRFALRFIRDPPSR TDPVGDIVSFMHSFEKYGRAHPVFYGGTYSQALNDAKRELS LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNI GYRVSQALRENTYPFLAMIMLKDRRE*PVVGRLEGLI\QPI INQLTFIMDANGTYLVSERLEREERROTQVLRQQDEAYLAR ADQEKERKKREBERERKKEVQQQKLAEBRRRONLQEKS LECLPPEPSPDDPSVKIIFKLPNDSRVERRFHFSQSLTVII LFSLKESP\EKFGIEA\NFPRR\VLPCTFSEB\WFNPFTLDI GLSHTSVLFVQDLTDE 5831 71 2897 FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQI TDDISSPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDJ FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMR EAAVQPHSRRAQEQLQLINNQLREBDDKWQDDLARWKSKRR. QDLIKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKEI REIHEAYKNARSGEAEGILQQYIERFFISEAVLERLEMPK RSHSTEPNLSSFLNDPPMKVLRQQSLPPPKFTATVETTIAI VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDULK VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFECVAA GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED GGKSRKONIELASSEPQHFTTTVTRCSPTVAPVEPSSSQL VSEKDQKKPENEMSGKVELVLSQKVVKPKSPSPERTLITFP KMPEANQLHLDPLNSQVDSPSSEKSPVTTPPKFWAWDPEEE QEKWQQSQERLLQERYQ\KEQDK\LKEN\WEXAGKEVEBEE YEEP1I\EDPVYPFTYSSSSADQLSTSSSNTEGSGTNNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEM AHSGNPVSKGVHEBHQLDTEAGAPHCGTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINIQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQGFRCG\ICKQQLGDAVSGTDV NGLINCNDCYMSRSAGGPTTL		ł	1	OKT*VTSPVKVK/VSIPLAVTDALEHIMEOLNVLTOTVSILEOR
5830 4496 3139 GKMAAPEERDLTQEQTEKLLQFQDLTGIESMQCRHTLEGE NIEAAVQDRINEGEGVPSVENPPSRPLQVNTADHRIYSYV PQPRGLLGGGYVLIMUP FFFTYTTILDIFRFALRFIRPPPRS TDPVGDIVSFMHSFEEKYGRAHPVFYQGTYSQALNDAKRELF LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTIN GYRVSQALRENTVPFLAMIKJRRE + PV\VGRLEGLI\QPI INQLFFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLAS ADQEKERKKREBERERKRKKEEVQQQKLABERRRONLQEEKS LECLPPEPSPDDPSVKIIFKLPNDSRVERRFHFSQSLTVII LFSLKESP\EKFQIEA\NFPRR\VLPCTPSEE\WFNPPTLQI GLSHTEVLFVQDLTDE 5831 71 2897 FCSKOKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQI TDDISSPKRSIRDSGYJTOWDSERSDSLSPPRHGRDDSFDSI FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREI KSWSTATSPAGLKKKALQVSGPT\PVS\DDABASTMFMNR EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKR. QDLIKKEEERKKWEKLLAGEDGTSERRKSIKTYREIVQSKEE RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFINDPNPMKYLRQQSLPPPKFTATVETTIA VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK* VDGKVSVNGETVHREEEKERCPTVAPAHSLTKSQMFPGVAI GSFLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED GKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL VSEKNQKVENENENSGKVELVLSQKVVKPKSEPERATLIFP KMPEANOLHLPNLNSQVDDSPSSEKSPVTTPFKFWAMPDFEE QEKWQDGGERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE YEERP + I 1\CDPVVPFTVSSSSADQLSTSSSMTEGSGTNNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTE AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ PTHSSEDVKRYHEDHQLSTANQFIESPERRKSISGKKLCSS PLGKGAMIIETLNLYFHIQGFRCG\ICKGQLGDAVSGTDV.				
NIEAAVQDRINEQEGYPSVFNPPPSRPLQVNTADHRIYSYVV PQPRGLLGMGYYLTMLPFRFTYYTILDI FRFALRFIRPDRES TDPVGDIVSFMHSFEEKYGRAHPVFYQGTYSQALNDAKRELI LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNF GYRVSQALRENTYPFLANIMLKDRRE*PV\VGRLEGII\QPI INQLTFIMDANQTYLVSERLERBERNQTQVLRQQQDEAYLAS ADQEKERKKREERERKRKKEEVQQXLABERRRQNLQEEKI LECLPPPPSPDDPESVKIIFKLPNDSRVERRFHFSQSITVII LFSLKSSP\EKFQIEA\MFPRR\VLPCIPSEE\WFNPPTLQI GISHTEVLFVQDLTDE 5831 71 2897 FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQT TDDIESPKRSIRDSGYIDCWDBERSDSLSPPRHGRDDSFDSI FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMR EAAVQPHSRARQEQLQLINNQLREEDDKWODDLARWKSRKR QDLIKKEEERKKMEKLLAGEDGTSERKSIKTYRSIVQEKEI RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFLNDDNPMKYLRQGSLPPPKFTATVETTIAI VLDTSMSAGSGSPSKTVTPFKAVPMLTPKPYSQPKNSQDVLK VDGKVSVNGETVHREEEKBRECPTVAPAHSLTKSGMFECVAL GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEPPSSPQL VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLPNLINSQVDSPSSEKSPVTTPFKYMAWDFEEE QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTGSGTMNK GNCQDEKQDRWKKSFQGDDSDLLLKTRESDFLEEKGSLTMN GNCQDEKQDRWKKSFQGDDSDLLLKTRESDFLEEKGSLTMN GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDFLEEKGSLTMN GNCQDEKQDRRWKSFGGDDSDLLLKTRESDFLEEKGSLTMN GNCQDEKQDRRWKSFGGDDSDLLLKTRESDFLEEKGSLTMN GNCQDEKQDRRWKSFGGDDSDLLLKTRESDFLEEKGSLTMN GNCQDEKQDRRWKSFGGDDSDLLLKTRESDFLEEKGSLTMN GNCQDEKQDRRWKSFGGDDSDLLLKTRESDFLEEKGSLTMN GNCQDEKQDRRWKSFGGDDSDLLLKTRESDFLEEKGSLTMN GNCQDEKQDRRWKSFGGDDSDLLLKTRESDFLEEKGSLTMN GNCQDEKQDRRWKSFGGDDSDLLLKTRESDFLEEKGSLTMN GNCQDEKQDRRWKSFGGDDSDLLKTRESDFLEEKGSLTMN GNCQDEKQDRRWKSFGGDDSDLLLKTRESDFLEEKGSLTMN GNCQDEKQDRRWKSFGGDDSDLLKTRESDFLEEKGSLTMN GNCQDEKQDRRWKSFGGDDSDLLKTRESDFLEKGSGTMNK GNCQDEKQDRRWKSFGGDDSDLLKTRESDFLEKGSGTMNK GNCGLINCCDCYYRSRSBAGQPTTL	F000	1405	2120	CCVMANDEEDDI.TOFOTEKLI.OFODI.TGIESMDOCRHTI.EOHNW
PQPRGLLGWGYYLIMLPFRFTYTTILDIFFFALRFIRPDPSS TDPVGDIVSFMHSFEEKYGRAHPVFYQGTYSQALNDAKRELE LVYLHGDDHQDSDBFCRWTLCAPEVISLINTRMLFWACSTNI GYRVSQALRENTYPFLAMIMLKDRRE*PV\VGRLEGLI\QPI INQLTFIMDANQTYI.VSERLERERRQTQVI.RQQQDEAYLAG ADQEKERKKRERERKRKEEVQQQKLABERRRQNLQEEKE LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHFSQSITVI LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WFNPPTLQI GLSHTEVLFVQDLTDE 5831 71 2897 FCSKDKCCLYLPDSINTSKSCTAKPGAHSQDRHAVMDSERQI TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSI FGSRSRQTPSPDVVLRGSSDGRSDSESDLHRRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKABREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMR EAAVQPHSRARQEQLQLINNQLREEDDKWQDLARWKSRKR QDLIKKEEERKKMEKLLAGEDGTSERKSIKTYREIVQEKEI REHHEAYKNARSQEBAGGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIA VLDTSMSAGSGSPSKTVTYKAVPMLTTKPYSQPKNSQDVLK VDGKVSVNGETVHREEKRECPTVAPAPHSLIKSQMFGEVAH GSFLELKQDNGSIEINIKRPNSVPQELAATTEKTEPNSQED GGKSRKGNIELASSEPQHFTTVTVTCSFTVAFVEFPSSPQL VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE GEKWQQEQERLLQERYQ\KEQDK\LKEE\WEXAQKEVEEEE YEEEP*II\EDPVVPFTVSSSADQLSTSSMTEGSGTWNK GNCQDEKQDRRWKKSFQGDSDLLLKTRESDRLERGSSTFNK GNCQDEKQDRRWKKSFQGDSDLLLKTRESDRLERGSSTFN GNCQDEKQDRRWKKSFQGDSDLLLKTRESDRLERGSSTFN GNCQDEKQDRRWKKSFQGDSDLLLKTRESDRLERGSSTFN GNCQDEKQDRRWKKSFQGDSDLLLKTRESDRLERGSSTFN GNCQDEKQDRRWKKSFQGDSDLLLKTRESDRLERGSSTFN GNCQDEKQDRRWKKSFQGDSDLLLKTRESDRLERGSSTFN GNCQDEKQDRRWKKSFQGDSDLLLKTRESDRLERGSSTFN GNCQDEKQDRRWKKSFQGDSDLLLKTRESDRLERGSSTFN GNCQDEKQDRRWKKSFQGDSDLLKTRSSSMTEGSGTWNK GNCQDEKQDRRWKKSFQGDSDLLKTRSSSMTEGSGTWNK GNCQDEKQDRRWKKSFQGDSDLLKTRSSSMTEGSGTWNK GNCQDEKQDRRWKKSFQGDSDLLKTRSSSRTEGSGTWNK GNCQDEKQDRRWKKSFQGDSDLLKTRSSSMTEGSGTWNK GNCQDEKQDRRWKKSFQGDSDLLKTRTRESDRLERGSSTFN GNCGLIKNCHCYYRSRSSAGQPTTL	5830	4496	3139	SOMETHER AND TO SECRET SERVICE SERVICES AND THE SECRET SERVICES.
TDPVGDIVSFMHSFEEKYGRAHPVFYQGTYSQALNDAKRELE LVYLHGDDHQDSDETCRNTTLCAFEVISLINTRMLFWACSTNH GYRVSQALRENTYPFLAMIMLKDRRE*PV\VGRLEGLI\QPI INQLTFIMDANQTYLVSERLERBERNQTQVLRQQQDEAYLAG ADQEKERKKREERERKRKKEEVQQQKLABERRRONLQEEKI LECLPPEPSPDDPESVKIIFKLPNDSRVERFFFSQSLTVII LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPFTLQI GLSHTEVLFVQDLTDE 5831 71 2897 FCSKDKCCLYLPDSINRSKSCTAKFGAHSQDRHAVMDSERQI TDDIESPKRSIRDSGYJICWDSERSDSLSDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKABREI KSWSTATSPAGLGKKALQDVGPRT\PVS\DDASSTSMEDMKS QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKEI RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFLNDENPMKYLRQQSLPPPKFTATVETTIA VLDTSMSAGSGSPSKTVTPFXAVEFPSSPQL VDCKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVA GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL VSEKDQKKPENEMSGKVELVLSQKVVKPKSPEPSATLTFP KMPEANOLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE QEKMQQEQERLLQERYQ\KEGDK\LKEE\MEEEEE YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMKK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTE AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINKGIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL			i	NIEAAVQDRINEQEGVESVENEFESKI EQVITADIKLISTVOK
LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTMI GYRVSQALRENTYPFLAMINLKDRRE*PV\VGRLEGLI\QPI INQLTFIMDANQTYLVSERLEREERNQTQURQQDEAYLAS ADQEKERKKREEREKRRKEEVQQQKLABERRRQNLQEEKI LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHFSQSLTVII LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPPTLQI GLSHTEVLFVQDLTDE FCSKDKCCLYLPDSINRSKSCTAKFGAHSQDRHAVMDSERQI TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSI FGSRSQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMR EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRI QDLIKKEEERKKMEKLLAGBGTSERRKSIKTYREIVQEKEI RELHEAYKNARSQEEAGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIA VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK VDGKVSVNGETVHREEEKERECPTVAPAHSLIKSQMFBEVAI GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQEDL VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE QEKMQQEGERLLQERYQ\KEDMK\LEWEKAGRUEEEEE YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRRWKKSFGGDDSDLLLKTRESDRLEEKGSLTE AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINIQIESFSERRKSIGKKLCSS PLGKGAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLINCNDCYMRSRSAGQPTTL			\	
GYRVSQALRENTYPFLAMIMLKDRRE*PV\VGRLEGLI\QPI INQLTFIMDANGTYLVSERLERERNGTQVURQQDEAYLAE ADQEKERKKREBERERKRKKEEVQQQKLAEBERRQNLQEEKE LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHFSQSLTVIE LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPPTLQE GLSHTEVLFVQDLTDE GLSHTEVLFVQDLTDE FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQI TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSI FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAERERI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMR: EAAVQPHSRARQCPLQLINNQLREEDDKWQDDLARWKSRKR: QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKEI RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIA VLDTSMSAGSGSPSKTVTPKAVPMLTPRYSQPKNSQDVLK VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVAL GSPLELKQDNGSIEINIKKPNSVPQELAATTRKTEPNSQED GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL VSEEKDQKKPENDEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE QEKNQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE; YEEEF+II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRRWKSFQGDDSDLLKTRESDRLEEKGSLTE AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLINCNDCYMRRSRSAGQPTTL				TDPVGDIVSFMMSFEERIGRAMPVFIQGIISQAMVDARREDRI
INQLTFIMDANQTYLVSERLERBERNQTQVLRQQQDEAYLAS ADQEKERKKREBERKRKKEEVQQQKLABERRRQNLQEEKI LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHFSQSLTVII LFSLKESSP\EKFQIEA\MFPRR\VLPCIPSEE\WPNPPTLQI GLSHTEVLFVQDLTDE GLSHTEVLFVQDLTDE 71 2897 FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQI TDDIESPKRSIRDSGYJDCWDSERSDSLSPPRHGRDDSFDSI FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRG EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKK; QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKEI RELHEAYKNARSOBEAEGILQOYIEFFTISEAVLERLEMPK RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIAI VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKY GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLPNLNSOVDSPSSEKSPVTTPFKWAWDEEEE QEKWQGEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE QEKWQGEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE GGCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTBG AHSGNPVSKGVHEDHQLDTEAGAPHCGTMPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINHQIESPEERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLINCNDCYMRSRSAGQPTTL		· ·		LVYLHGDDHQDSDEFCRNTECAPEVISLINIRILEWACSINRPE
ADQEKERKKBERERKRKKEEVQQQKLAEERRRQNLQEEKI LECLPPEESPDDPESSVKIIFKLPNDSRVERRFHFSQSLTVII LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPPTLQI GLSHTEVLFVQDLTDE 5831 71 2897 FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQY TDDIESPKRSIRDSGYIDCMDSERSDSLSPPRHGRDDSFDSI FGSRRRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREEI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRG EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKR; QDLIKKEEERKKMEKLLAGBDGTSERRKSIKTYREIVQKEI RELHEAYKNARSQEEAEGILQQYIEFTISEAVLERLEMPK RSHSTEPPLISFLNDPNPMKYLRQQSLPPPKFTATVETTIAI VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFFGVAI GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED: GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP: KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE: QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE: YEEEP+II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTB: AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ PTHSSEBVKPKTLPLDKSINIQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL		1		GYRVSQALRENTYPFLAMIMLKDRRE*PV\VGRLEGLI\QPDDL
LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHFSQSLTVII LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPPTLQI GLSHTEVLFVQDLTDE GLSHTEVLFVQDLTDE FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQI TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSI FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRG EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKR: QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKEI RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFINDPNPMKYLRQQSLPPPKFTATVETTIA VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK VDGKVSVNGETVHREEEKERCPTVAPAHSLTKSQMFGVAI GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLPNLNSQVDSPSSEKSPVTTPPKWAWDPEEE QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE YEEEP+IIFDPVVPFTVSSSADQLSTSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEG AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSGNQQ PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL				INQLTFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLASLR
LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPPTLQI GLSHTEVLFVQDLTDE 5831 71 2897 FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQI TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSI FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRG EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRI QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKEI RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIAI VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVAI GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQLI VSEEDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP: KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE QEKWQQQEGRLLQGRYQ\KEQDK\LKEE\WEKAQKEVEEEE: YEEEP+II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTB: AHSGNPVSKGYHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQIGDAVSGTDV NGLLNCNDCYMRSRSAGQPTTL				ADQEKERKKREERERKRRKKEEVQQQKLAEERRRQNLQEEKERK
GLSHTEVLFVQDLTDE 5831 71 2897 FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSEROT TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSI FGSRRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAVVPAPLRKKKABREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRG EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRI QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKEI RELHEAYKNARSQEAEGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIA VLDTSMSAGSGSPSKTVTPKAVPMLTPKRYSQPKNSQDVLK VDGKVSVNGETVHREEEKERCCPTVAPAHSLTKSQMFEGVAL GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFFSSPQL VSEEKDQKKPENSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE QEKWQQEQRLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE! YEEEP+II\EDPVVPFTVSSSADQLSTSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTB AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQP PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV NGLLNCNDCYMRSRSAGQPTTL				LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHFSQSLTVIHDF
FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQY TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSJ FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRG EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSKKRS QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKEI RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK: RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIAI VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK: VDGKVSVNGETVHREEKERECPTVAPAHSLTKSQMFEGVAI GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED: GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQLI VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP; KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE: QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE: YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRRWKKSFCQDDSDLLLKTRESDRLEEKGSLTB: AHSGMPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ' PTHSSEDVKPKTLPLDKSINHQIESPSERKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCDCYMRSRSAGQPTTL				LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPPTLQE\A
TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSI FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKAEREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRG EAAVQPHSRARQEQLQLINNQLRBEDDKWQDDLARWKSRKRI QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKEI RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK: RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIAI VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK; VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVAI GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED: GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL: VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPBFEATLTFP KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE: QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE: YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTGGSTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTB: AHSGNPVSKGVHEDHQLLTEAGAPHCGTNPQLAQDPSQNQQ' PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV		1		GLSHTEVLFVQDLTDE
TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSI FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKAEREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRG EAAVQPHSRARQEQLQLINNQLRBEDDKWQDDLARWKSRKRI QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKEI RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK: RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIAI VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK; VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVAI GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED: GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL: VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPBFEATLTFP KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE! QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE: YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTGGSTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTB: AHSGNPVSKGVHEDHQLLTEAGAPHCGTNPQLAQDPSQNQQ' PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL	5831	71	2897	FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQVKD
FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDI ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMR EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKEI QDLIKKEEERKKMEKLLAGEDGTSERKSIKTYREIVQEKE RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIAI VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVAI GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKWAWDPEEE QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEEI YEEEP*II\BDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRWKKSFQGDDSDLLLKTRESDRLEEKGSLTE AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV NGLLNCNDCYMRSRSAGQPTTL	2031	· -	1	TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSLDS
ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREI KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRG EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRI QDLIKKEEERKKMEKILAGEDGTSERRKSIKTYREIVQEKEI RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIAI VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVAI GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQEDI GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQLI VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFPI KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEEI QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEEI YEEEP*II\EDPVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRWKKSFQGDDSDLLLKTRESDRLEEKGSLTE AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQI PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDVI NGLLNCNDCYMRSRSAGQPTTL			1	
KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRG EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRS QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKEI RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK. RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIAL VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK. VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVAL GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED. GGKSRKGNIELASSEPQHFTTTVTRCSPTVAPVEFPSSPQL. VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP. KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEEL QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEEL YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTKE AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL				APPTSHGEPKSAVPFNOYLPNKSNOTAYVPAPLEKKKARREEYR
EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKR. QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKEI RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK. RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIAI VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK. VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVAI GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED. GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL. VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP. KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEEI QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEEE YEEEP+II\EDPVVPFTVSSSSADQLSTSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLKTRESDRLBEKGSLTE AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQO' PTHSSEDVKPKTLPLDKSINHQIESPSERRSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL				NEMCTATE DAGICKKALODYGDDT DVS DDARSTSMEDMBCER
QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKEI RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK: RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIAI VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK: VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVAI GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED: GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL: VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP: KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE! QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE! YEEEP+II\EDPVVPFTVSSSSADQLSTSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLKTRESDRLBEKGSLTE AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQO' PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL			1	PARTODUCARDOROLOT TABIOLOPPINARIOLA ABRACAMORIA PARTODUCA A PROPERTIONAL A POPULA DE PROPERTIONAL DE PROPERTIONAL DE PROPERTIONAL DE PROPERTIONAL DE PROPERTIONAL DE PROPERTIONAL DE PROPERTIONAL DE PROPERTIONAL DE PROPERTIES DE
RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPK: RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIAI VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK: VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVAI GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED: GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL: VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP: KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEEI QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEEE YEEEP+II\EDPVVPFTVSSSSADQLSTSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTE AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQO' PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL				ENTITY OF THE PROPERTY OF THE
RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIAL VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK* VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVAL GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED: GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL. VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP. KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEEL QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEEL YEEEP+1I\EDPVVPFTVSSSADQLSTSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEG AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQO' PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL				QULIKKEEEKKKMEKDLAGEDGTSEKKKSIKTIKEIVQEKEKKE
VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLK VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVAL GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANOLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEEL QEKWQQEERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEEN YEEEP+1I\EDPVVPFTVSSSADQLSTSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTE AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL				
VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVAL GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED: GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL: VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP. KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE! QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE! YEEEP+II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEG AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ' PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL			1	RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS
GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED: GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL: VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPBPEATLTFP: KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE: QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE: YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEG AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ' PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL				VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK
GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQED: GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQL: VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPBPEATLTFP: KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE: QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE: YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEG AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ' PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL		1	-	VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVARVH
GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQLIVSEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP KMPEANQLHLPNLNSQVDSPSSEKSPVTTFFKFWAWDPEEE QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE YEEEP*II\DPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEE AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV NGLLNCNDCYMRSRSAGQPTTL				GSPLELKODNGSIEINIKKPNSVPQELAATTEKTEPNSQEDKND
VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFP: KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEE! QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE! YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTMS AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL		1	-	GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQLKND
KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEEL QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEEL YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEG AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQO PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL				VSEEKDOKKPENEMSGKVELVLSOKVVKPKSPEPEATLTFPFLD
QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEE YEEEP+II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTE AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV NGLLNCNDCYMRSRSAGQPTTL				KMDEANOLHLDNINSOVDSPSSEKSPYTTPEKEWAWDPERERER
YEEEP+II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNK GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEG AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQG PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV NGLLNCNDCYMRSRSAGQPTTL				ORKMOODOEDITOEDAO/ KEODK/ I'KEE/ MEKYOKKAKEEEEBBA
GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEG AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV NGLLNCNDCYMRSRSAGQPTTL				ABBED + 1.1/ BUDINIDE MIGGGGYDULG GEGGWEDGGGWWINIDI.
AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQ' PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV NGLLNCNDCYMRSRSAGQPTTL				XEERA*II/EDAAAALA22222DDD211122DD1EGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSS PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV NGLLNCNDCYMRSRSAGQPTTL				GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEGAL
PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDV. NGLLNCNDCYMRSRSAGQPTTL				AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN
NGLLNCNDCYMRSRSAGQPTTL		ĺ		PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL
NGLLNCNDCYMRSRSAGQPTTL				
				NGLLNCNDCYMRSRSAGQPTTL
5832 2454 829 PGRRFRHGSCAFQKQCIMLHICQYFLQGECKFGTSCKRSHD	5832	2454	829	PGRRFRHGSCAFQKQCIMLHICQYFLQGECKFGTSCKRSHDFSN
SENLEKLEKLEMSSDLVSRLPTIYRNAHDIKNKSSAPSRVP			· -	SENLEKLEKLGMSSDLVSRLPTIYRNAHDIKNKSSAPSRVPPLF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
140:	location	corresponding	
			H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
Ĺ	sequence		\=possible nucleotide insertion)
			VPQGTSERKDSSGSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH
			RVHFHLPYRWQFLDRGKWEDLDNMELIEEAYCNPKIERILCSES
	1		ASTFHSHCLNFNAMTYGATQARRLSTASSVTKPPHFILTTDWIW
			YWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGV*R
	ł		PGSHLEVPGRKAQLRVRFQSLRSEKPGLWHN*KGLPQTQIR\AP
		ĺ	QDVTTMQTCNTKFPGPKSIPDYWDSSALPDPGFOKITLSSSSEE
			YQKVWNLFNRTLPFYFVQKIERVQNLALWEVYQWQKGQMQKQNG
			GKAVDEROLFHGTSAIFVDAICOONFDWRVCGVHGTSYGKGSYF
1			ARDAAYSHHYSKSDTQTHTMFLARVLVGEFVRGNASFVRPPAKE
			GWSNAFYDSCVNSVSDPSIFVIFEKHOVYPEYVIQYTTSSKPSV
1			TPSILLALGSLFSSRO
5833	170	3289	SILCLLSPCVVQFGKPVVSILSSRSRHSPCTKKGWEGMRKHLHT
, ,,,,,	1,0	3403	RQGHK*VHVEISKALWYYRDDYFIRHSISVSAVIVRAWITHKYR
1			
1			GRDWNVKWEENLLHAVAKNYTLLQTIPPFERPFKDHQVCLEWNM
1			GYIWNLRANRIPQCPLENDVVALLGFPYASSGENTGIVKKFPRF
1		ļ.	RNRELEATRRORMDYPVFTVSLWLYLLHYCKANLCGILYFVDSN
			EMYGTPSVFLTEEGYLHIQMHLVKGEDLAVKTKFIIPLKEWFRL
			DISFNGGQIVVTTSIGQDLKSYHNQTISFREDFHYNDTAGYFII
f			GGSRYVAGIEGFFGPLKYYRLRSLHPAQIFNPLLEKQLAEQIKL
			YYERCAEVQEIVSVYASAAKHGGERQEACHLHNSYLDLQRRYGR
			PSMCRAFPWEKELKDKHPSLFQALLEMDLLTVPRNQNESVSEIG
1	•		GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYYLAV
1			FYETGLNVPRDQLQGMLYSLVGGQGSERLSSMNLGYKHYQGIDN
1	•		YPLDWELSYAYYSNIATKTPLDQHTLQGDQAYVETIRLKDDEIL
}			KVQTKEDGDVFMWLKHEATRGNAAAQQRLAQMLFWGQQGVAKNP
			EAAIEWYAKGALETEDPALIYDYAIVLFKGQGVKKNRRLALELM
		,	KKAASKGLHQAVNGLGWYYHKFKKNYA\KAAKYWLKA\EB\MGN
			PDASYNLGVLHLDGIFPGVPGRNQTLAGEYFHKAAQGGHMEGTL
	1 *		WCSLYYITGNLETFPRDPEKAVVWAKHVAEKNGYLGHVIRKGLN
			AYLEGSWHEALLYYVLAAETGIEVSQTNLAHICEERPDLARRYL
			GVNCVWRYYNFSVFQIDAPSFAYLKMGDLYYYGHQNQSQDLELS
ŀ			VQMYAQAALDGDSQGFFNLALLIEEGTIIPHHILDFLEIDSTLH
ĺ		,	SNNISILQELYERCWSHSNEESFSPCSLAWLYLHLRLLWGAILH
	,		SALIYFLGTFLLSILIAWTVQYFQSVSASDPPPRPSQASPDTAT
			STASPAVTPAADASDODOPTVTNNPEPRG
5834	17	4020	RFRRGGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG
		. = +	SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV
	i		TLEDALSNVDLLEELPLPDOOPCIEPPPSSLLYOPNFNTNFEDR
1			NAFVTGIARYIEOATVHSSMNEMLEEGOEYAVMLYTWRSCSRAI
	,		POVKCNEOPNRVEIYEKTVEVLEPEVTKLMNFMYFORNAIERFC
· '			GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV
1			KNDHSAYKRAAOFLRKMADPOSIOBSONLSMFLANHNKITOSLO
1			QQLEVISGYEELLADIVNLCVDYYENRMYLTPSEKHMLLKVMGF
			GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKOLQVVPLFGDMQI
			ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM
j l			RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL
	1		SOWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS
			EEKFALVEVIAMIKGLOVLMGRMESVFNHAIRHTVYAALODFSO
			1
			VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL
]	ŀ		RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK
			KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL
			WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVL
'	l		YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDQFVYKLADQ
			IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKQR
			HVQLLGRSIDLNRLITQRVSAAMYKSLELAIGRFESEDLTSIVE
			LDGLLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL
			HVFWELNYDFLPNYCYNGSTNRFVRTVLPFSQEFQRDKQPNAQP
			QYLHGSKALNLAYSSIYGSYRNFVGPPHFQVICRLLGYQGIAVV
			MEELLKVVKSLLQGTILQYVKTLMEVMPKICRLPRHEYGSPGIL
			EFFHHQLKDIVEYAELKTVCFQNLREVGNAILFCLLIEQSLSLE
	ļ		EVCDLLHAAPFQNILPRVHVKEGERLDAKMKRLESKYAPLHLVP
			<u></u>

PCT/US00/34263

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartit Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	residue of	amino acid	Codon, /=possible nucleotide deletion,
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	i	\=possible nucleotide insertion)
			LIERLGTPQQIAIAREGDLLTKERLCCGLSMFEVILTRIRSFLD
1		1	DPIWRGPLPSNGVMHVDECVEFHRLWSAMQFVYCIPVGTHEFTV
1	Į.	1	EQCFGDGLHWAGCMIIVLLGQQRRFAVLDFCYHLLKVQKHDGKD
l			EIIKNVPLKKMVERIRKFQILNDEIITILDKYLKSGDGEGTPVE
1			HVRCFOPPIHOSLASS
5835	4209	1904	SGNIRMAQGSHQIDFQVLHDLRQKFPEVPEVVVSRCMLQNNNNL
			DACCAVLSQESTRYLYGEGDLNFSDDSGISGLRNHMTSLNLDLQ
1	ì	1	SQNIYHHGREGSRMNGSRTLTHSISDGQLQGGQSNSELFQQEPQ
			TAPAQVPQGFNVFGMSSSSGASNSAPHLGFHLGSKGTSSLSQQT
	ł	1	PRFNPIMVTLAPNIQTGRNTPTSLHIHGVPPPVLNSPQGNSIYI
	1		RPYITTPGGTTRQTQQHSGWVSQFNPMNPQQVYQPSQPGPWTTC
1	1		VETTITEGGTTVÄTÄÄNGOUNDERNUMBLEEBAAGUBBATREGGE
			PASNPLSHTSSQQPNQQGHQTSHVYMPISSPTTSQPPTIHSSGS
	Į.		SQSSAHSQYNIQNISTGPRKNQIEIKLEPPQRNNSSKLRSSGPR
1		1	TSSTSSSVNSQTLNRNQPTVYIAASPPNTDELMSRSQPKVYISA
			NAATGDEQVMRNQPTLFISTNSGASAASRNMSGQVSMGPAFIHH
			HPPKSRAIGNNSATSPRVVVTQPNT\EYTFKITVSPNKPPAVSP
	1		GVVSPTFELTNLLNHPDHYVETENIHHLTDPTLAHVDRISETRK
1	1		LSMGSDDAAYTQDI*RISNSWLGMVAHACNSSALGGQDGRII*A
[Í	QEFETSWGNIWRLRLYRRF*NYAGMVAHTCSPSYSVD*ALLVHQ
	1		OEFETSWGNIWKEKEIKKF NIAGWVAHICSFSISVD ALLIVING
1		1	KARMERLQRELBIQKKKLDKLKSEVNEMENNLTRRRLKRSNSIS
			QIPSLEEMQQLRSCNRQLQIDIDCLTKEIDLFQARGPHFNPSAI
1		1	HNFYDNIGFVGPVPPKPKDQRSIIKTPKTQDTEDDEGAQWNCTA
			CTFLNHPALIRCEQCEMPRHF
5836	361	2303	FHITMCGICCSVNFSAEHFSQDLKEDLLYNLKQRGPNSSKQLLK
3030	1 302		SDVNYQCLFSAHVLHLRGVLTTQPVEDERGNVFLWNGEIFSGIK
]	1	}	VEAEENDTQILFNYLSSCKNESEILSLFSEVQGPWSFIYYQASS
i			HYLWFGRDFFGRRSLLWHFSNLGKSFCLSSVGTQTSGLANQWQE
1	1		HYLMFGRDFFGRRSLLWHFSNLGRSFCLSSVGTQTSGLARQWQS
1	i	ł	VPAS\DFSELILSLLSFPDALFYNCILGNIFLGRILLKKMLIA*
	1	1	VKFQQTYQHLYQR*QMKPNCILKNLLFL*I*CCHKLHWRLIAVI
1			FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR
i	1.	1	DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE
}·	ļ	1	PIDLLNVAFIAEEKTMPTTFNREGNKQKNKCEIPSEEFSKDVAA
l		1	AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME
1			ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG
1			
Į.	1	1	VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM
1	1		MELGRISSRNLGRDDRVIGDHGKEARFPFLDENVVSFLNSLPIW
ı	1	1	EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA
1	1		KMEKINEKASDKCGRLQIMSLENLSIKKETKL
5837	4792	903	NGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL
303/	=134	1	KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT
			QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD
1	1		RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG
ı	1		KDAYCMDTATPEC9A LPA9PGGLAT9BAL92ADTG9BUTGAGAG
1	[MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT
i	1	1	DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE
1		1	GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY
1	1	1	KLPVHTBISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH
1		1	HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC
1	Į.		P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL
1		1	VFCFPIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL
1			ALCENTIGASEGCMD / VELEGREVANTERS / UKORUBCANNOLD
			DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIELEKKRLSQ
		1	PKAKPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ
1			EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV
1		1	ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKBELHQDCL
1			VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG
I		į.	HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA
1			WITHOUT THE STAND CONDOLOGY TO THE TAILURE AND AUTHORS AND AUTHORS.
-		1	GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS
1			NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK
1		1	CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA
1		1	LRCAOELLLANNWVGAQEALQLHESLQGQRLVFCLLBLLSRHLB
1			RKOLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPEQY
1	į.		QEAFQKLQNIKYPSATNNTPAKQLLLHICHDLTLAVLSQQMASW
i	į.	i i	ABUL AUDRITUTE DUTING TELEVISION OF THE SECTION OF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion) DEAVQALLRAVVRSYDSGSFTIMQEVYSAFLPDGCDHLRDKLGD
1			HOSPATPAFKSLEAFFLYGRLYEFWWSLSRPCPNSSVWVRAGHR
ŀ	;		TLSVEPSQQLDTASTEETDPETSQPEPNRPSELDLRLTEEGERM
			LSTFKELFSEKHASLONSORTVAEVOETLAEMIROHOKSOLCKS
			TANGPDKNEPEVEAEQPLCSSQSQCKEEKNEPLSLPELTKRLTE
1			ANQRMAKFPESIKAWPFPDVLECCLVLLLIRSHFPGCLAQEMQQ
			QAQELLQKYGNTKTYRRHCQTFCM
5838	110	98	KTMPHLLVTFRDVAIDFSQEEWECLDPAQRDLYRDVMLENYSNL
			ISLDLESSCVTKKLSPEKEIYEMES\PSGRIWGNVSTITFQYNG
			LGDNMECKGNLEGQVSKSEGLYMCVKITCEEKATESHSTSSTFH
			RII/HYQGKIVKCKECRQGFSYLSCLIQHEENHNI*KCSEVNKH
			RNTFSKKPSYI*HQ\KFRLGEKPYECMECGKAFGRTSDLIQHQK IHTNEKPYOCNACGKAFIRGSOLTEHORVHTGEKPYDCKKCGKA
]	FSYCSQYTLHQRIHSGEKPYECKDCGKAFILGSQLTYHQRIHSG
			EKPYECKECGKAFILGSHLTYHORVHTGEKPYICKECGKAFLCA
			SQLNEHQRIHTGEKPYECKECGKTFFRGSQLTYHLRVHSGERPY
		· ·	KCKECGKAFISNSNLIQHQRIHTGEKPYKCKECGKAFICGKQLS
			EHQRIHTGEKPFECKECGKAFIRVAYLTQHEKIHGEKHYECKEC
			GKTFVRATQLTYHQRIHTGEKPYKCKECDKAF/HLWLTILSEHQ
			RIHRGEKPYECKQCGR/LFIRGSHL/NEHLRIHTGEKPYECKEC
			GRAFSRGSEHTLHQRIHTGEKPYTCVQCGKDFRCPSQLTQHTRL
5839	1	2425	HN*EYSSHKICMHSIALASLDFAHLQEKNPEN GRPFPRPPRALPRLPLRGRRQDGRWTVDFEBCLKD\SPRFRAAL
5039	*	2425	EEVEGDVAELELKL\DKLVKLCIA\MIDTGKAFCVANKQFMNGI
			RD\LAQNS\NNDA\VVETKFAPSFLDSLQEMINFHTIL/L*PNS
ł			EIN+GHSFQNFVKEDLRKFKDAKKQFENSQ+KRKKIALVKNAPV
1			PSRPASLEL*KPPNILTATRKCFRHIALDYVLQINVLQSKRRSE
			ILKSMLSFMYAHLAFFHQGYDLFSELGPYMKDLGAQLDRLVGDA
İ			AKEKREMEQKHSTIQQKDFSRDDSKLKYNVDAANGIVMEGYLFK
1			RASNAFKTWNRRWFSIQNNQVVYQKKFKDNPTVVVEDLRLCTVK
			HCEDIERRFCFEVVSPTKSCMLQADSEKLRQAWIKAVQTSI\AT
ļ	;		AYREKDDESEKLDKKSSPSTGSLDSGNESKEKLLKGESALQRVQ CIPGNASCCDCGLADPRWASINLGITLCIECSGIHRSLGVHFSK
			VRSLTLDTWEPELLKLMCELGNDVINRVYEANVEKMGIKKPOPG
1			QRQEKEAYIRAKYVERKFVDKIFL*SLSPP\EQQKK\FVSKSSE
	1.4		EKRLSISKFGP\GDQVRASAQSSVRSNDSGIQQSSDDGRESLPS
	,		TVSANSLYEPEGERQDSSMFLDSKHLNPGLQLYRASYEKNLPKM
			AEALAHGADVNWANSEENKATPLIQAVLGGSLVTCEFLLQNGAN
	· .		VNQRDVQGRGPLHHATVLGHTGQVCLFLKRGANQHATDEEGKDP
	•		LSIAVEAANADIVTLLRLARMNEEMRESEGLYGQPGDETYQDIF
		2011	RDFSQMASNNPEKLNRFQQDSQKF
5840	698	3610	KHLHLPRQHLTTLWQISSPRWRSPQRAFMSALSKTQTQSAPALQ
	İ		GLSSLLQSVTGNPVPASEAASQSTSASPANTTVYTIKGRNLPSS AOPFIPKSFNYSPNSSTSEVSSTSASKASIGOSPGLPSTAFKLP
			SNTKGFTATHNTSPAAPPTEVTICQSSEVSKPKL\ESESTSPSL
1			\EMKIHNFLKGNPGFSVA*NLKHPNPAGSLGSSAPSESHPSDFQ
1			RGPTSTSIDNIDGTPVRDERSGTPTQDEMMDKPTSSSVDTMSLL
			SKIISPGSSTPSSTRSPPPGRDESYPRELSNSVSTYRPFGLGSE
1			SPYKQPSDGMERPSSLMDSSQEKFYPDTSFQEDEDYRDFEYSGP
	•		PPSAMMNLQKKPAKSILKSSKLSDTTEYQPILSSYSHRAQEFGV
			KSAFPPSVRALLDSSENCDRLSSSPGLFGAFSVRGNEPGSDRSP
			SPSKNDSFFTPDSNHNSLSQSTTGHLSLPQKQYPDSPHPVPHRS
		,	LFSPONTLAAPTGHPPTSGVEKVLASTISTTSTIEFKNMLKNAS
			RKPSDDKHFGQAPSKGTPSDGVSLSNLTQPSLTATDQQQQBEHY RIETRVSSSCLDLPDSTERKGAPIETLGYHSASNRRMSGEPIQT
			RIETRVSSSCLDLPDSTEBRGAPIETLGTHSASNRRMSGEPIQT VESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDNGPSSASELA
			SLGGGGSGGLTGFKTAPYKERAPOFQESVGSFRSNSFNSTFEHH
			LPPSPLEHGTPFQREPVGPSSAPPVPPKDHGGIFSRDAPTHLPS
			VDLSNPFTKEAALAHAAPPPPPGEHSGIPFPTPPPPPPPGEHSS
			SGGSGVPFSTPPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP
		·	KDHSSLLQGTLAEHFGVLPGPRDHGGPTQRDLNGPGLSRVRESL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location		Grutamic Acid, Fernenylatanine, GeGrycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		1	TLPSHSLEHLGPPHGGGGGGGSNSSSGPPLGPSHRDTISRSGII
		,	LRSPRPDFRPREPFLSRDPFHSLKRPRPPFARGPPFFAPKRPFF
ļ	1	ł	PPRY
5841	1908	762	GLRLFLVLTVWPMMKPSWLSRTEFSKRLLCRTLWCOSGWSSRSY
			TRSMLKMTTSINRRSRTSTKSTRTSARPGLTATVSIGLSDSPTW
ļ	!		RHCWMTARSCSGEKGGHWAPRQVGVYLLPGRVGCVSSRVSPSFP
İ		1	GDGLDSGLARRGSAVSALASGLVEEPMLGPPFHPTPRFKAVSAK
ļ			
			SKEDLVSQGFTEFTIEDFHNTFMDLIEQVEKQTSVADLLASFND
		[QSTSDYLVVYLRLLTSGYLQRESKFFEHFIEGGRTVKEFCQ\QE
]	j	}	\VEPMCKESDHIHIIALAQGLQRVHPGWEYMGPRPRAATTNPHI
1			FP*GLPSPKVYLLYRPG\HYDILYKIGLGSSPLGCPGCPLLARA
	<u>L</u>	1	LGHCYRGFSVVVKWSYFTPFFLSHDPPPMFY
5842	307	1918	QEPTADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVPRVRKL
1	1		WSSRRPRTRRNLLLGTACAIYLGFLVSQVGRASLQHGQAABKGP
[HRSRDTAEPSFPEIPLDGTLAPPESQGNGSTLQPNVVYITLRSK
			RSKPANIRGTVKPKRKKHAVASAAPGQEALVGPSLQPQEA\EG
			KLML*HLGTLREQTWLRLESDPGGWCGVRE/WRAGGPDFLQPSS
	1	ļ	RESNIRIYSESAPSWLSKDDIRRMRLLADSAVAGLRPVSSRSGA
	1		RLLVLEGGAPGAVLRCGPSPCGLLKOPLDMSEVFAFHLDRILGL
			NRTLPSVSRKAEFIQDGRPCPIILWDASLSSASNDTHSSVKLTW
			<u> </u>
			GTYQQLLKQKCWQNGRVPKPESGCTEIHHHEWSKMALFDFLLQI
1		1	YNRLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAALAHIIQRKH
İ	\	ı	DPRHLVFIDNKGFFDRSEDNLNFKLLEGIKEFPASAVYVLKSQH
	1	1	LRQKLLQSLFLDKGYWESQGGRQGIEKLIDVIEHRAKILITYIN
			AHGVKVLPMNE
5843	500	1453	GTARLVTCWVLHGQ*VKKPAWEPGVVWL*Q*RCRPKGWGLGAGM
į			RGSRMSQPPQCLRRAQSSCCHFMVKLLDDGTFMIPGEKVAHTSL
ł		1	DALVTFHQQKPIEPRRELLTQPCRQKDPANVDYEDLFLYSNAVA
İ			EEAACPVSAPEEASPKPVLCHQSKERKPSAEM/RQNNHQGSHFL
ļ			LPPKIPSWRDPPETLEEPQNAPRERPEGPAAAKKPPRHCELVVT
l		1	LGCPEIHGDLRPWDRKRQPRSLRGSHLGGQRLHGSLCGHISQKP
1	1	1	LTAPGTKRQKGPHOEGREVGOLH*GDPRGOELAPNGSESPILPG
	1	1	VOARAPGLGRA
5844	202	2471	FDSAVLSSINVMAVLPGPLOLLGVLLTISLSSIRLIOAGAYYGI
3044	202	24,1	
			KPLPPQIPPQMPPQIPQYQPLGQQVPHMPLAKDGLAMGKEMPHL OYGKEYPHLPQYMKEIQPAPRMGKEAVPKKGKEIPLASLRGEOG
Į .	.]		1 7 7 7
	1		PRGEPGPRGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM
			PGKPGAMGMPGAKGEIGQKGEIGPMGIP*PQGPPGPHGLPGIGK
1			PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV
			KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP
1	1		GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL
1			PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA
			PGIGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPG
			PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP
			GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI
1			PGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPQGQPGL
ı		1	PGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHAYG
			AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRONY
]			NPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYD
1			EYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHS
			SFSGYLLYPM
5845	215	2007	
2042	215	2061	HASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER
		1	GPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLP
	J	}	KPI*KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK
[PFPNNRANYNFQVMYNQRYHCPIPKIFYVQLTVGNNBFFGEGKT
1	İ	1	RQAARHNAAMKALQALQNEPIPERSPQNGESGKDMDDDKDANKS
l ·		1	EISLVFEIALKRNMPVSFEVIKESGPPHMKSFVTRVSVGEFSAE
ĺ			GEGNSKKLSKKRAATTVLQELKKLPPLPVVEKPK\HFFKKRPKT
	Į		IVKAGPEYGQGMNPISRLAQIQQAKKEKEPDYVLLSERGMPRRR
1		1	EFVMQVKVGNEVATGTGPNKKIAKKNAAEAMLLQLGYKASTNLQ
1			DOLEKTGENKGWSGPKPGFPEPTNNTPKGILHLSPDVYQEMEAS
			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l .	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			RHKVISGTTLGYLSPKDMNQPSSSFFSISPTSNSSATIARELLM
İ		1.	NCTCCTAPATCL VCCCDTDDCCDVCDCVCV CVCADACCTARELLM
	1		NGTSSTAEAIGLKGSSPTPPCSPVQPSKQLEYLARIQGFQVHYC
	1		DRQSGKECVTCLTLAPVQMTFHAIGSSIEASHDQV*YATAILLC
1			YGPARKWKAIKMEAMCAHAALLSLIHYLLAPSARLBKSKLFALG
5846	1126	150	N.
3046	1126	456	FSKLIMKTFIIGISGVTNSGKTTLAKNLQKHLPNCSVISQDDFF
			KPESEIETDKNGFLQYDVLEALNMEKMMSAISCWMESARHSVVS
1			TDQESAEEIPILIIEGFLLFNYKPLDTIWNRSYFLTIPYEECKR
1	1		RRSTRVYQPPDSPGYFDGHVWPMYLKYRQEMQDITWEVVYLDGT
1]	KSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTTNPS/CK*IRK
L			LQGVI
5847	2769	505	APEMEDLSSPDSTLLQGGHNLLSSASFQESVTFKDVIVDFTQEE
1		1	WKQLDPGQRDLFRDVTLENYTHLVSIGLQVSKPDVISQLEQGTE
		1	PWIMEPSIPVGTCADWETRLENSVSAPEPDISEEELSPEVIVEK
		1	HKRDDSWSSNLLESWEYEGSLERQQANQQTLPKEIKVTEKTIPS
1		· ·	WEKGPVNNEFGKSVNVSSNLVTQEPSPEETSTKRSIKQNSNPVK
		1	KEKSCKCNECGKAFSYCSALIRHQRTHTGEKPYKCN*/CVEKAF
1		1	SRSENLINHQRIHTGDKPYKCDQCGKGFIEGPSLTQHQRIHTGE
			KPYKCDECGKAFSQRTHLVQHQRIHTGEKPYTCNECGKAFSQRG
ł		{	HFMEHQKIHTGEKPFKCDECDKTFTRSTHLTQHQKIHTGEKTYK
			CNECGKAFNGPSTFIRHHMIHTGEKPYECNECGKAFSQHSNLTQ
			HQKTHTGEKPYDCAECGKSFSYWSSLAQHLKIHTGEKPYKCNEC
Į.			GKAFSYCSSLTQHRRIHTREKPFECSECGKAFSYLSNLNQHQKT
1			HTQEKAYECKECGKAFIRSSSLAKHERIHTGEKPYQCHECGKTF
1	Ī		SYGSSLIQHRKIHTGERPYKCNECGRAFNQNIHLTQHKRIHTGA
ł			KPYECAECGKAFRHCSSLAQHQKTHTEEKPYQCNKCEKTFSQSS
			HLTQHQRIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGEKPYK
		. ,	CNECGK/TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN
			KHORLHPGI
5848	22	2961	AAPRRILRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK
			GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL
1	1	. ,	DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG
1			
1	}	•	YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV
1			GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL
	į į	.,	VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV
1		,	SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY
i			PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA
1	'		ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA
]		SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN
· i	[APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD
	.		TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ
			APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL
[į į		CSVPTRALLLSTYIKFVNLFPEVKPTIQDVLRSDSQLRNADVEL
	,		
	l		QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK
		I	GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG
			GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA
			GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL
			GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD
			GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD
			GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ
			GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP
		·	GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQPL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV
5849	3545	. 1895	GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF
5849	3545	. 1895	GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ
5849	3545	. 1895	GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGSGSLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQPL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES
5849	3545	1895	GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGSGSLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSBFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW
5849	3545	1895	GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGSGSLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDMNVKGTTLPRIAVHEPSFMI
5849	3545	1895	GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGSGSLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSBFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVSI
5849	3545	1895	GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGSGSLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER
5849	3545	1895	GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGSGSLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSBFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER LBKAQEENRNVAVEKQNL*RKMMDEINYAKEEACRLRELREGAE
5849	3545	1895	GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGSGSLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			AHSSSLDEVDHKILEAKKALSELTTCLRERLFRWQQIEKICGFQ
			IAHNSGLPSLTSSLYSDHSWVVMPRVSIPPYPIAGGVDDLDEDT
			PPIVSQFPGTMAKPPGSLARSSSLCRSRRSIVPSSPQPQRAQLA PHAPHPSHPRHPHHPOHTPHSLPSPDPDILSVSSCPALYRNEEE
ļ			
			BEAIYFSAEKQWEVPDTASECDSLNSSIGRKQSPP/SKPRDIPN
5850	3	1895	IIS/DERYQEMRCP*RIPSGGIL KAVLNFSASGSVISLTGSNPMHDASMWHLKKNGIIVYLDVPLLN
5850	3	1895	LICRLKLMKTDRIVGQNSGTSMKDLLKFRRQYYKKWYDARVFCE
			SGASPEEVADKVLNAIKRYQDVDSETFISTRHVWPEDCEQKVSA
ļ	ł		EFFIEAVIEGLASDGGLFVPAKEFPKLSCGEWKSLVGATYVERA
1		-	OILLERCIHPADIPAARLGEMIETAYGENFACSKIAPVRHLSGN
			OFILELPHGPTGSFKDLSLQLMPHIFAQCIPPSCNYMILVATSG
			DTGSAVLNGFSRLNKNDKORIAVVAFFPENGVSDFOKAOIIGSO
			RENGWAVGVESDFDFCQTAIKRIFNDSDFTGFLTVEYGTILSSA
			NSINWGRLLPQVVYHASAYLDLVSQGFISFGSPVDVCIPTGNFG
			NILAAVYAKMMGIPIRKFICASNONHVWTDFIKTG\HYDLRGKE
ŧ			N*AQTFFTVQ*IFLPNLSNLERHLHLMANKDGQLMTELFNRLES
Ì			QHHFQIEKALVEKLQQDFVADWCSEGECLAAINSTYNTSGYILD
	İ		PHTAVAKVVADRVQDKTCPVIISSTAHYSKFAPAIMQALKIKEI
			NETSSSQLYLLGSYNALPPLHEALLERTKQQEKMEYQVCAADMN
ļ			VLKSHVEQLVQNQFI
5851	3120	1802	RCYLOFLALLLTSTSARAAAAIAAAEEPAGSPSVMTRAGDHNRQ
			RGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVELY
1			GNSLLLTAVYGLVVAGSVLVLGAIIGDWVDKNARLKVAQTSLVV
			QNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANI
	1		ANLASTATAITIQRDWIVVVAGEDRSKLANMNATIRRIDQLTNI
1			LAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWKVYQKT
1	1	,	PALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIH
			ELEHEQEPTCASQMAEPFRTFRDGWVSYYNQPVF/LGWHGSCFP
ì	1		LYDCPGL*LHHHRVRLHSGTEWFHPQYFDGSISYNWNNGNCSFY
1			LATSKMWFGSDRSDLRIGTAFLFDLVCDLCIHAWKPPGLVRFSF
5852	1	422	KTTFPSSLCPLRQLPEVRGYSGQPLTDPLISLCRSHKCRGKGWG
1			SSSYPSLPALLRARSAPGHCTHRSCGPEWRIDSISRLEMQGARR
1			SGWAQAQPTILLLVPRLRKSLPSIWG/SLMGPFITSGPG/WFRQ
			YYFFISGRH*VLFTESDFYYVAMDFGGHGLSSHYSPGVPYYLQT
			FVSEIRRVVAGKKQSVYFRRCGGCSRAPPLITGGGVGSRKQRWP
		<u> </u>	ESGAWALAPGLPAIHGRSWES
5853	223	1346	RLLGLSRVKGLHGPAASAWISDPETRGDPGGPWGMWRGSDLRPR
			PVSLTGLTLVCK*AAQGPQV\HSVKLCFGLGG\PCLL\FPIFRP
]			LLLHPRRPRLHPGTRGVAVEPHALRVVHVAHGEEAGIRAAGPGH
	1		GGVEIPQG/VGSLGARRGLRPSRPSSRHRNRVPAPPPGRPLATP
			HRRRFPPDPALTCPGLGQDQGPREQQKQGSGRHDTILGDWGESE
	1		SRWVRGNFRTGTAATLIGFSRNPTLNGSENWGSLVSIQEEGPDT
			GWEREKRNPAEMGNPQRWASPIHTPPLGPEILRAMPEALRAMPE ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNQGETLGMGPVP
			LSSLCITESPSQNWTPCLLLLTCPRGLF
5854	86	938	KGRNTAPEKKGAALNNRENASS*NGY/SRWKODIRRIENHIIOE
3034		930	LKHLCAMIKRVLLERLENTRKLRELTEGRTLDWPONRITEVSAK
			ROIVTEYREKGKRN*EEKKRDLEGRSRRYNLCIIGIPETEDRAS
	}		GAETIKDLLE/ENFPELKNELDLQMEKAHRIPLKFNEKKAASRH
}			IRVTFL/KFORRNILOASSORKOVTYKGAKVRLTSDFSPAILNA
	ļ		RROW/N/PISRVLRENNFEPRIIYSAKLSFLYKGNWKTFLDIQG
			LGKYINQELSLKILLKDLLQLTENLN
5855	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSESPPPITDSWAP
3333	336	2331	FISLTHHVLSQSQSPLSSNCWICLSTHTQ*FTALPADLLTWTQS
			NVSLHISYLAIPFLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS
1	1		GRAVALLHLIASGLTSIQTNTASSKPPIWGY\LSTQTSFISPPP
			LCLSRTYPNPAHATMVGQVPQSLCGLIFTL/RTPCRPSILHPNY
			KIISTSAWQKVLCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAA
			NSALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGSN/RLTVDKDN
L			

SEQ	Predicted	1 0 12 1 1	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
10.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
-	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
,	sequence	sequence	\=possible nucleotide deletion,
	bequence		FFLSPKPNSLHQLPSQ\TPYQALTGAALAGSYPIWENENTLSWL
1			PTFTYNFCLSTPSLFFLCDTN*YLCLPANWSGTCTLVFQAPTIN
1) ·	
			ILPPNQTILISVEASISSSPIRNKWALHLITLLTGLGITAALGT
			GIAGITTSITSYQTLFTTLSNTVEDMHTSITSLQRQLDFLVGVI LQNWRVLDLLTTEKGGTCIYLQEECCFCVNESGIVHIAVRRLHD
			RAAEL*HQVADSWWQGSSLLRWIPWVAPFLGPLIFLFLLLMIGP
	ł		CIFNLVSRFISQRLNCFIQASMQKHIDNIFHLCHV*YQSLRGNH
ŀ			SEAPEPRP
5856	173	1137	PWLHGLGLSAVFLFYL*/YVTFHLYGGIILLLLIFISIAGILYK
3030	1/3	1137	
	}		FQDVLLYFPEQPSSSRLYVPMPTGIPHENIFIRTKDGIRLNLIL IRYTGDNSPYSPTIIYFHGNAGNIGHRLPNALLMLVNLKVNLLL
ŀ			
Į .			VDYRGYGKSEGEASEEGLYLDSEAVLDYVMTSPDLDKTKIYLSG
			RSLG\GAAAIHLASDNSHRISAIMVENTFLSIPHMASTLFSFFP MRYLPLWCYKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMMKQ
			LYELSPSRTKRLAIFPDGTHNDTWQCQGYFTALEQFIKEVVKSH
1	. :		SPEEMAKTSSNVTII
5857	1597	563	KLIGKVLVLSVVADAMAAFAVEPQGPALGSEPMMLGSPTSPKPG
	2331	503	VNAQFLPGFLMGDLPAPVTPQPRSISGPSVGVMEMRSPLLAGGS
			PPQPVVPAHKDKSGAPPVRSIYDDISSPGLGSTPLTSRROPNIS
			VMQSPLVGVTSTPGTGQSMFSPASIGQPRKTTLSPAQLDPFYTQ
			GDSLTSEDH\LDDSWGDCIWGFLKASA\SYILL\QFAQYGGIS*
1 1			NMWMSNTGNWMHIRYQSKLQARKALSKDGRIFGESIMIGVKPCI
			DKSVMESSDRCALSSPSLAFTPPIKTLGTPTQPGSTPRISTMRP
			LATAYKASTSDYQVISDRQTPKKDESLVSKAMEYMFGW
5858	355	1419	PPHQPAAASTSXHQQQQPPPPPQDSSKPVVAQGPGPAPGVGSAP
1	,		PASSSAPPATPPTSGAPPGSGPGPTPTPPPAVTSAPPGAPPPTP
1 1			PSSGVPTTPPQAGGPPPPPAAVPGPGPGPKQGPGPKGGKMP
		•	GGPKPGGGPGLSTPGGHPKPPHRGGGEPRGGRQHHPPYHQQHHQ
			GPPPGGPGGRSEEKISGPRRGFKANLSLLRRPGEKTYTORCRFC
			LLGIYLLISRRMNSRRLFAKIWENQEKFLSTKAKDSEFIKLESR
			ALA*NCPKPELG*YTP*GGRQLPSSLFPTHACLPLSCSVIFSPF
1 1			MFPQ*NCWGRKPFRPNLGPHLKGAVCNRWDDPWEGPTGKGHCLN
}			FAS
5859	307	1503	GGSSARPRASSRRMLSRKKTKNEVSKPAEVOGKYVKKETSPLLR
1.			NLMPSFIRHGPTIPRRTDICLPDSSPNAFSTSGDGVVSRNOSFL
	· 1		RTPIQRTPHEIMRRESNRLSAPSYLARSLADVPREYGSSOSFVT
]		EVSFAVENGDSGSRYYYSDNFFDGQRKRPLGDRAHEDYRYYEYN
1 . 1			HDLFQRMPQNQGRHASGIGRVAATSLGNLTNHGSEDLPLPPGWS
			VDWTMRGRKYYIDHNTNTTHWSHPLEREGLPPGWERVESSEFGT
1 1	` [YYVDHTNKKAQY\RHPCAPTCTSV*STTSCHI/AS/RQOTERNO
	Į.		SLLVPANPYHTAEIPDWLQVYARAPVKYDHILKWELFQLADLDT
	f		YQGMLKLLFMKELEQIVKMYEAYRQALLTELENRKQRQOWYAQO
1 1			HGKNF
5860	2956	1270	TIRVEEFPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFP
	1		LLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQI
]			SWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSLNDATI
1 1			TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG
ļ	ļ	i	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFP
	ĺ		NETATI ISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDI
			QYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG
		ļ	QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTOK
	1	l	VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LATEP*KIA
		ļ	PSPLSTL\ATIKGWTQLPTIIA*CSGVGALFIV\LVKCFGLGIF
]		j	CYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDBLDPYPDSV
1			KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL
	·		KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
5861	2051	1305	EVCACVQAFWLVASSGDDSQGDKCGCEVGSWVGSMRVVMARLL
į [- = =		SEGEQGIPTACAAFAQQPAG/EPRRGLAGVGEGGPQCSWVNYRC
	1		TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI
j (i	1	LE*RMNSGSPARDNAPSQRFCTNLSEGLRFGISPSWREALYGCH

Predicted Predicted Predicted Namino acid segment containing signal peptide Cocation Corresponding Contrain Contrainent Cocation Corresponding Contrainent Cocation Contrainent Cocation Contrainent Cocation Contrainent Cocation				
Notestation Corresponding	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
corresponding to first amino acid areidue of amino acid residue of amino acid sequence sequen		location	corresponding	H=Histidine. I=Isoleucine, K=Lysine.
to first anino acid residue of anino acid residue of anino acid sequence 8-Sestien, T-Threenine, V-V-Billine, W-Tryptophan, Y-Tyrosine, X-Unknown, *-stop Codon, /-possible nucleotide deletion, \-__________________\				LeTeucine MaMethionine NaAsparagine.
amino acid residue of amino acid sequence 8-8-1-1556 1567 1577				D-Broline O-Clutamine P-Arginine
residue of amino acid sequence (2000, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide insertion) A PSIRCELLINE PROPERTION PROVINCENT DE P				
amino acid sequence A A A A A A A A A A A A A A A A A A				S=Serine, T=Threonine, V=Valine,
Sequence A Spossible nucleotide insertion	l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
\$862 1956 483 PPPQLIMBEIKVSPDYNNPRGTVPLKKIIVDDDDSKIMSLYDAG PRSIRCPLIFLEPVSGTADVPPRQILALIGNGYRVIALOGYPVYN DHEEFCOPFRILIDHOLDKVHLEFGALGGELAGKRAFYNFHYSE RVHSLILLCNSPDTSI PROTWIANSFMIMPAPHIKKIULGNPSYS GPUDPMADAIDPWINDLESLAGGELAGKRAFYNFHYSEPK RUSLILLCNSPDTSI PROTWIANSFMIMPAPHIKKIULGNPSS GPUDPWADAIDPWIDLESLAGGELAGKARIALIGNGYRVPK RDIPVIIMDVPQSALSTEAKEEMYKLYPNARRAHLKTGGNPPY LGSRAFWILVYGILK, PRINNENTPRIPLINGWSVPBEIGCKA ALASARSSSSVSLAVMDELTRCULV*SVASAPVSRPFFSGSSGS PVITYGGK 8 PPPRRGSEPTALAPEEDTWCPLMULFCLLELYPGLADSAPSCOM VISGGTTILSIGSMAGALUTYSCOGLYPSPASILCKSSGMQ TTGATTSLSKAVCKPWCCPADVSFENGI VTDRIGSSTPWGGNVSGTE CROPT ILRGSPVEGCPHOMMADETAVCONGAGHCPWGISL GPLYGRYSTDPFEDVAPALOTSPSSHMLAGSTPYGVTKRSGGWK GROPT TAGATTSLSKAVCKPWCCPADVSFENGI VTDRIGSSTPWGGNVSGTE PICCQPSYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGHCPWGISL GPLYGRYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGHCPWGISL GROPT TAGATTSLSKAVCKPWCCPADVSFENGI VTDRIGSSTPWGGNVSGTE PICCQPSYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGHCPWGISL GROPT TAGATTSLSKAVCKPWCCPADVSFENGI VTDRIGSSTPWGGNVSGTE PICCQPSYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGHCPWGISL GROPT TAGATTSLSKAVCKPWCCPADVSFENGI VTDRIGSSTPWGGNVSGTE PICCQPSYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGNVSGTE PICCQPSYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGNVSGTE PICCQPSYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGNVSGTE PICCQPSYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGNVSGTE PARTICLAR TO ALMONICAL TO ALMON)	amino acid	sequence	Codon, /=possible nucleotide deletion,
\$862 1956 483 PPPQLIMBEIKVSPDYNNPRGTVPLKKIIVDDDDSKIMSLYDAG PRSIRCPLIFLEPVSGTADVPPRQILALIGNGYRVIALOGYPVYN DHEEFCOPFRILIDHOLDKVHLEFGALGGELAGKRAFYNFHYSE RVHSLILLCNSPDTSI PROTWIANSFMIMPAPHIKKIULGNPSYS GPUDPMADAIDPWINDLESLAGGELAGKRAFYNFHYSEPK RUSLILLCNSPDTSI PROTWIANSFMIMPAPHIKKIULGNPSS GPUDPWADAIDPWIDLESLAGGELAGKARIALIGNGYRVPK RDIPVIIMDVPQSALSTEAKEEMYKLYPNARRAHLKTGGNPPY LGSRAFWILVYGILK, PRINNENTPRIPLINGWSVPBEIGCKA ALASARSSSSVSLAVMDELTRCULV*SVASAPVSRPFFSGSSGS PVITYGGK 8 PPPRRGSEPTALAPEEDTWCPLMULFCLLELYPGLADSAPSCOM VISGGTTILSIGSMAGALUTYSCOGLYPSPASILCKSSGMQ TTGATTSLSKAVCKPWCCPADVSFENGI VTDRIGSSTPWGGNVSGTE CROPT ILRGSPVEGCPHOMMADETAVCONGAGHCPWGISL GPLYGRYSTDPFEDVAPALOTSPSSHMLAGSTPYGVTKRSGGWK GROPT TAGATTSLSKAVCKPWCCPADVSFENGI VTDRIGSSTPWGGNVSGTE PICCQPSYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGHCPWGISL GPLYGRYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGHCPWGISL GROPT TAGATTSLSKAVCKPWCCPADVSFENGI VTDRIGSSTPWGGNVSGTE PICCQPSYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGHCPWGISL GROPT TAGATTSLSKAVCKPWCCPADVSFENGI VTDRIGSSTPWGGNVSGTE PICCQPSYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGHCPWGISL GROPT TAGATTSLSKAVCKPWCCPADVSFENGI VTDRIGSSTPWGGNVSGTE PICCQPSYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGNVSGTE PICCQPSYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGNVSGTE PICCQPSYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGNVSGTE PICCQPSYSTDPFEDVAPALOTSPSSHMLAGATVCONGAGNVSGTE PARTICLAR TO ALMONICAL TO ALMON	i	sequence		\=possible nucleotide insertion)
Sec		bequence		I - 7
PRISTROPLIFLE POYSTADVERGILLALIGNG/TRVITALOTEVTY HHISCHICLENS PROTECTION OF THE PROTECTION OF THE PROPERTY HESP HYSISLILCENS PROTECTION OF THE PROTECTION OF THE PROPERTY HESP GPUDMMADAIN PROMITE, SLOGGS LAS, SELLIALCONS YVERY HE RD P PUT IMOUP DO SALS TEAKERWYKLYPONARBAHLATGON PPY LOSS ARVAIN VOILING, PRISH PROTECTION OF THE PROPERTY OF THE PROPER		ļ.,		, ·
DHLEPCOPPRILITIONTOLING HINTORAL GENERAL VILLAMES BY MYMILLICIANS SINTERIONTONINS WIN PAPARLIKULUMINS GPUDPHMADAID PHYDRILES LOGGELASRITINCONS YVERHIR RD 1 PVY INDVPOLOSAL STRAKERYKLYPNORAL VILLAMES ALASARS SINTERION TOLING WITH HINTORY BY STRAKERY ALASARS SINTERION OF THE WASHINGTON TO THE WASHINGT	5862	1556	483	I =
RYISLILLONS SIDTS IF NOT THAN SPWI MAPAGELIKKULGUNGS VERPEKT BD 19VT IND VPD CALLS ALSARITATION SYVEPHEKT BD 19VT IND VPD CALLS ALSARITATION SYVEPHEKT BD 19VT IND VPD CALLS ALSARITATION SYVEPHEKT BD 19VT IND VPD CALLS ALSARITATION SYVEPHEKT BD 19VT IND VPD CALLS ALSARITATION SYVEPHEKT CALLS BD 19VT IND VPD CALLS ALSARITATION SYVEPHEKT CALLS BUTTYSGK PFERSSISTIAN BEING FLANT PLANT CALLS ALSARITATION SYVERIST YPD CALLS SOW WITSOGTPTILS ING AND PLANT PLANT PLANT SYPOLOGIVED BE CEBER TO A CHARGE STATE AND A CHARGE SYME AND A CHARGE	l .	į.		PRSIRCPLIFLPPVSGTADVFFRQILALTGWGYRVIALQYPVYW
GPUDPMMADAIDPWIDLESIGGSELASRITINGONSVEPRIL RD 1PVTINDVPDGALSTEARERWIKL/PNORRALIKTIGGNEPY LCRSARVAILYQIHL/E/RANMEDTRIPLITHQWSVPERSIGGS ALASARSSSYSLAVMDELTRCVLV*SVASAPVSRPPSGSGS PVLTVSGG PFERGSLPLAAPREDTMGPLWLFCLLFLYYQIAADASPSCPON VNISGGTFILSKRANGSLLTYSCPQGLYPSPASRLCKSSQQWQ TPGGTFISISKRANGSLLTYSCPQGLYPSPASRLCKSSQQWQ TPGGTFISISKRANGSLLTYSCPQGLYPSPASRLCKSSQQWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQQWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQQWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQQWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQGWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQGWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQGWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQGWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQGWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQGWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQGWQGGFISISKLANGSULTYSCPQGTSTAVCHANGSULTYSCPQGGTSULTYSCRANGSULTYSCPQGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ļ	1	!	DHLEFCDGFRKLLDHLQLDKVHLFGASLGGFLAQKFAEYTHKSP
GPUDPMMADAIDPWIDLESIGGSELASRITINGONSVEPRIL RD 1PVTINDVPDGALSTEARERWIKL/PNORRALIKTIGGNEPY LCRSARVAILYQIHL/E/RANMEDTRIPLITHQWSVPERSIGGS ALASARSSSYSLAVMDELTRCVLV*SVASAPVSRPPSGSGS PVLTVSGG PFERGSLPLAAPREDTMGPLWLFCLLFLYYQIAADASPSCPON VNISGGTFILSKRANGSLLTYSCPQGLYPSPASRLCKSSQQWQ TPGGTFISISKRANGSLLTYSCPQGLYPSPASRLCKSSQQWQ TPGGTFISISKRANGSLLTYSCPQGLYPSPASRLCKSSQQWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQQWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQQWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQQWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQGWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQGWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQGWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQGWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQGWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQGWQ TPGGTFISISKRANGSULTYSCPQGLYPSPASRLCKSSQGWQGGFISISKLANGSULTYSCPQGTSTAVCHANGSULTYSCPQGGTSULTYSCRANGSULTYSCPQGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			RVHSLILCNSFSDTSIFNOTWTANSFWLMPAFMLKKIVLGNFSS
RDIPVTINDVPDQSALSTERAKEMYKLYPNARRAILKTGGRYPY LCRSARVALVYQIH.// KYMBEMPTRPLITHQWSYPRSIRCRKY ALASARRSSYSIAVNDELTRCVLV*SVASAPVSRPPPSGSSG PVLTVSGK PPEPSRGSIPLAAPREDTMGPLMVLPCLLFLYPGLADSARSCON WNISGGTFILSHGHAPGSLLTYSCPQGLYPSPASRLCKSSQWQ TPGATTSLSKGVAVCKPWCCPAVSTERMGITYPGLADSARSCON TPGATTSLSKGVAVCKPWCCPAVSTERMGITYPGLAGSTPVOGNVSF ECEBGFI/LRGSPVACCFRMMMDETAVCUNGAGHCPNETSI GPLVATGFREGHGDKVWINCSSHLVTGSSERGCGMGVWSGTE PICRQPYSTPPEDVARALGTSFSHMLGATHPTQKTKESLGKKY QIGRSGHLMIVLLLDCSQVSSRDFLITKRSSSLWVDRIFSFEI NVSWAITTFASEPKVLMSVLNDNSRDMTEVISSLENANKYBURG GTGTNTYAALNSYLMSNANGDRETFWHVIKKRSGET/C\RGALISDGWT ARHOPECHNELLDCSQVSSRDMCHIRTHAUDVSKLTDTI CCVCKINSANASDGERTSFHULDKETMAVQCFTRAILLL\T DGK\SHMGGSPKTAVDHIREILATNOKENDYLDIVALGVSKLTDTI CCVCKINSANASDGERTSFHULDKETMAVQCFTRAILLL\T AAHCPPGCHDIBLAWAVGOPSGKEFLIERAVLSGFDVFA KKNOGILLFPYGD\DIALL\KLAGKVSM\STHCOGPSCLP\CTM \ARHOPECHNELLFYNSTGCTC\DHENLYVNNKGVS\PHV\ALSGFDVFA KKNOGILLFPYGD\DIALL\KLAGKVSM\STHCOGPSCLP\CTM \ARHOPECHNELLFYNNKGVS\PHV\ALSGFTALT\DHEN\ALSGFTALT\ CSKLEHLITRMGVEWTSCCRGLSPKKKTM\FPNLT\DVRR\VVT D\QTL\CS\GPGEDESP\CX*E\S\GGA\VTIERRFRLSAGVVT SKGL\YNP\CLGSAQLNNSPKKGESVAVPPFTR\VALN\ GSKLEHLITRMGVEWTSCCRGLSPKKKTM\FPNLT\DVRR\VVT D\QTL\CS\GPGEDESP\CX*E\S\GGA\VTIERRFRLSAGVVT SKGL\YNP\CLGSAQLNNSPKKGESVAVPPFTR\VALN\ SKGL\YNP\CLGSAQLNNSPKKGESVAVPPFTR\VALN\ GSKLEHLITRMGVEWTSCCRGLSPKKKTM\FPNLT\DVRR\VVT D\QTL\CS\GPGEDESP\CX*E\S\GGA\VTIERRFRLSAGVT KLDMSK\PENGTFFFSILQVLDNSCHKMGKSEVPDVQAFF\ KLDMSK\PENGTFFFSILQVLDNSCHKMGKSEVPDVQAFF\ KLDMSK\PENGTFFFSILQVLDNSCHKMGKSEVPDVQAFF\ KLDMSK\PENGTFFFSILQVLDNSCHKMGKSEVPDVQAFF\ KLDMSK\PENGTFFFSILQVLDNSCHKMGKSEVPDVQAFF\ KLDMSK\PENGTFFFSILQVLDNSCHKMGKSEVPDVQAFF\ KLDMSKLTQPSSWLINCOP KLDMSK\PENGTFFFSILGVLDNSCHKMGKSEVPDVQAFF\ KLDMSKLTQPSSWLINCOP S665 1684 1684 1684 1684 1685 1685 1686 1686 1686 1686 1686 1686 1686 1686 1687	ĺ	į	ĺ.	
LCRSAEVALTVOLHL/A/RAMSHENTRELITHOMSVPRESURCES ALASARRSSSVSLAVNDELTRCVLV-SVASARVSPEPSGSGS PVLTVSGK PPEPSGSIPLAAPREDTMSPLMVLPCLLFLYPOLADSAPSCPON VNTSGGTTTLSHGHARDSSLLTVSCPOGLVPSPASRLCKSSGOV VNTSGGTTTLSHGHARDSSLLTVSCPOGLVPSPASRLCKSSGOV TRGATRSLSKAVCKSVEVCDAPSERG YTPPRIGSTSPAGGSVSPAGGBVSF ECROST\LAGSPVRQCPPROMMDGETAVCDNGAGHCHNGISL GP\VRTGFRGHGDXVRTRCSSKIVLTGSSEREQQNGVWSOTE PICRGP*SVDPPEDVDALGTSSEREQQNGVWSOTE PICRGP*SVDPEDVDALGTSSEREQQNGVWSOTE PICRGP*SVDPEDVALGTSSEREMIALATIVPGXTKESLGRKKI QTGRSGHLHUYLLLDCSQSVSENDFLIFRESASLAVVRLFSFST NVSVALTTFASEFEXIMSVLKDINGSREMTEVISLSELANAYKOHEN GTGTTNTTAALNSVYLMMNNQWRLLGHETMAV\QBLTRGATLTAGUSKLDV DKKSSMGGSFRFAVILOTRALHGVVSRKMDVRLFST CQVGNNSANASDGRFTHWTVITKSKSGNTLVAGGVCKLDV DWRELMBLGSKKDGRHAPTLQDTKALHGVVSRKMDVLTAGUSKLDV DWRELMBLGSKKDGRHAPTLQDTKALHGVVSRKMDVLTAGUSKLDV DWRELMBLGSKKDGRHAPTLQDTKALHGVVSRKMDVLTAGUSKLDV AAHCFREGONDHSLMSUNVODPKSQMCKEFLIERAVISPGGDVLT AAHCFREGONDHSLMSUNVODPKSQMCKEFLIERAVISPGGDVLT AAHCFREGONDHSLMSUNVODPKSQMCKEFLIERAVISPGGDVLT AAHCFREGONDHSLMSUNVODPKSQMCKEFLIERAVISPGGDVLT AAHCFREGONDHSLMSUNVODPKSQMCKEFLIERAVISPGGDVLT ACHCHEMENVETSCCRGLSFKKTM\FPRILT\DVRK\VT D\QDFL\CS\GPGGDESP\CK*S\GGGA\TFLERAFILSAGGVLT\DVRK\VT D\QDFL\CS\GPGGDESP\CK*S\GGGA\TFLERAFILSAGGX\TPVR\TDVRK\VT D\QDFL\CS\GPGGDESP\CK*S\GGGA\TFLERAFILSAGGX\TDVRK\VT SMATLETL 5864 173 1013 PEJSVPGSLTSEOPLLCPGGGPFSADSPCLYSFLANGSFTMG KLPPSTPSSSPLACUMRUNKEPULTPDLXPKCLIFFTXHDPQY KLDDGK*PERKOTFESILQVLDNSCHKMKKKSEVPDUQAFF\S HWSLFSLCSQC/GLIPALSSTSPCSFC/PPQTVPSFTATMSPQT KLDDGK*PERKOTFESILQVLDNSCHKMKKKSEVPDUQAFF\S HWSLFSLCSQC/GLIPALSSTSPCSFC/PPQTVPSFTATMSPQT KLDDGK*PERKOTFESILQVLDNSCHKMKKKEVEVPDUQAFF\S HWSLFSLCSQC/GLIPALSSTSPCSFC/PPQTVPSFTATMSPQT KLDDGK*PERKOTFESILQVLDNSCHKMKKKKAPPSLSQCT*C\CCCCTACTACTACTACTACTACTACTACTACTACTACTAC	l		1	DD T DUMENDUEDO CAL CHEA VEENVUL VONADDAUL VECCUEDV
ALASARSSSVALANDELTRCULY-SVASAPVSRPPESSSSS PVLTVSGK 5863 2714 249 FPESSSLELAAPREDTINGPLAVLECLLELYSGLADSAPSCOM VNISGOTPTLSHGNAPGSLLTYSCPQALYSPASRLCKSSGOM TPGATRSISKAVCKEVRCPAPVSFENGITTPRIGSYPVGGWOGNUS GCROFTLLRGSPVRQCPRGWMODETAVCINGAGHCHPROTISL GPLYRTGRFROHDKVRYRCSSINUL/IGSSSEECQONGWSGTE PICROPYSYDPPEDVARALGTSSSMMUGATHTCKYKESLGRKI QIQRSGHLINLYLLLDCSGSVSENDFLIFKESSLEMDIRTSFSELIGRI QIQRSGHLINLYLLLDCSGSVSENDFLIFKESSLEMDIRTSFSSHLIKGHR GTGTTYTAALULLDCSGSVSENDFLIFKESSLEMDIRTSFSSHLIKGHR GTGTTYTAALUSHULDCSGSVSENDFLIFKESSLEMDIRTSFSSHLIKGHR GTGTTYTAALUSHULDCSGSVSENDFLIFKESSLEMDIRTSFSSHLIKGHR GTGTTYTYALUSHULDCSGSVSENDFLIFKESSLEMDIRTSFSSHLIKGHR GTGTTYTAALUSHULDCSGSVSENDFLIFKESSLEMDIRTSFSSHLIKGHR GTGTTYTAALUSHULDCSGSVSENDFLIFKESSLEMDIRTSFSSLERGKI QIQRSGHLINGVILDDTAALUCYBHLIADISLUSHTITUL DGK\SHMGGSPKTAVDHIREILININQKRIDYLDIYATGVGKLDV DWEBLEMEISSKKGBRHAPILODTAALUCYBLOPTALUSKLDDY LOGKLSHAMGSSENTAVDHIREILININQKRIDYLDIYATGVGKLDV MKNGGIL\EPYGD\DIALL\KLAQKVKM\STHCQOPSCLP\CTM AAHCPEDGNIBLINARNONDFSOGNGKEFLISHTAILIDIOKSLDFTIC CCVUNNSANASDGERTPHVTTKFKSSTC) HARREL/VANROSKIPSFOFGVAR KKNGGIL\EPYGD\DIALL\KLAQKVKM\STHCQOPSCLP\CTM AAHCPEDGNIBLINARNONDFSOGNGKEFLISHFOKSVTAV GSKLEHLTRNOVEWISCCRGLSPKKKTM\PFNLT\DVRR\VTT D\QFL\CS\GCPGEDESP\CS\SGGAV\PFLERF\LSAGGVWC SWGIL\TNP\CLSSAQLNISHESPRACPSTMG VSBULRGIPGGRSFIFFLDLANGHLSPFACCARICCPHIT\DVRR\VTT D\QFL\CS\GCPGEDESP\CS\SGGAV\PFLERF\LSAGGVWC SWGIL\TNP\CLSSAQLNISHESPRACPSTMG KLIPPSSPLACVLKRILKPLQLTPDLIKRKGLIFFCNTAMPGVY KLIDDISKF\FERGYTSFSSILGVULDINSCKIKMGKNSEVPDVOPSYFTSFFS MDSSDLIPPSQAAPKSRAGFTSVGCTIFFCNTAMPGVY KLIDDISKF\FERGYTSFSSILGVULDINSCKIKMGKNSEVPDVOPSYFTSFFS MDSSDLIPPSQAAPKSRAGFTSVGCTIFFCNTAMPGVY KLIDDISKF\FERGYTSFSSTCSTGT\GFPQVPSFYFTSFTS MDSSDLIPPSQAAPKSRAGGNSEVFTSSTSTSTSTTGTATTTTTATT SLEFFERGYTSTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		j	i	
PVITYSGK PFPSRGSILLANPREDTMGPLMVLFCLLFLYFGLADSAPSCPON VNISGGTFTLSHGMAPGSLLTYSCPQGLYPSPASRLCKSSGQWQ TPGATTSLSKAVCKEVERPAPYSFEMGITTFELGSPYPGGBVSF ECEBGFILLRGSPYSQCPRGWMDETAVCDMGAGHCPBPGISI GP\VRTGFRFGHGDKVRYRCSSDNLVLTGSSEBECQGGWWSTE PICRQPYSYDPSDVAPALGTSSHMLGATHYTQKTESBLGVRGWWSTE PICRQPYSYDPSDVAPALGTSSHMLGATHYTQKTESBLGVRGWWSTE PICRQPYSYDPSDVAPALGTSSHMLGATHYTQKTESBLGVRGWWSTE ORKSHLMLYLLLDCSGSVSENDFLIFKESASLMVDRIFSFEI NVSWAIITFASEFKVLMSVLTMNNSDMTEVISISLENANTKOHEN GTGTNTYAALMSVYLMMNOMRLLGMETMAW\QEIRRAIILL\T DGK\SHMGGSFKTAVHHTPEILTINNOKRNDVTAWM\QEIRRAIILL\T CGVGNSAMADDGEPTPHHYTIP YESGET\CALLSQUWLTD- CGVGNSAMADDGEPTPHHYTIP KPSGET\CALLSQUWLTD- CGVGNSAMADDGEPTPHHYTIP KPSGET\CALLSQUWLTD- AAHCPRDGNDHSLMRVNVGDPKSQWGKEFLIEKAVISPGFDVPA KRONGILLEFYGO\DIALL\KLAQKVVM\STHCQGPSCLD\CTM \{ EANLAGFREFFFKSTCR\ PHREML-/WNKGSV\ PAIF\VAL\N GSKLEHLTLRWGVEWTSCCKGLSPKKETM\ FFNIT\"\DVSR\ VAT\ \{ CSKLEHLTLRWGVEWTSCCKGLSPKKETM\ FFNIT\"\DVSR\ VAT\ \{ CSKLEHLTLRWGVEWTSCCKGLSPKKETM\ FFNIT\"\DVSR\ VAT\ \{ CSKLEHLTLRWGVEWTSCCKGLSPKKETM\ FFNIT\"\DVSR\ VAT\ \{ CSYBLIRGHUGGMS\ *TFPLIALMKGLS\ FFNIT\"\AL\N\ SMGL\ YNP\CLGSA\ DKMSPKKGPSVAKVPPPTR\ DHITN\ LFP BWATLETL \$1013 \$\$PLISVPGSLTSLPPLCPPGGGEPSAPSPCLYSFLWAGSFTMG KLPPSTPPSSLACVLKNILKPLDLTPDLKPKCLIFFFCNTAWDY KLDDSK\ *PENGTFFFSSTLC\ UNDICKLMSCHKGMSVEPVDVAF\ *S\ KLPPSTPPSSPLACVLKNILKPLDLTPDLKPKCLIFFFNTAPDY KLDDSK\ *PENGTFFFSSTLC\ UNDICKLMSCHKGMSVEPVDVAF\ *S\ KLPPSTPPSPAQOFTLKKVAGAKGTVKVAGAKSTVKVEPPTR\ SLGPHSVTSPPSPAQOFTLKKVAGAKGTVKVAGAKSTVKUCLCIGVF\ VEXCUSMBLAGECLCVTHITGCAGTRWWAGSARGSSLSTLP\ CKAPGPGLSLPPSCPSVEQGLAGGGGQLOGGARALGSHGHT GSTALV-YWYMCSVCVCVGCTLDVKCAHCVLCLGVA*AC\ TCVMCVCHHENCM\ VVCAGCGGGQCQLOGBRALGSHGHT GSTALVSNTAGSPSTLAGHT SRAVCSSNCTVSPRRGADCFEAPDVPKOPPGWGRASFEEGG GRGMVVAGPBLNGPGCCFSTLFB\ NELKTRNTFFSNTFGTA\ KKEVANTBEKNSUESUCKKNTDCVGGLTTSKAGSTLAGGBTAG GRGMVVAGPBLNGPGCCFSTLFB\ NELKTRNTFFSNTFGTA\ KKEVANTBEKNSUESUCKKNTDCVGGLTTSKAGSTLAGBGTAG GRGMVVAGPBLNGFGCCFSTLFB\ LENKTKKKERRDLDDL KKEVANTGBRYTMQCTATHARVALFFILGTSTTICSKTGTTLTONRM\ TVAHMMEPOLITURGLAGTVAGLAGSTLAUNALFFTILLONGAR TVAHMFBOLITURGLAGT	ŀ	}		
PFPERGSUPLAPREDTINGPLAWLECLLFLYNGLADSAPSCPON VNISGSTPILLGHANGSGLITYSCPOQL PSPELKESSGOW, TPGATRSLSKAVCKPVRCPAPVSFENGIYTPRIGSSYPUGGNVSF GCROFT/LRGSPVRQCPRGWMODETAVCDNGAGHEPROTISL GPVATGREFROHDKVRYRCSSINLVLYGSSEERCQORGWWSGTE PICRQPYSYDPPEDVARALGTSSHMUGATNITOKTKELGRKI QIQRSGHLNIYLLLDCGSGVSERDFLIFKESSGOWGWSGTE PICRQPYSYDPPEDVARALGTSSHMUGATNITOKTKELGRKI QIQRSGHLNIYLLLDCGSGVSERDFLIFKESSLMVDRIFSFEI NVSVAIITFASEFKVLMSVLMNDNSDMTEVISSLENANKOHEN GTGTTYTAALNSVYLMNNOMBLICHMTFMAVLDVSLMTDII GGKNSHMASVYLMNNOMBLICHMTFMAVLDVSLMTDII GGKNSHMASVYLMNNOMBLICHMTFMAVLDVSLMTDII GGKNSHMASVYLMNNOMBLICHMTFMAVLDVSLMTDII GGKNSHMASVYLMNNOMBLICHMTFMAVLDVSLMTDII GGKNSHMASVYLMNNOMBLICHMTFMAVLDVSLMTDII GGKNSHMASVYLMNNOMBLICHMTFMAVLDVSLMTDII GGKNSHMASVYLMNNOMBLICHMTFMAVLDVSLMTDII GGKNSHMASVYLMNNOMBLICHMTFMAVLDVSLMTDII GGKNSHMASVYLMNOGDPSCMP\CTM KKNGGILSEPTGSTCN\HENEL/WNNCGSV\PASITAJDQWVLT AAHCPKDGNDISLMRXNNOGDPSCMP\CTM KKNGGILSEPTGSTCN\HENEL/WNNCGSV\PASIT\HINDOX GSKLEHLTIRGVSVMSTSPTKCSVTMSVTMSQSV\PASIT\HINDOX GSKLEHLTIRGVSVMSTSPTKGSTCN\HENEL/WNNCGSV\PASIT\HINDOX GSKLEHLTIRGVSVMSTSPTKGSTCN\HENEL/WNNCGSV\PASIT\HINDOX SWGL\NYPSTCHSSAVKKGSPXAVVPTERFRICATORPOY KLINDAK*PERGNTFFSTSLOULDNSCKKMKNSKSVPDVQAFF\S MSGLENGTSTSTLOULDNSCKKMKNSKSVPDVQAFF\S MSGLENGTSTSTLOULDNSCKKMKNSKSVPDVQAFF\S MSGLENGTSTSTLOULDNSCKKMKNSKSVPDVQAFF\S MSGLENGTSTSTLOULDNSCKMKNSKSVPDVQAFF\S MSGLENGTSSMTKLOULDNSCKMKNSKSVPDVQAFF\S MSGLENGTSSMTKUNDOX GKRSMTKUNDOX			1	ALASARRSSSVSLAVNDELTRCVLV*SVASAPVSRPFPSGSSGS
UNISGITPTI.SHOWADGILITYSCPOGLYPSPASRICKSSGOWQ TPGGATRSISKAVCKUPUCAPUSY FENGITYTPGSYPUGGNUSH ECROFIL/RGSPURQCPYGFMOMOCTAVCDWGAGHCPROFISI GF\TGTGFFGHGDKVRYRGSSILVLTGSSERECQGMUSWSGTE PICRQFYSTPSPBOVAPALOTSFSHMIGATIPTTQXTKESLGRKI QIQRSGHLMIYLLLDCSGSVSENDFLITFESSLENANTKOHEN HVSVAIITHASEFKVLMSVLNDNSEDHTEVISSLENANTKOHEN GTGTTTYAALMSVYLMWANOMELLGMSTMAW, QEITRAILLL\T DGK\SHMGGSFKTAVHHTESILNINGKRUDYLDIYAIGWGKLDV DWRELBELGSKKDGRHAFILDOTKALHQVFSHMIDDVSKLTDTI CCVGNISMANASDGETFHHYTIKFSGOTCHGASLSDGWUTT AAHCFBORDISLWRNWGDPSGWGKFFLIEKAVISPGFDVFA KKNOGTLA PFYGDO DIALLKARQKVMA\TSHALISDGWLTT QASHLGFLGSKKDGRHAFILOTKALHQVFSHMIDVSKLTDTI CCVGNISMANASDGETFHHYTIKFSGOTCHGSCLGSCAVCH \{RANLGFLRETFKGSTCR\DHENEL/WNKGSV\PAHF\VAL\N GSKLBHLTIRKGVEWTSCCKGLSFKKKTM\FFNIT\DVRK\VT D\QPL\CS\GGGDESP\CS\CS\CS\CS\CS\CS\CS\CS\CS\CS\CS\CS\CS\		1	1	PVLTVSGK
UNISGITPTI.SHOWADGILITYSCPOGLYPSPASRICKSSGOWQ TPGGATRSISKAVCKUPUCAPUSY FENGITYTPGSYPUGGNUSH ECROFIL/RGSPURQCPYGFMOMOCTAVCDWGAGHCPROFISI GF\TGTGFFGHGDKVRYRGSSILVLTGSSERECQGMUSWSGTE PICRQFYSTPSPBOVAPALOTSFSHMIGATIPTTQXTKESLGRKI QIQRSGHLMIYLLLDCSGSVSENDFLITFESSLENANTKOHEN HVSVAIITHASEFKVLMSVLNDNSEDHTEVISSLENANTKOHEN GTGTTTYAALMSVYLMWANOMELLGMSTMAW, QEITRAILLL\T DGK\SHMGGSFKTAVHHTESILNINGKRUDYLDIYAIGWGKLDV DWRELBELGSKKDGRHAFILDOTKALHQVFSHMIDDVSKLTDTI CCVGNISMANASDGETFHHYTIKFSGOTCHGASLSDGWUTT AAHCFBORDISLWRNWGDPSGWGKFFLIEKAVISPGFDVFA KKNOGTLA PFYGDO DIALLKARQKVMA\TSHALISDGWLTT QASHLGFLGSKKDGRHAFILOTKALHQVFSHMIDVSKLTDTI CCVGNISMANASDGETFHHYTIKFSGOTCHGSCLGSCAVCH \{RANLGFLRETFKGSTCR\DHENEL/WNKGSV\PAHF\VAL\N GSKLBHLTIRKGVEWTSCCKGLSFKKKTM\FFNIT\DVRK\VT D\QPL\CS\GGGDESP\CS\CS\CS\CS\CS\CS\CS\CS\CS\CS\CS\CS\CS\	E963	2714	249	
TPGATESLEKAVCEPVRCPAPUS PERGI YTPRIGS YPOGRVSS ECROSI). LINGSPYDGYDROMMOGETANGAGHCYMPGUTE GP\VRTGPFRGHGDKVRYRCSSNLVLTGSSERECQONGWSGTE PICRQPYSYDPPBUVAPALGTSFSHALGATNPTQKTKESLGRKI QIQRSGHLIMILILLDCSGSVESDMFLIFESSALMVDRIFSFSI NVSVAIITTASEFRYLMSVIAMNSRDMTEVISSLERANIKDHER GTGTNTYTAALNSVIAMNSQRIMGNELGGETHAWN\QBIRHAILLL\ DGK\SHMGGSPKTAVDHIREILAINQKRNDVLDIYALGVGKLDV DWRELMELSKKDGERHAFILQDYKALHQVFREMILDVSKLTDTI CGVGNMSANASDQRTPHHVTIFKSQET\CRGALLSDGWULT AAHCPRORDHSLAWRIVODDFSGWGKEFLEAVISPGEVDFVA KRNGGIL\EPFUD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM \CANGGIL\EPFUD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM \CANGGIL\EPFUD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM \CANGGIL\EPFUD\CGLSA\KNGSVEPFTK-YFNLT\DVRE\VTI D\QPL\CS\GPQEDESF\CK-E\SGGA\YFLERFIFKSGGTV D\QPL\CS\GPQEDESF\CK-E\SGGA\YFLERFIFKSGGTV D\QPL\CS\GPQEDESF\CK-E\SGGA\YFLERFIFKSGGTV SGGL\TNP\CGLSA\KNGSVEPFTK-DPHTN\LFP Q*SPURQHDGSMS+IFLDLLANGHLSPPACPARICRPLHFLPS BWATLRTL 5864 173 1013 PLISVPQSLISLPQPLCPFGGQFSAPSPCLXSFLARGSFYMC KLPPSIPPSPLACVLKNLKPLQLIPDLKPFKCITFCNTAWPOY KLDDDSK-PENGTPESILQVLUDNSCHKWGSWSVPDVQAFF\S HMSLPSLCSGC/GLIPNLSSFSPPCFG/PPOVPSPTEFFFS MDSSDLPPSPQAPRGABEGNSHLSAPPYNDFTISPPHWS SLQFHSVTSPPPPAQOFTLKKVAGAKGIVKVSAPFSLSQIR*RL SGFSSNIKTJOPSSLLIMQP 5865 5865 568 1684 CLEPGPRGBGWRAGHTIVGCIFFKIAIISHKKGMYLCVOMCT LSVCLVCVQVSSNICV/CVGCACCUSCLCT\CCGISMYTREHAC ACTRV-VYMCMS/VCTCVSTCIDVRVCAHVCVYNCLLGYAFAG CVYAVCGUCWARCHMSTCTVLUVGS-ACTCVMHM/CSGTCR/C VINCCMSHBAGECLCVYLHIGGCAGTRRWMGSRGSGSCRLD CWAPGGGLSLPGSPSSVORGCVSSLCTVLGGRGSGSGSCRLD CWAPGGGLSLPGSPSSVORGCVSSLCTVLGGRGSGSGSGREGGERGG GSPANVCSNNCTVSPRRGADCFEAPDVPROPGGRAFFERGG GSPANVCSNNCTVSPRRGADCFEAPDVPROPGGRAFFERGG GSPANVCSNNCTVSPRRGADCFEAPDVPROPGGRAFFERGG GSPANVCSNNCTVSPRRGADCFEAPDVPROPGGRAFFERGG GSPANVCSNNCTVSPRRGADCFEAPDVPROPGGRAFFERGG GSPANVCSNNCTVSPRRGADCFEAPDVPROPGGRAFFERGG GDRAVCSNPTHAGGCAGTRRWMAGSRAGGSCSLL CWAPGGGLSLPGSPSCRIPGFOTHE NPLKTRNITFFSNNTVCGTTA RCVVVATGGSTVMAGSTALTASSLEWGERGRAFFRIDDT DPSGDMIYLGVFRAWVDGULGTTANGAGTED DPSGDMIYLGVFRAWVDGULGTTANGAGSRCSLLATUT CLTLTAKRMARKNCLVKNLEAVFLIGGIUGRTVPALLATITGNKTMTTGORM TVAHHWEDRGTHEADGGTSFDKS	3003	4123		
ECEGGFI\LRGSPVRQCRPNGMBDETAVCDNGAGHCHPBGISL GP\VRTGPFFGHGDKVRTXCSSNLVLTUSERCOONGWSGTE PICQPYSYDFPBDVAPALGTSFSHMLGATNPTQKTKESLGRKI QIGRSGHLMINLLLDCSQSVSENDFLIFKESAGLMVRDFFSFBI NVSVAIITASEPEVLMSVLMDNSRDMTSVISLENANYKUHEN GTGTNTYAALNSVILMMNGWRLLGMETMAW\QSIRRAILL\T BGK\SHMGGSPKTAVBHIRETLININGKRDLDYAIGUGKLDV DWRELMELGSKKDGERHAFILQDTKALHQVFEHHLDYAIGUGKLDV DWRELMELGSKKDGERHAFILQDTKALHQVFEHHLDYAIGUGKLDV DWRELMELGSKKDGERHAFILQDTKALHQVFEHHLDYSLTDTI CGVGNMSANADQRFTPWHTVITKYSGGF\C\RGALISDGWUT AAHCFRGDDIBLMFUNVGDPKSQMGREFLIEKAVISPGFDVFA KKNQGIL\EPFGDDIBLL\KLAUGHENL\WNKGSV\PAHF\VAL\N GSKLBHILTLRMGVEWISCCRGLSPKKTTW\FPNIT\DVRE\VVT D\QFD\C\GSQFDEESS\F\GVE\S\GGGA\FLERAVISPGFDVFA KNQGIL\SPYGDDIBLL\KLAUGHENL\WNKGSV\PAHF\VAL\N GSKLBHILTLRMGVEWISCCRGLSPKKTTW\FPNIT\DVRE\VVT D\QFD\C\GSQFDEESS\F\GVE\S\GGGA\FLERAVISPGFDVFA KNGGIL\NP\CGSGPDEESS\F\GVE\S\GGGA\FLERAVISPGFDVFA GSKLBHITLRMGVEWISCCRGLSPKKTTW\FPNIT\DVRE\VVT D\QFD\LC\GSQFDEESS\F\GVE\S\GGGA\FLERAVISPGFDFT\DVRA\GFT\LF\FLATATISPGFDVFA GSKLBHITLRMGVEWISCCRGLSPKKTTW\FPNIT\DVRE\VVT D\QFD\LK\GSQFDEESS\F\GVE\S\GGG\FLATA\GGGWC SWGL\YNP\CGSGPDESS\F\GVE\S\GGG\FLATA\GGGWC SWGL\YNP\CGSGPDESS\F\GVE\S\GGG\FLATA\GGGWC SWGL\YNP\CGSGPDESS\F\GVE\S\GGG\FLATA\GGGWC SWGL\YNP\GS\GGG\FLATA\GGG\GGG\FLATA\GGG\GGG\FLATA\GGG\GGG\FLATA\GGG\GGG\FLATA\GGG\GGG\FLATA\GGG\GGG\GGG\FLATA\GGG\GGG\GGG\GGG\GGG\GGG\GGG\GGG\GGG\	1			
DP\PRTGERFOHDKÜRYRCSSILVLTGSSEREQGNGWSGTE PICROPYSYDPEDVAPALGTSPSHMLGATNPTOKTKESLGRKI QIGRSCHLMILTLLDCSGVSENDFLIFESSALMVDRIFSFEI NVSVAIITTASEPKYLMSVIADNSRMTEVTSSLEMNIKDHEN GTGTNTTAALNSVIAMNOKRLIGMETHAW\QSIRRAIILL\T DGK\SHMGGSPKTAVHIREILAINQKRNDVLDIVALGVGKLDV DWRELBELGSKKDGERHAFILOTKALHQVFREMLDVSKLTDTI CGVGNMSANASDQERTPWHVTIKPKSQET\CRGALISDQWVLT AAHCFROGNDIBLMRUNVGDPKSGMGKEFLIERAVISPGFVDFA KKNGGIL\SPYGDQLTALL\ALAQKVMM\SVAYSPGFVDFA KKNGGIL\SPYGDQLTALL\ALAQKVMM\SVAYSPGFVDFA KKNGGIL\SPYGDQLTAL\ALAQKVMM\SVAYSPGFVDFA KKNGGIL\SPYGDQLTAL\ALAQKVMM\SVAYSPGFVDFA KKNGGIL\SPYGDQLTAL\ALAQKVMM\SVAYSPGFVDFA KKNGGIL\SPYGDQLTAL\ALAQKVMM\SVAYSPGFVDFA KKNGGIL\SPYGDQLTAL\ALAQKVMM\SVAYSPGFVDFA KKNGGIL\SPYGDLTANCHLSPYDAKUSPYDFALDFALDFALDFALDFALDFALDFALDFALDFALDFAL	l			1
PICROPYSTOPPEDVAPALGTSSPHALGATNPTOKTYRESLGRKY QIQNSGHLAILALLALDGOSQUSENDFLIFASALMVORIFSFEI NVSVAIITFASEPKVLMSVLMDNSRDMTEVISSLENANYKDHEN GTGTNTYAALNSVYLMNNOQRELGMETMAN\QSIEATIALLAL DGK\SIMGGSPKTAVHRIELLAINDKRANDVEDYALGVGKLDV DWRELMELGSKKDGERHAPILQDTKALHQVFERMLDVSKLUTTI CGVGNINSAMADDGRTPMVTVIRKSGEPK(AGALISDGWVLT AAHCPROGNDISLMRVINVADPKSGWCKEFLIEKAYTSGFDVPKA KKNQGIL\EPVGD\DTALLI\KLAGKVUM-STECTGGPSCLP\CTM \QSKLEHLTLRMGVEWTSCCRGLSFKKTM\FPNLT\DVRE\VTV D\QFL\CS\GPGEBSF\CS\eta\S\GGA\FFLERAYTSGFDVFXA KKNQGIL\EPVGD\DTALLI\KLAGKVUM-STHEORFSCLP\CTM \QSKLEHLTLRMGVEWTSCCRGLSFKKTM\FPNLT\DVRE\VTV D\QFL\CS\GPGEBSF\CS\eta\S\GGA\FFLERAYTGGPSCLP\CTM \QSKLEHLTLRMGVEWTSCCRGLSFKKTM\FPNLT\DVRE\VTV D\QFL\CS\GPGEBSF\CS\eta\S\GGA\FFLERAYTGGPSCLP\CTM \QSKLEHLTLRMGVEWTSCCRGLSFKKTM\FPNLT\DVRE\VTV D\QFS\WLROJHGGMS*FLEDLLANGHLSFPACGFTKGFHINLSF GSKLEHLTLRMGVEWTSCCRGLSFYKKTM\FPNLT\DVRE\VTV D\QFS\WLROJHGGMS*FLEDLLANGHLSFPACGFTKGFHINLSF SWATLRTL FLISVPQSLISLPQFLLCFPGGGEFSAPSCLYSFLWACSFTMG KLPPSIPPSSPLACVLKNLKFLQLTPDLKPKCLIFFCNTAWPQY KLDMDSK*PENSTTEFSILQVLDNSCKKNGKNESVPUQAFF\S HNSLPSLCSCG\GJIENTLSSFSPCTGF\GPPQOPPSF\TESFFS MDSSDLPPSPQAAPRQARPGDNSHLASAPPPYNFTISPPHTWS SLGPHSVTSPPPPAQOFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKLOPSSHLINQOP CLEGPRWGESWRAGHTIVGCIFFKTAIISHFRGGMYLCVCMCTC LSVCVCQVGSNICV\CVSMCACVSLCTC\LGCISMYTRHAC ACTRV*VYYNCMS\VCTCVSTGLDVRVCARVCYNCLLGYA*AC TCV*MCCVGHREVCMC\VCAGSCCLL\CGGHICM\FMCMSAYICI \/CVVVCULCVMACMRMSTCVMLVYG*ACTCVMMEN\GCSTCR\C VHVCCMSMIACCLCVVALIG\CGGAGTERDVD FXQFRGRASFEERG CWAPGPGLSLPGPSCPSVEQGLGGGPQLQGRSGEARLGEHRGW GSPAAVCSNCTVSPRRGADCFRAPOVFXQFTCSTCL\C VHVCCMSMIACCLCVVALIG\CGGAGTERDVD FXQFRGRAFEERGD CWAPGPGLSLPGPSFCPSVEFTAPDVTRYQLTHSKAQEILATTVV CLTHTAKRMSVEEVTRADVQLSTHKAGESTDLSGKTGTLQAGTED DPSGDNLYLGIVAAVVITTGCFSYYQEAKSKKIMESFROMVDO QALVIREGRKMVABERVVODLVEIKGGDRVPADLRIISAHG KVDNSILTGSSRYTMGRAGATHASGLSVACHTRITFSINTVSGTA RGVVVATGGTVTMGTAITLASGLSVGTTALEEHFIQLITGV AVFIGVSFTILLIGVTRUEAVTFLIGGIVANVLEGUHTYTU CLTTLTAKRMRRNCLVKNLRAAFATCLISSGSVULMRE RNKVXBIPSNSTKYQLSHILLBAVTFLIGGIUTSVLLGFCHYYL CLTTLTAKRMRRNCLVKNLRAAFATCLISSGSVULME	I	,		1
QIQRSGRIANITALLDCSQSVSENDFLIFKESASLAMDRIFSFBI NVSVAIITFASEPKVLMSVLNDNSRDMTEVISSLENANYKHEN GTGTNTYAALNSVLWNNNQMELLGHETMAW\QBIRHAIILL\T DGK\SHMGGSPKTAVDHIREILNINQKRNDYLDIVAIGVGKLDV DWRELMELGSKKDGERHAFILQOTEALHQVBERMLDVSKLTDTI CGVGNMSANASDGRTFWHVTTKPKSQBT\C\GRALISD\GWUT AAHCPROENDHSLHRWAVGDPKSQMGKFLIERAVISSPGFUVFA KKNQGIL\EFYGD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM \EARLGFLRETFKGSTCR\DHBNEL\FWNNXGSYPAPR\VAL\N GSKLEHLTRMGVEWTSCCRGISPKKTM\FPHIT\DVRB\VVT D\QFL\CS\GPQEDESP\CR*E\SGGAV\FILERFALSAGGWC SWGL\TMP\CLGSA\DKDSFKKGSPAVVPPTR\DFHIT\DVRB\VVT D\QFL\CS\GPQEDESP\CR*E\SGGAV\FILERFALSAGGWC SWGL\TMP\CLGSA\DKDSFKKGSPAVVPPTR\DFHIT\D\LFP O*SPHLRQHEGGMS*IFLPLLANGHLSPFACPARICRPLHFLDS EMATLRTL 5864 173 1013 PLISVPQSLISILPQFLLCFPGGQEPSAPSPCLYSFLWACSFTMG KLPPSIPPSEPLACVLKNLKPLQLTPDLKFRCLIFFCNTAWPGY KLDNDSK*PNOTTPSFSILQVLDNSCKHMGKWSEVPDVQAFF\S HWSLPSLCSQC\GLIPBLSSFSPCSFG\PPPQVPSP\FTSPFSFM MDSDLPPSPQAAPRQAEPGPNSHLASAPPYNPFTTSPBTHWS SLQFHSVTSPPPPAQQFTLKKVAGAKUTVKXAPFSLSQIR*RL GSFSSNIKLQPSSWLIMQQP 5865 568 1684 1	1			GP\VRTGFRFGHGDKVRYRCSSNLVLTGSSERECQGNGVWSGTE
QIQRSGRIANITALLDCSQSVSENDFLIFKESASLAMDRIFSFBI NVSVAIITFASEPKVLMSVLNDNSRDMTEVISSLENANYKHEN GTGTNTYAALNSVLWNNNQMELLGHETMAW\QBIRHAIILL\T DGK\SHMGGSPKTAVDHIREILNINQKRNDYLDIVAIGVGKLDV DWRELMELGSKKDGERHAFILQOTEALHQVBERMLDVSKLTDTI CGVGNMSANASDGRTFWHVTTKPKSQBT\C\GRALISD\GWUT AAHCPROENDHSLHRWAVGDPKSQMGKFLIERAVISSPGFUVFA KKNQGIL\EFYGD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM \EARLGFLRETFKGSTCR\DHBNEL\FWNNXGSYPAPR\VAL\N GSKLEHLTRMGVEWTSCCRGISPKKTM\FPHIT\DVRB\VVT D\QFL\CS\GPQEDESP\CR*E\SGGAV\FILERFALSAGGWC SWGL\TMP\CLGSA\DKDSFKKGSPAVVPPTR\DFHIT\DVRB\VVT D\QFL\CS\GPQEDESP\CR*E\SGGAV\FILERFALSAGGWC SWGL\TMP\CLGSA\DKDSFKKGSPAVVPPTR\DFHIT\D\LFP O*SPHLRQHEGGMS*IFLPLLANGHLSPFACPARICRPLHFLDS EMATLRTL 5864 173 1013 PLISVPQSLISILPQFLLCFPGGQEPSAPSPCLYSFLWACSFTMG KLPPSIPPSEPLACVLKNLKPLQLTPDLKFRCLIFFCNTAWPGY KLDNDSK*PNOTTPSFSILQVLDNSCKHMGKWSEVPDVQAFF\S HWSLPSLCSQC\GLIPBLSSFSPCSFG\PPPQVPSP\FTSPFSFM MDSDLPPSPQAAPRQAEPGPNSHLASAPPYNPFTTSPBTHWS SLQFHSVTSPPPPAQQFTLKKVAGAKUTVKXAPFSLSQIR*RL GSFSSNIKLQPSSWLIMQQP 5865 568 1684 1	j	j	J	PICROPYSYDFPEDVAPALGTSFSHMLGATNPTQKTKESLGRKI
NUSVALITRASEPKULMSVLINDISRDMTEVISSLENABYKDHEN GTGTNTYAALNSVYLMMNNOMRLIGHETMANQEIRHAIILL\T DGK\SHMGGSPKTAVDHIREILNINQKRNDYLDIYAIGVGKLDV DWRELMELGSKKDGERHAFILQDTKALHQVFERMLDVSKLTDTI CGVOUMSAMANDSDGRTFWHVITKPRSQT\C\RGALISDQWLT AAHCPROGNDHSLWRUVVGDPKSQWGKEFLLEKAVISPGFDVFA KKNQGIL\EPYGD\DIAL\KLAQKVKM\STHCQGPSCLP\CTM \EANLGFLRETPKGSTCR\DHSNEL\VWNKQSV\PAHP\VAL\N GSKLEHLTLRMGVEWTSCCRGLSPKKTM\FPHIT\DVREN\VUT D\QTA\CS\QPQEDESP\Cx\e\S\GGAQ\VFLERRFLASGGWC SWGL\YMP\CLGSA\DKNSPKKGDEVAKVPPTR\DFHIT\LFUR\SGGGWC SWGL\YMP\CLGSA\DKNSPKKGDEVAKVPPTR\DFHIT\LFUR\SGGGWC SWGL\YMP\CLGSA\DKNSPKKGDEVAKVPPTR\DFHIT\LFUR\SGGGWC SWGL\YMP\CLGSA\DKNSPKKGDEVAKVPPTR\DFHIT\LFUR\SGGGWC SWGL\YMP\CLGSA\DKNSPKKGDEVAKVPPTR\DFHIT\LFUR\SGGGWC SWGL\YMP\CLGSA\DKNSPKKGDEVAKVPPTR\DFHIT\LFUR\SGGGWC SWGL\YMP\CLGSA\DKNSPKKGDEVAKVPPTR\DFHIT\LFUR\SGGGWC SWGL\YMP\CLGSA\DKNSPKKGDEVAKVPPTR\DFHIT\LFUR\SGGGWC SWGL\YMP\CLGSA\DKNSPKKGDEVAKVPPTR\DFHIT\LFUR\SGGGWC SWGL\YMP\CLGSA\DKNSPKKGDEVAKVPPTR\DFHIT\LFUR\SGGGWC SWGL\XMPSIPPSSPLACVINLKEPQLUTPDLKPKCLIFFCTNTAWFQY KLDNDSK*PENGTFFFSILQVLDNSCHKMGKWSEVDVQAFF\S HWSLDSLPPSSQAARQAEPGPNSHLASAPPPYNFFITSPEHTWS SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPPSLSGIR*RL SSFSNIKLOPSSWLINGKQP SSFSNIKLOPSSWLING\QP SSFSNIKLOPSSWLING\QP SSFSNIKLOPSSWLING\QP SSFSNIKLOPSSWLING\QP CLEGPRWGGWRAGHTVGCIFFKTAIISHKGGMYLCVGMCTC LSVCVCVQVGMCACVSLCTC\ICCIGNYTRHAC ACTEV*YYMCMS\VCTCVSTCIDVEVCAHVCVMEM\GSTCTC\ICCISNYTRHAC ACTEV*YYYMCMS\VCTCVSTCIDVEVCAHVCVMEM\GSCTC\ICCISNYTRHAC CYVMCVCHUEHKPCC\VCACSCVLL\CRGGBCC\MMSANICLGYAA\AC TCV*MCVCHEHKPCC\VCACSCVLL\CRGGBCQD\GMGGABGEARLGERGW GSPAAVCSRCTVSPRRGADCFEAPUV KQPOWGRASFEERGC GGRGWCAPPLNSPCCCFSIKPELKAKKK KEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQE ILARDGNA LTPPTTPEWAVKCRQUFGGFSILLIMGAILCFLAYGQAGTED DPSGNILVGSSEPQTRSPDCTHS\FYLLIMGAILCFLAYGQAGTED CXDNSSLTGSSEPQTSPDCTHS\FYLLIMGAILCFLAYGGAGTED DPSGNILVGSSEPQTSPDCTHS\FYLLIMGAILCFLAYGGAGTED AVFIGSSEPQTSSPDCTHS\FYLLIMGAILCFLAYGGAGTED CXDNSSLTGSSEPQTSSPDCTHS\FYLLIMGAILCFLAYGGAGTED NAVFIGSSEPQTSSPDCTHS\FYLLIMITSFSNINVEGTA TVAMWFONGIHEADTTEDGSGTSFDKSSHTWALP*H\LLOFT TVAMWFONGIHEADTTEDGSGTSFDKS]			
GTGTNTYALINSVILMONNOMILLGMETMAW\QBIRHAIILL\T DGK\SHMGGSPKTAVDHIREILNINQKRNDYLDIYAIGVGKLDV DWRELBELGSKEDGERIAFILQDTRALHQVFERMLDVSKLTDTI CGVGNMSANASDGRTFWHUTIKPKSQGT\C\GALISDQWTL AAHCFRGROHSLHURWVGDPKSQMGEFILERAVISPGFDVFA KKNGGIL\EPYGD\DIALL\KLAQKVM\STHCQGPSCLP\CTM \RANLGFLRETFKGSTCR\DHENEL\VMNKQSV\PAHP\VAL\N GSKLEHLILRMGVEWTSCCRGLSPKKTM\FFNLT\DVRE\VVT D\QPL\CS\GPQEDESP\CX*E\SGGA\VFLERFLSAGGWWC SWGL\TMP\CLGSA\DKNSPKKGPSVAKVPPFTR\DFHIN\LFP Q*SPWLRQHEGGMS*IFLPLLANGHLSPFACPARICRPLHFLPS SWATLRTL 5864 173 1013 PLISVPQSLISLPQFLLCFPGGQEPSAPSPCLYSFLWACSFTMG KLPPSIPPSEPLACVLKNLKPLQLTPDLKFRCLIFFCNTAWPQY KLDMDSK*PENGTFFSTLQVLDNSCKHMGKWSEVPDVQAFF\S HWSLPSLCSQC\GLIFNLSSFSFCSG\PPPQWSP\TESFFS MDSSDLPSPQAARRAGPEQPNSHLASAPPPWFFITSPFHWS SLQFHSVTSPPPPAQQPTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSNIKLQPSSWLINGQP 5865 568 1684 CLFGFRWGESWRAGHTVGCTFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVSSWLCV\CVSMCACVSLCTC\CXGTSMYTREHAC ACTRV*VYMCMS\VCTCVSTCLDXCAHVCVVMCMCLCLSM*AC TCV*MCVCVGMSWLCV\CVSMCACVSLCTC\CXGTSMYTREHAC CCHPCFWGESWRAGHTVGCTFFKTAIISHFKGGMYLCVCMCTC \CXTVCVCVCMHENVCCVC\CXGSCVLL\CRGHICM\MMSAYICI \CVVVCVCMHENVCCC\CYGSCCVLL\CRGHICM\MMSAYICI \CVVVCVCMHENVCCCYCSCCDAGGGGQLQGGGGAGGGGARLGEHRGW GSPANCSSRCTVSFRRADCFFEAPVCPFOMGRAFEERGC GGRGWCAPPLNGPGCSTSFDKKKKKK SPANCSSRCTVSFRRADCFFEAPVCPFOMGRAFEERGC GGRGWCAPPLNGPGCCFSIKPELKAKKKK ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHMSVESVCRKYNTDCVQGLTHSKAQBILARDGFNA LTPPPTPEWVKFCQLFGGFSILWIGALLCHAYGIQAGTED DPSGNILVLGIVLAAVUTTGCFSYQFAKSKIMBSFREERGC GGRGWCAPPLNGPGCGFSILWIGALLCHAYGIQAGTED DPSGNILVLGILAGVUTTTGCTFSYQFAKSKIMBSFREERGC GRCWVCATGDRTWMGKIATLASGLBGKTTIATEILBHFQLITGV CLUTLTAKRMARNCLVUTVITGCFSYQFAKSKIMBSFREERGC AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPGGLLATVTV CLUTLTAKRMARNCLVUKNILAVETISTSTCSDKTGTLONKM TVAHMWENGIHEADTTEDGSGSFPKSSTWWALP*H\LLGF RYVKAGBIPPNSTNKYQLSTHETEDBNDRYLLVMKGAPERILD RCSTILLQGKEGDFLDERMEAPQNAYLBLGGLGERVLGFCHYTL BROWFKGGQDNIPVLRTDVAGADASSALLKCIELSSGVLARE RNKKVABIPPNSTNKYQLSTHETEDBNDRYLLVMKGAPERILD RCSTILLQGKEGDFLOFFTTDDLCFTTDNTCVMIGAPPDAVDAU	1			
DGK\SHMGGSPKTAVDHIREILMINOKRNDYLDIYALGVGKLDV DWRELNELGSKKDGERHAFILQDTKALHQVFEHMLDVSKLTDTI CGVGNMSANASDGERTPHVTITKSGET\C\RGALISDGWVLT AAHCPRDGNDHSLWRNNYGDPKSGWGKEFLIEKAVISGFDVFA KKNGGIL\EPYGD\DIALL\LLAKW\STRGGPSCLP\CTM \EANLGFLRSTFKGSTCX\DHENSL\VMNKGSV\PAHF\VAL\N GSKLEHLTLRMGVEWTSCCRGLSPKKTM\FPHIT\DVRE\VVT D\QPL\CS\GPQEDESP\CX**E\SGGA\VFLERRFRLSAGGSWC SWGL\YMP\CLGSA\DKNSFKKGFSVAKVPPPTR\DFHIT\DVFE\VVT Q*SPWLQHEGMS*IFLPLLANGHLSPFACPARICRPHFLPS EWATLRTL FLISVPQSLISLPQPLLCFPGQEPSAPSPCLYSFLMACSFTMG KLPBSTISLPQSPLLCFPGGQEPSAPSPCLYSFLMACSFTMG KLPBSTISLSCQC\GIPNLSSSSFSG\PPDVVBSP\TESFFS HWSLPSISLCSC\GIPNLSSSSFSG\PPDVVBSP\TESPS\TESPSPLLSCG\GIPNLSSSSPS\FSP\PPDVPSP\TESPS\TESPS\TESPS\TESP\PPDVPSP\TESPS\TESP\TESPS\TESP\TESPS\TESP\TESP				
DWRELNELGSKKDGERHAFILJOTKALHQVFERMLDVSKLTDTI CGVGNMSANASDQERTPWHVTIKPKSQET\C\RGALISDQWULT AAHCPROGNDHSLWRNNUGDKSQMCREFLIEKAVISBGFDVFA KKNGGIL\EFYGD\ITALL\LAQKVEM\STRCQGPSCLP\CTM \EANLGPRETFKGSTC\DHENELVWKGSV\PAHP\VAL\NA\ GSKLEHLTLRMGVEWTSCCRGLSPKKKTM\FPNLT\DVRE\VVT D\QFL\CS\GPOEDESP\CK* E\SGGA\VFLERRFKLSAGGVWC SGKLEHLTLRMGVEWTSCCRGLSPKKKTM\FPNLT\DVRE\VVT D\QFL\CS\GPOEDESP\CK* E\SGGA\VFLERRFKLSAGGVWC SGML\TMP\CLGSA\DKNSPKKGSSPAKVPPFTR\DFHIN\LFP Q*SPWLRQHPGGMS*IFLPLLANGHLSPFACPARICRPLHFLPS EMATLRTL 5864 173 1013 1013 PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG KLDPSIPSSPLACVLKRLKPLQLTPDLKFKCLIFFCKTAMPQY KLDRDSK*PENGTFFSSILQVLDNSCKKMGKWSEVPDVQAFF\S HWSLPSLPSSPLACVLKRLKPLQLTPDLKFKCLIFFCKTAMPQY KLDRDSK*PENGTFFSSILQVLDAKGKKWSEVPDVQAFF\S HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPPQVPSP/TESFFS MDSSDLPPSPQAPRQAEPGNSHLASAPPPNPPITSPFHTWS SLQFHSVTSPPPPAQPTFLKKVAGAKGIVKVSAPPSLSQIR*RL GSFSSNIKLQPSSWLIWQQP S4FSNIKLQPSSWLIWQQP S4FSNIKLQPSSWLIWQQP CLFGFRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSWLCV/CVSMCACVSLCTC\ICRCISMYTRBHAC ACTRV*YYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYX*AC TCV*MCVCMEHHCMC/VACSCYLICRGHLCM/MGMSAYICI /CVYVCVLCVWACMRMSTCVLLVYG*ACTCVSMCHMSAYICSI /CVYVCVLCVWACMRMSTCVLLVYG*ACTCVSMCHMSAYICSI /CVYVCVLCVWACMRMSTCVLLVYG*ACTCVSMCHACMSANICI /CVYVCVLCVWACMRMSTCVLLVYG*ACTCVSMCHACMSANICI /CVYVCVLCVWACMRMSTCVLLVYG*ACTCVSMCHACMSANICI /CVYVCVLCVWACMRMSTCVLLVYG*ACTCVSMCHACMSANICI /CVYVCVLCVWACMRMSTCVLLVYG*ACTCTSAGERERGC GGRGWCCAPPLNGPCCCFSIKPELKAKKK 5866 98 3197 ARPEVPAPPAMISRRGAAKMCDKKDKDSPKNNKKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQCLTHSAQEILLARDCPNA LTPPPTTPEWKYRCRQLFGGPSILLMIGALLCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSKIMESFXNMVPQ QALVIRRGERMQVNAEEVVVGDLUEIKGGGRVADLRIISAHGC KXDMSSITGSSESFGTFSSPCTHER,NNFVEGTA RGVVVATGDRTVSFTPSCTHERVPLKTRNIFTSSTNSVESTA RGVVVATGDRTVSFTILLIGGTTSSTSTICSDKTGTLTDNTM TVAHMWFDNQIHEADTTEDQSGTSFDRSSSTKIMVAF*H/LLGFC NRPVKKGGQNNIEVLKRDVAGDASALLKCIELSSGSVKLMER RNKKVAEIPPNSTNKYQLSHETEDPNDNRYLLVMKGADERILD RESTILLQGKGQDDIEBKKGAFQDANYLLGGGERVLGFCHYYL PEEGFPFKKAFFCDDVNFTTDNLCFLAMM	i	ı		
CCVCNMSANSDOERTPHHTTERESOET\C\RGALISDQWVLT AAHCFRORDHSLWRVNVGDPKSQWGEFLIEKAVISPGFDVFA KKNGGIL\EPYGD\DIALL\KLAQKVRM\STHCQGPSCLP\CTM \{EANLGFLRETFEGSTCR\DHENEL\VWNKQSV\PAHF\VAL\N GSKLEHTLTRMGVWFTSCRGLSFKTM\FPNLT\DVRR\VTD D\QFL\CS\GPQEDESP\CK*E\SGGA\VFLERRFRLSAGGWC SWGL\YNP\CLGSA\DKNSYKKGFSVAKVPPPTR\DFHIN\LFP Q*SYBLHQHEGGMS*IFIPLLANGHLSPPACPART CRPLHFLPS EWATLRTL 5864 173 1013 PLISVPQSLISLPQPLCFPGGQEPSAPSPCLYSFLWACSFTMG KLPPSIPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY KLDMDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S HWSLPSLCSC\G'C\GILNLSSSSPFSG\FPQPVLVSP\TSSPFTMS SLQPHSVTSPPPAQAPFLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKLQPSSWLIWOQP 5865 568 1684 CLFGPRWGESWRRGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSWICV\CVSMCACVSLCTC\ICRCISMYTREHAC ACTRV*VYMCMS\VCTCVSTCIDURVCAHVCVYMCLCIGYA*AC TCV*MCVGHEVCKC\VCNSCACVGSCVLL\CRGHICM\MCMSAYICI \CVVYUCVLCVWACMMNSTCVWLUVGS*ACTCVMMHM\CSCTCR\C VHVCCMSMHACECLCVYLHIGGCAGTRRWWAGSARGSRSCRLP CWAPGPGLISLPPSCPSVEQGLGGOLQGRSGERLGEHRYW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFERGC GGRGWVCAPPLNOPQCCCFSIKPBLKAKKK **SAPAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFERGC GGRGWVCAPPLNOPQCCCFSIKPBLKAKKKK DPSTRAMSVERGCRYFTDLVALAVVIITGCSTYQEAKSKKIMESFRINDVDGT **LTPPFTTPEWVKPCRQLPGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCSTYQEAKSKKIMESFRINDVDG ALVIRRGERKQVNAEEVVVGDLVEIKGGDRVFADLRIISAHGC KVDNSSITGSSEDFTSSPDCTHB\CKTYTINLYPGELLATVTV CLTLTAKRMAKKCHINKIAEVETLGSTSTICSDKTGTLTDNTM TVAHMWFNOLHRADTTEDGSGTSFDRSSITIUVALF*H\LLGFC NEPVFKGGQDNIPUKRDVARDSALLKCIBLSSGSWLLMR TVAHMSPNOLHRADTTEDGGGTSFDRSSITIUVALF*H\LLGFC NEPVFKGGQDNIPUKRDVARDSALLKCIBLSSGSWLLMR TVAHMSPNOLHRADTTEDGGGTSFDRSSITIUVALF*H\LLGFC NEPVFKGGQDNIPUKRDVARDSALLKCIBLSSGSWLLMR TVAHMSPNOLHRADTTEDGGGTSFDRSSITIUVALF*H\LLGFC NEPVFKGGQDNIPUTTDNLCKGLMSMIDEPRAAVPDAVG PEEGFPKGFAFCDDVNFTTDNLCVGLMSMIDEPRAAVPDAVG PEEGFPKGFAFCDDVNFTTDNLCVGLMSMIDEPRAAVPDAVG PEEGFPKKFAFCDDVNFTTDNLCVGLMSMIDEPRAAVPDAVG PEEGFPKKFAFCDDVNFTTDNLCVGLMSMIDEPRAAVPDAVG PEEGFPKKFAFCDDVNFTTDNLCVGLMSMIDEPRAAVPDAVG PEEGFPKKFAFCDDVNFTTDNLCVGLMSMIDEPRAAVPDAVG PEEGFPKKFAFCDDVNFTTDNLCVGLMSMIDEPRAAVPDAVG PEEGFPKKFAFCDD	1	1	ì	
AAHCPRDGNDHSLWRUNVGDPKSQWGKEFLIEKAVISBGFDVFA KKNQGILLEFYGD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM \text{PanligPlantlyklaykvkm\sthcqgpsclp\ctm} \text{PanligPlantlyklokvkm\sthcqgpsclp\ctm} \text{PanligPlantlyklokvkm\sthcqgpsclp\ctm} \text{PanligPlantlyklokvkm\sthcqgpsclp\ctm} \text{PanligPlantlyklokvkm\sthcqgpsclp\ctm} \text{D\QFL\cS\GpQEDESP\cks\tm\prnlt\purplykl\vtp} \text{D\QFL\cS\GpQEDESP\cks\tm\prnlt\purplykl\vtp} \text{D\QFL\cS\GpQEDESP\cks\tm\prnlt\purplykl\vtp} \text{D\QFL\cS\GpQEDESP\cks\tm\prnlt\pphin\lpp} \text{Q\sthchmorespect} \text{D\QFL\cs\GpQEDESP\cks\tm\prnlt\pphin\lpp} \text{Q\sthchmorespect\sthchmorespect\pphin\lpp} Q\sthchmorespect\pphin\sthchmorespect\pphin\sthchmorespect\pphin\sthchmorespect\pphin\sthchmorespect\pphin\sthchmorespect\pphin\pphin\sthchmorespect\pphin\sthchmorespec				DWRELNELGSKKDGERHAFILQDTKALHQVFEHMLDVSKLTDTI
KKNQGIL\EFYGD\DTALL\KLAQKVIM\STHCQGPSCLP\CTM \EARLIGFLRETFKGSTCR\DHENEL\VWNKQSV\PAHF\VAL\M GSKLEHLTLRMGVEWTSCCGELSFKKKTM\FPNLT\DVRB\VVT D\QFL\CS\GFQBDESF\CK*E\SGGA\VFLERRFRISAGGVWC SWGL\YNP\CLGSA\DKNSFKKGPSVAKVPPTR\DFHIN\LFP Q*SPWLRQHBGGNS*IFLPLLANGHLSFFACPARICRPLHFLPS EWATLRTL 5864 173 1013 PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG KLPPSIPPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY KLDMDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S HWSLSPLSCSC\GLIFNLSSFSPCSFG\PPPQVPSP\TESFFS MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPYNPFITSPPHTWS SLQFHSVTSPPPPAQOFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKLQPSSWLIWQQP 5865 568 1684 CLFGPRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVGMTC LSVCVCVQVGSWLCV\CVSMCACVSLCT\LGCCISMYTREHAC ACTRY*YYMCMS\VCTVSTCIDVRVCAHVCYMCHLGGX*AC TCV*MCVCMHEHVCMC\VCACSCVLL\/CRGHICM\MCMSAYICI /CVYVCVLCVWACMHENTCVWLVYG*ACTCVWMHM\CSCTCR\/C VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEGGLGGGFGOLQGRGGARATGERIGW GSPAAVCSRNCTVSPRRGADCFEAPVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIRPBLKAKKKK 5866 98 3197 ARPEVPAPPAWLSRRGARKNGKCBKDDDD LTPPPTTPEWKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGNLYLGIVLAAVVITTGCFSYYGAKSKIMESFRNVPQ QALVTREGEKMQVMAEEVVCRYNTDCVQGLTHSKAQE ILARDGPNA KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQE ILARDGPNA VPFLAVSFFILSLILGYTWLSTGGDRVPADLRIISAGI KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVKKFIAELEHFIQLITGV CLTLTAKMMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHWMFNOQTHEADTTEDGSTSFDKSSHTWALF+H\LLGFC NRPVFKGQDDNIPVLKRDVRGDASSBALLKCELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSTHFTEDDNDNRYLLVMKGABERILD RCSTILLGGKSQPLDEGRKRAPGONAYLELGGGGRVLAGFCHYLI RCSTILLGGKSQPLDEGRKRAPGONAYLELGGGLGERVLAGFCHYLI BEGGPFKGFAFDCDDWNFTTDNLCFVGLMSMIGPPRAAVPDAVG		i	<u> </u>	CGVGNMSANASDQERTPWHVTIKPKSQET\C\RGALISDQWVLT
KKNQGIL\EFYGD\DTALL\KLAQKVIM\STHCQGPSCLP\CTM \EARLIGFLRETFKGSTCR\DHENEL\VWNKQSV\PAHF\VAL\M GSKLEHLTLRMGVEWTSCCGELSFKKKTM\FPNLT\DVRB\VVT D\QFL\CS\GFQBDESF\CK*E\SGGA\VFLERRFRISAGGVWC SWGL\YNP\CLGSA\DKNSFKKGPSVAKVPPTR\DFHIN\LFP Q*SPWLRQHBGGNS*IFLPLLANGHLSFFACPARICRPLHFLPS EWATLRTL 5864 173 1013 PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG KLPPSIPPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY KLDMDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S HWSLSPLSCSC\GLIFNLSSFSPCSFG\PPPQVPSP\TESFFS MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPYNPFITSPPHTWS SLQFHSVTSPPPPAQOFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKLQPSSWLIWQQP 5865 568 1684 CLFGPRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVGMTC LSVCVCVQVGSWLCV\CVSMCACVSLCT\LGCCISMYTREHAC ACTRY*YYMCMS\VCTVSTCIDVRVCAHVCYMCHLGGX*AC TCV*MCVCMHEHVCMC\VCACSCVLL\/CRGHICM\MCMSAYICI /CVYVCVLCVWACMHENTCVWLVYG*ACTCVWMHM\CSCTCR\/C VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEGGLGGGFGOLQGRGGARATGERIGW GSPAAVCSRNCTVSPRRGADCFEAPVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIRPBLKAKKKK 5866 98 3197 ARPEVPAPPAWLSRRGARKNGKCBKDDDD LTPPPTTPEWKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGNLYLGIVLAAVVITTGCFSYYGAKSKIMESFRNVPQ QALVTREGEKMQVMAEEVVCRYNTDCVQGLTHSKAQE ILARDGPNA KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQE ILARDGPNA VPFLAVSFFILSLILGYTWLSTGGDRVPADLRIISAGI KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVKKFIAELEHFIQLITGV CLTLTAKMMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHWMFNOQTHEADTTEDGSTSFDKSSHTWALF+H\LLGFC NRPVFKGQDDNIPVLKRDVRGDASSBALLKCELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSTHFTEDDNDNRYLLVMKGABERILD RCSTILLGGKSQPLDEGRKRAPGONAYLELGGGGRVLAGFCHYLI RCSTILLGGKSQPLDEGRKRAPGONAYLELGGGLGERVLAGFCHYLI BEGGPFKGFAFDCDDWNFTTDNLCFVGLMSMIGPPRAAVPDAVG			1	AAHCFRDGNDHSLWRVNVGDPKSOWGKEFLIEKAVISPGFDVFA
RANLGFLRETFKGSTCR\DHENEL\VMNKQSV\PAHF\VAL\M GSKLEHLTLEMGVEWTSCCRGLSPKKKTM\FRNIT\DVRF\VTI D\QF\CS\GFQEDESP\CK*\SGQA\VFLERFRFLSAGGVWC SWGL\YMP\CLGSA\DKMSPKKGPSVAKVPPPTR\DHIN\LFP Q*SFWLRQFBEGSP\CK*\SGAQ\VFLERFRFLSAGGVWC SWGL\YMP\CLGSA\DKMSPKKGPSVAKVPPPTR\DHIN\LFP Q*SFWLRQFBEGMS*IFPLLANGHLSPFACPARICRPLHFLPS EWATLRTL				
GSKLEHLTLRRGVEWTSCCRGLSPKKKTM\FPRLT\DVRR\VVT D\QFL\cs\GPQEDESP\CK*E\SGGA\VFLERRFRLSAGGVWC SWGL\YRP\CLGSA\DKNS*EKGPSVAKVPPPTR\DHIIN\LFP Q*SPWLRQHPGGMS*IFLPLLANGHLSPFACPARICRPLHFLPS EWATLRTL 5864 173 1013 PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG KLPPSIPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY KLDNDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S HWSLPSLCSQC/GLIPALSSTSPFCSFG/PPPQVPSF/TESFFS MDSSDLPPSQAAPQAEPGPNSHLASAPPPYNPFITSPPHTWS SLQPHSVTSPPPPAQQPTLKXVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSSWLIMQQP 5865 568 1684 CLPGPRWGEGRRAGHTVGCIFFTATISHFKGGMYLCVCMCTC LSVCVCVQVGSWLCY/CVSMCACVSLCTC\ICRCISMYTRRHAC ACTRV*YYMCMS/VCTVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHENCMC/VCACSCVLL\CRGHICM/MCMSAYICI /CVYVCVLCVMACRMEMSTCVL\UVGFACTCVMEMM/GSCTCR/C VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSSCSRLP CWACPGLSLEGPSCPSVEQQLGGGPQQLQGRSGEARLGEHRGW GSPBAVCSRNCTVSPRRADDFEAPDVPKOPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK ARPEVPAPPAMLSRRGAKMGDKKDDKDSPKRNGKERRDLDDL KKEVAMTEHKWSVEVCKKYNTDCVQGLTTSKAGE ILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLTLGTVLAAVVIITGCFSYYQEAKSSKTMESFKNNVPQ QALVIREGEKMVANEEVVCKYNTDCVQGLTTSAAGE ILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLTLGTVLAAVVIITGCFSYYQEAKSSKTMESFKNNVPQ QALVIREGEKMVANEEVVCKYNTDCVGLTTSAAGE ILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLTLGTVLAAVVIITGCFSYYGEAKSSKTMESFKNNVPQ QALVIREGEKMVANEEVVCKNTEAVTFILGIITVANPVEGILAATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMMFDNQTHEADTTEDGSGTSFDKSHTWALF+H/LLGFC NEPVYKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSHETEDPDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEMKEAPQNAYLELGGLECVVLGFCHYYL PEGGPFKGFAPPCDDVNFTTTONLCFVGLMSMIGEPRAAVPDAVG				
D\QFL\CS\GPQEDESP\CK*E\SGGA\VFLERFFILSAGGVWC SWGL\YMP\CLGSA\DKNSFKKGFSVAKVPPPTR/DPHIN\LFP Q*SPWLRQHEGMS*IFLPLLANGHLSPFACPARICRPLHFLPS EWATLRTL 5864 173 1013 PLISVPQSLISLPQPLLCFPGGGEPSAPSPCLYSFLWACSFTMG KLPPSIPSSPLACULKNLKPLQLTPDLKPKCLIFFCNTAWPQY KLDNDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S HWSLPSLCSQC/GLIPNLSFSPPCSFG/PPPQVPSF/TESFFS MDSSDLPPSPQAAPRQABPGPNSHLASAPPPYNFFITSPPHTWS SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSSWLIWQQP 5865 568 1684 CLPGPRWGEGRAGHTTUGCIFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC CWACVCMHEHVCMC/VACASCVLL/CRGHICM/MCMSAYICI /CVYVCVLCWACMHEHVCMC/VACASCVLL/CRGHICM/MCMSAYICI /CVYVCVLCWACMHEHVCMC/VACASCVLL/CRGHICM/MCMSAYICI /CVYVCVLCWACMHEHVCMC/VACGSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCWACMHEHVCMC/VAGGGGGGGGGAGGARGERGERIGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFERGC GGRGWVCAPPLINGGCGGFSILBLKKKKK GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFERGC GGRGWVCAPPLINGPQCCCFSIKPBLKAKKK 5866 98 3197 ARPEVPAPPAWLSRRGAAKMGKKDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLITHSKAQE ILARGSPNA LTPPPTTPEWWKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNABEVVVODLVEIKGGRVPADLRI ISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAEIEHFIQLITGV AVFIGVSFILSLIGYTWLEAVTFLIGIIVANVPEGLATVTV CLTLTAKRMAKKNCLVKNLEAVETIGSTSTICSNKTGTLITONRM TVAHMMFDNQIHEADTTEDQSGTSFDKSSHTWALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSCSVKLMRE RNKKVABIPFNSTNKYQLSHHETDSPDNNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAPQNAYLELGGLGERVLGFCHYYL PEEQPFKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	1	1	1	
SWGL\YNP\CLGSA\DKNSPKKGPSVAKVPPPTR/DFHIN\LFP Q*SFWLRQHPGGMS*IFLPLLANGHLSPFACPARICRPLHFLPS EWATLRTL 5864 173 1013 PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG KLPPSIPPSSPLACVLKNLKPLQLDTPDLKPKCLIFFCNTAWPQY KLDNDSK*PENGTFEFSILQVLDNSCKKMGKWSEVPDVQAFF\S HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPPQVPSP/TESFFS MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPNNPFTTSPPHTWS SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSSWLIWQQP 5865 568 1684 CLPGPRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC LSVCVCVOVGSWLCVCVGNCACVSLCTC\ICRCISMYTREHAC ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMMMSTCVWLVYG*ACTCVWMHM/CSCTCR/C VHVCCMSMHAGECLCVYLHICGCAGTRRWAGSARGSRGSCRLP CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAMLSRRGAKMGDKKDDKDSFKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRYNTDCVQGLTTHSKAQEILARDGPNA LTPPPTTPEWKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGNNLVLIGIVLAAVVIITGCFSYYQEAKSSKIMESFKNNVPQ QALVIREGEKMQVNAEEVVVQDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESSEPGTNSPDCTHEINPLKTRNITFFSNNFVBGTA RGVVVATGDSTTVMGRIATLASGLEVKKTPIALEIHFIQLITGV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTCDNRM TVAHMMFDNQIHEADTTEDGSGTSFDKSSHTWVALF+H/LLGFC NRPVEKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSHTETEDPNDNRYLLVMKGAPERILD RCSTILLQGKGQPLDEEMKEAPQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVC	1	1	l	
Q*SPHLRQHPGGMS*IFLPLLANGHLSPFACPARICRPLHFLPS EWATLRTL 5864 173 1013 PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG KLPPSIPPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY KLDNDSK*PENGTFESTLQVLLDNSCHKMGKWSEVEDVQAFF\S HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPDQVPSP/TRSFFS MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPYNPFITSPPHTWS SLQFHSVTSPPPPAQQFTLKKVAGARGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSWLIWQQP 5865 568 1684 CLPGFRWGEGWRAGHTIVGCTFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSNICV/CVSMCACVSLCTC\ICRCISMYTRSHAC ACTRV*VYMCMS/VCTCVSTCTDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCWAMCMRMSTCVWLVYG*ACTCVWHMM/CSCTCR/C VHVCCMSHACCLCVYLHIGCGAGTRRWWAGSARGSRSCSRLP CWACPGGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAWLSRRGAAKMGNKKDDKDSFKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAVGIQATED DPSGDNLYLGIVLAAVUITGCFSYYQEAKSSKIMESFKKNVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGSSEPQTSPDCTHE\NPLKTRNITFFSNNFVBGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIALEIHFIQLLTGV AVFLGVSFFILSLIIGYTMLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKKMARKNCLVKNLEAVETLSSTSTICSDKTGTLTCDNRM TVAHMMFDNQIHEADTTEDQSGTSFDKSSTHWVALF+H/LLGFC NRPVFKGGQDNITPULKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKGQPLDEEMKEAPQNAYLELGGLGECKPLYJL PEEQFFKGFAFDCDDVNFTTDNLCFYGLMSMIGPPRAAVPDAVG	j	1	j	
Q*SPHLRQHPGGMS*IFLPLLANGHLSPFACPARICRPLHFLPS EWATLRTL 5864 173 1013 PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG KLPPSIPPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY KLDNDSK*PENGTFSFSILQVLLDNSCHKMGKWSEVPUVQAFF\S HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPDQVPSP/TRSFFS MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPYNPFITSPPHTWS SLQFHSVTSPPPPAQQFTLKKVAGARGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSWLIWQQP 5865 568 1684 CLPGPRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSNICV/CVSMCACVSLCTC\ICRCISMYTRSHAC ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCWAMCMRMSTCVWLVYG*ACTCVWHMM/CSCTCR/C VHVCCMSHACCLCVYLHIGCGAGTRRWWAGSARGSRSCSRLP CWACPGGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPPCCCFSIKPELKAKKKK 5866 98 3197 APBEVPAPPAWLSRRGAAKMGNKKDDKDSFKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAVGIQATED DPSGDNLYLGIVLAAVUITGCFSYYQEAKSSKIMESFKKNVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGSSEPQTRSPDCTHE\NPLKTRNITFFSNNFVBGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIALEIHFIQLLTGV AVFLGVSFFILSLIIGYTMLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLSSTSTICSDKTGTLTCDNRM TVAHMMFDNQIHEADTTEDQSGTSFDKSSTHWVALF+H/LLGFC NRPVFKGGQDNITPULKRDVAGDASESALLKCIELSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKGQPLDEEMKEAPQNAYLELGGLGECKLUMGCAPERILD RCSTILLQGKGQPLDEEMKEAPQNAYLELGGLGERVIGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFYGLMSMIGPPRAAVPDAVC	[SWGL\YNP\CLGSA\DKNSPKKGPSVAKVPPPTR/DFHIN\LFP
EWATLRTL PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG KLPPSIPPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY KLDNDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S HWSLPSLCSQC/GLIPNLSSFSPCSFG/PPPQVPSP/TESFFS MDSSDLPPSPQAAPQAEPGPNSHLASAPPPYNPFITSPPTWS SLQFHSVTSPPPPAQAPQAEPGPNSHLASAPPPYNPFITSPPTWS SLQFHSVTSPPPPAQAPQAERGHTVVGCIFFKTAIISHFKGGMYLCVCMCTC GSFSSNIKIQPSSWLLWQQP 5865 568 1684 CLPGFRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSWICV/VSMCACVSLCTC\ICGCISMYTREHAC ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLVWACMRMSTCVWLVVG*ACTCVWMHM/CSCTCR/C VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGFGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPBLKAKKKK 5866 98 3197 ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVANTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARGPNAA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVATGDRTVMGGIATLASGLEVGKTPIAEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKKMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMMFDNQIHEADTTEDQSGTSFDKSSHTWALP*H/LLIGFC NRPVFKGGQDNIFVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVABIPFNSTNKYQLSTHETEDPNDNYYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFFKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	l	1	l	O*SPWLROHPGGMS*IFLPLLANGHLSPFACPARICRPLHFLPS
173 1013 PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG KLPPSIPEDACVLKNIKPLQLTPDLKPKCLIFFCNTAWPQY KLDNDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S HWSLPSLCSQC/GLIPNLSSFSPCSFG/PPPQVPSP/TESFFS MDSSDLPPSPQAAPRQAEPGPNSHLASAPPYNPFITSPPHTWS SLQPHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPPSLSQIR*RL GSFSSNIKLQPSSWLLWQQP 5865 568 1684 CLPGPRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCHHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAWLSRGAAKWGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKPCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKMVPQ QALVIREGSKMQVNAEEVVVQDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGBRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSILLGYTWLEAVIFLIGIIVANVPEGILATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTTCSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSTHETEDPNDNYTLUVMKGAPERILD RCSTILLQGKEQPLDEEMKEAPQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVMFTTDNLCFVGLMSMIGPFRAAVEDAVG	i	İ		
KLPPSIPPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY KLDNDSK*PENGTTEFSILQVLDNSCHKMGKWSEVPDVQAFF\S HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPPQVPSP/TESFFS MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPNPFITSPPHTWS SLOPHSVTSPPPAQOFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSSWLIWQQP 5865 568 1684 CLPGPRWGEGWRAGHTVGCTFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC ACTRV*VYMMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMRMSTCVWLVYG*ACTCVMMEM/CSCTCR/C VHVCCMSMHACECLCVVLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAMLSRRGAAKMGPKKDDKDSFKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWKFCRQLFGGFSILLNIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVODLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVKKTPIAIEIEHFIQLITGV AVFLGVSFFILSLILGYTWLEAVFILGI IVANVPEGILATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQTHEADTTEDQSGTSFFKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHSTEDDNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFFKGFAFDCDDVNFTTDNLCFVGLMSNIGPPRAAVPDAVG		155	 	
KLDNDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPPQVPSP/TESFFS MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPVNPFITSPPHTWS SLQFHSVTSPPPPAQOFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSSWLIWQQP 5865 568 1684 CLPGPRWGEGWRAGHTIVGCTFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSWICV/CYSMCACVSLCTC\ICRCISMYTREHAC ACTRY*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMRMSTCVULVYG*ACTCVWMEM/CSCTCR/C VHVCCMSMHACECLCVYLVIUVYG*ACTCVWMEM/CSCTCR/C CWAPGPGLSLPGPSCPSVEQGLGGGPQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAMLSRRGAAKMGDKKDDDSPKNKGKERRDLDDL KKEVAMTEHKMSVESVCKKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKPCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGGFSYVQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPGTTSPDCTHE\NPLKTRNITFFSNNTVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIEHFIQLITGV AVFLGVSFFILSLILGYTWLEAVFFIGIIVANVPEGLAATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDYNFTTDNLCFVGLMSMIGPPRAAVPDAVG	5864	173	1013	The state of the s
HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPPQVPSP/TESFFS MDSSDLPPSPQAAPRQABFBGPNSHLASAPPPYNPFITSPPHTWS SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSSWLIWQQP 5865 568 1684 CLPGPRWGGGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMTTREHAC ACTRV*VYMCMS/VCTCVSTCIDVRVCABVCVYMCLCLGYA*AC TCV*MCVCMEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCWACMMSTCVWLVYG*ACTCVWMEH/CSCTCR/C VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPSPSCPSVEGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFERRGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KEVANTEHKMSVESVCRKYNTDCVQGLTHSKAQE ILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVITTGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNABEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGBSEPQTRSPDCTHE\NPLKTRNITFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIEHFIQLITGV AVFLGUSFFILSLILGYTWLEAVTIGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPPNSTNRYQLSTHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	1		1	
MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPYNPFITSPPHTWS SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSSWLIWQQP CLPGPRWGEGWRAGHTTVGCIFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCCYYMCLCLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWARCMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEQGLGGGGQQQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLMGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAMLSRGAAKMGDKKDDKDSPKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCPLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLBVGKTPIALBIEHFIQLITGV AVFLGVSFFILSLILGYTWLEAVFILIGIIVANVPEGLLATVTV CLTLTAKRMARRNCLVKNLEAVETLGSTSTICSDKTGTLTONRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*+/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKVQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAPQNAYLBLGGLGERVLLOFCHYYL PEEQFFRGFARFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	Ì	1]	
SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSSWLIWQQP 5865 568 1684 CLPGPRWGGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTRBHAC ACTRY*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMRMSTCVWLVYG*ACTCVMMHM/CSCTCR/C VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAMLSRRGAAKMGDKKDDKDSPKRNKGKERRDLDDL KKEVANTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRAITALASGLEVGKTPIALEIEHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLBLGGLGERVLGFCHYYL PEEQFFRGFAFFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG		1		HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPPQVPSP/TESFFS
SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSSWLIWQQP 5865 568 1684 CLPGPRWGGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTRBHAC ACTRY*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMRMSTCVWLVYG*ACTCVMMHM/CSCTCR/C VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAMLSRRGAAKMGDKKDDKDSPKRNKGKERRDLDDL KKEVANTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRAITALASGLEVGKTPIALEIEHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLBLGGLGERVLGFCHYYL PEEQFFRGFAFFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	1			MDSSDLPPSPOAAPROAEPGPNSHLASAPPPYNPFITSPPHTWS
GSFSSNIKIQPSSWLIWQQP 5865 568 1684 CLPGPRWGEGWRRGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C VHVCCMSMHACECLCVVIHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVITGCFSYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTUMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLITLTAKRMARKNCLVKNLEAVETLGSTSTCSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFFRGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG				
5865 568 1684 CLPGPRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC ACTRV*YYMCMS/VCTCVSTCIDVRVCAHVCVYMCLLCLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCWACMRMSTCVWLVYG*ACTCVWMEM/CSCTCR/C VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKK 5866 98 3197 ARPEVPAPPAWLSRRGAAKMGDKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQBILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVQDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLBLGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	1		1	
LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C VHVCCMSMHACECLCYYLHICGCAGTRRWAGSARGSRSCSRLP CWAPGPGLSLFGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQBILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVBGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG				
ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQBILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNNVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIEHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	5865	568	1684	CLPGPRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC
TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAWLSRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGATLCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	I			
TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAWLSRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGATLCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	1		1	ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC
/CVYVCVLCWACMRMSTCVWLVYG*ACTCVWMEM/CSCTCR/C VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAMLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLITAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	1			
VHVCCMSMHACECLCVYLHICGCAGTRRWAGSARGSRSCSRLP CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFSNNFVEGTA RGVVVATGGRTVMGRIATLASGLEVGKTPIAIEIEHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*+H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGPCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	I		j	The state of the
CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFSNNFVEGTA RGVVVATGGRTVMGRIATLASGLEVGKTPIAIEIEHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGPCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	1			
GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGPCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG		1		
GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGPCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG		1		
GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK 5866 98 3197 ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGPCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	ì			GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC
3197 ARPEVPAPPAWLSRRGAAKMGDKKDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGPCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG			l	1
KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	5066	00	2107	
LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATILASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKKMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	3000	30	3191	
DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*+H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	1		1	
QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLITLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*+H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG		1	1	
QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLITLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*+H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	1			DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ
KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLITAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG				OALVIREGEKMOVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC
RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG				KVDNSSLTGESEPOTESDDCTHE\NDLKTENTTERSNNFVEGTA
AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG				POTENTA DE DESTACTO DE LA COLONO DEL COLONO DE LA COLONO DEL COLONO DE LA COLONO DE
CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG				
TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG		1		
TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	}			
NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	1			TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC
RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	1		1	NR PUFKGGODNI PVI. KROVAGDA SESALLKCI ELS SGSVKLMRE
RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	1			DMYCOAPT DPMCTMVVOI CTUPPPDOMDMDVI.I.MVCADPDTI.D
PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	1			MANAMETALISTIKLIČESTUGI DELIMITET DO
PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG KCRSAGIKVIMVTGDHPITAKAIAKGVGIIFEGNETVEDIAARL	I			RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL
KCRSAGIKVIMVTGDHPITAKAIAKGVGIIFEGNETVEDIAARL	1			PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG
, 120-1 1 - 120-				KCRSAGIKVIMVTGDHPITAKAIAKGVGIIFEGNETVEDIAARL

SEO	Predicted	Predicted end	I having a seld respect to the self-time of the self-time
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ĺ	sequence	- Jodgesman	\=possible nucleotide insertion)
		 	NIPVSQVNPRDAKACVIHGTDLKDFTSEQIDEILQNHTEIVFAR
ŀ			TSPQQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGI
l l			AGSDVSKQAADMILLDDNFASIVTGVBEGRLIFDNLKKSIAYTL
1			TSNIPEITPFLLFIMANIPLPLGTITILCIDLGTDMVPAISLAY
			EAAESDIMKRQPRNPRTDKLVNERLISMAYGQIGMIQALGGFFS
1	1	1	YFVILAENGFLPGNLVGIRLNWDDRTVNDLEDSYGQQWTYEQRK
			VVEFTCHTAFFVSIVVVQWADLIICKTRRNSVFQQGMKNKILIF
			GLFEETALAAFLSYCPGMDVALRMYPLKPSWWFCAFPYSFLIFV
			YDEIRKLILRRNPGGWVEKETYY
5867	3	1485	LPGRRARGGRGLGWPPAQALDGSRMGKAKVPASKRAPSSPVAKP
İ		1	GPVKTLTRKKNKKKKRFWKSKAREVSKKPASGPGAVVRPPKAPE
			DFSQNWKALQEWLLKQKSQAPEKPLVISQMGSKKKPKIIQQNKK
1			ETSPQVKGEEMPAGKDQEASRGSVPSGSKMDRRAPVPRTKASGT
1			EHNKKGTKERTNGDIVPERGDIEHKKRKAK\GQPQPHPPR/IDI
1			WFDDVDPADIEAAIGPEAAKIARKQLGQSEGSVSLSLVKEQAFG
1		j	GLTRALALDCEMVGVGPKGEESMAARVSIVNQYGKCVYDKYVKP
1			TEPVTDYRTAVSGIRPENLKQGEELEVVQKEVAEMLKGRILVGH
			ALHNDLKVLFLDHPKKKIRDTQKYKPFKSQVKSGRPSLRLLSEK
			ILGLQVQQAEHCSIQDAQAAMRLYVMVKKEWESMARDRRPLLTA
		į	PDHCSDDA+QSCPAAAAAPLQRQCDQSQGQITSPQSGNSGETFS
			ESWQRGVAWCY
5868	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
1			AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
l			LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
1			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
			CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
			DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5869	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
		*	AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
1	,		LESRV*T\MTLDGHNLPSLVCVITGKGPLRBYYSRLIHQKHFQH
ł	[]		IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
1			CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
5870	2122	833	DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
1 3070	2122	633	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
	'		AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
	.		TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
	, ,		CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
			DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5871	. 3	3465	FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS
-	_	3.43	VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP
}			LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT
1		1	CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI
			KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS
			YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF
			CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ
]			L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR
[1		SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR
	}		FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG
[VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE
			KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI
			DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV
			FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR
			PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID
			DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA
			LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTBELPEFKS
		}	FEELEPPKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHEIL
			QKLNDCSCLASQAILLGILLKREGPNFITKEGTVSDHIERVYRR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1.	sequence		\=possible nucleotide insertion)
——	Doguesto		AGSQKLWSVVRRAASLLSKVVDSLAPSITNVLVQGKQVTLGAFG
	•		HEEEVISNPLSPRVIONIIYYKCNTHDEREAVIOOELVIHIGWI
1			-
		· ·	ISNNPELFSGTLKIRIGWIIHAMEYELQIRGGDKPALDLYQLSP
			SEVKQLLLDILQPQQNGRCWLNRRQIDGSLNRTPTGFYDRVWQI
	ŀ		LERTPNGIIVAGKHLPQQPTLSDMTMYEMNFSLLVEDTLGNIDQ
	i		PQYRQIVVELLMVVSIVLERNPELEFQDKVDLDRLVKEAFNEFQ
1	ł		KDQSRLKEIEKQDDMTSFYNTPPLGKRGTCSYLTKAVMNLLLEG
(!		EVKPNNDDPCLIS
5872	68	665	VQGYMYRFVIKINSCYSEKTSICRHRCCPELPATQPWPTPTVFF
			NIAIDSESLGCI\SFKLFADKV/PKRWKKNFVLLNTGEKVLGDK
	1		GPCFYRIIPG\LCQGGDFTHHNGTGGKSLYSKEFDDENFI/LKH
			TAPGVLSTANAGPTTNGSQFFICTAKTEDG*QHVVFGKVKDGMS
	1	1	IVEALERSGSRNGKTSKKITAANCGQL
5873	2240	506	RRPPEGGSGGGRRTRARMPLPWSLALPLLLSWVAGGFGNAASAR
			HHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCEATCEPGCKF
	1		GECVGPNKCRCFPGYTGKTCSODVNECGMKPRPCOHRCVNTHGS
		l	YKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCP
1		1	SSGLRLAPNGRDCLDIDECASGKVICPYNRRCVNTFGSYYCKCH
1		ł	IGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKC
			KOGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMK
			1 ~
			KKAKIKNVTPEPTRTPTPKVNLQPFNYEEIVSRGGNSHGG\KKG
ļ		1	NEEKMKEGLEDEKREEKALKD*HRRERPFRG\DVFFPKVNEAGE
			FGLIL\VQRKALTSKLEHKADLNISVDCSFNHG\ICDW\KQDR\
		<u> </u>	EDDFDW\NPADR\DNAI\GFY\MAVPGLWQGHK\KDIGRLKLLL
İ			PDLQPQSNFCLLFDYRLAGDKVGKLRVFVKNSNNALAWEKTTSE
1		1	DEKWKTGKIQLYQGTDATKSIIFEAERGKGKTGEIAVDGVLLVS
	<u> </u>		GLCPDSLLSVDD
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD
1			AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD
			VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD
1		<u> </u>	SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW
l		ſ	EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\
į			SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG
1			.KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI
		İ	QKNTPSPDVTLGTNPGTEDIOFPIOKIPLGLDLKNLRLPRRKMS
		ŀ	FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSOLFOTLFELET
1			ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL
l		İ	NMLLDKGAVKTKNCFFEIIKPFDKYIMRLODRLLKSVTPLLMAC
l .		1	NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGOTFSLAS
I		Į.	SFROEKIL*AVGLODIAPSPAAFPNFEDSTLFGREYIDHLKAWL
1			VSSGCPLOVKKAEPEPMREEEKMIPPTKPEIOAKAPSSLSDAVP
1			_ ~
1			QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN
1		1	SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV
i	!	1	RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR
1		Į.	APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP
ļ		1	QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE
1		1	KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK
1			FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME
1		1	GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEEAPA\PGRG
ļ			GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG
ŀ			RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS
I	ļ		KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK
I			GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL
			IFVF
5875	296	1848	LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA
3073	2,0	1040	LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP
1		1	1
			WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK
			VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL
	,	1	VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS
			VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS
	I	1	/SGDPSCPRRGAAPDIWPYPQQECLHSPNWQHQT\SHGTESSGS
L		<u> </u>	

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
"""	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
ŀ	sequence	Bedgettee	\=possible nucleotide insertion)
}	100420000	 	GLFALCTLDGTLKLMEEMEEADKLLWSVQVDHQLFALEKLDVTG
	•		NGHEEVVACAWDGQTYIIDHNRTVVRFQVDENIRAFCAGLYACK
			EGRNSPCLVYVTFNQKIYVYWEVQLERMESTNLVKLLETKP\ST
			TACCRSWAWILTTSL*LVPCFTKRSTIQTSHHSVLPQASRIPPS
			WTCLIAGEGFF*TPTLPPKGVFGSHCAAAGSITKO
5876	1122	224	HLPLGVPSKVAGAAAMEPQEERETQVAAWLKKIFGDHPIPQYEV
33.73		221	NPRTTEILHHLSERNRVRDRDVYLVIEDLKQKASEYESEAKYLQ
1			DLLMESVNFSPANLSSTGSRYLNALVDSAVALETKDTSLASFIP
			AVNDLTSDLFRTKSKSEEIKIBLEKLEKNLTATLVLEKCLOEDV
ł		1	KKAELHLSTER\AKVDNRRQNM\DFLKAKSEEFRFGIQAAGEQL
			SARGQ\DAFSVPIQSLVALIRENWPRLKQQTIPLK\KKLESYLD
			LMP\NPSHCSK*RIEBAK\RELA\SIEAELTRRVS\MMEL
5877	2030	1907	
3077	2030	130/	GTLGKMAASSSGEKEKERLGGGLGVAGGNSTRERLLSALEDLEV LSRELIEMLAISRNOKLLOAGEENOVLELLIHRDGEFOELMKLA
1			
1		•	LNQGKIHHEMQVLEKEVEKRDSDIQQLQKQLKEAEQILATAVYQ
			AKEKLKSIEKARKGAISSEEIIKYAHRISASNAVCAPLTWVPGD
			PRRPYPTDLEMRSGLLGQMNNPSTNGVNGHLPGDALA/RRKIAR
5878	950	2113	CPCSTVS/NGSQMTCR*INIILILQKSVCEL
3878) 950	2113	GLWKCMQLQGPHTHRVQP*PTPRQQGPQ\VPVAVIAGNRPNYLY
1	1		RMLRSLLSAQGVSPQMITVFIDGYYEEPMDVVALFGLRGIQHTP
			ISIKNARVSQHYKASLTATFNLFPEAKFAVVLEEDLDIAVDFFS
1 .	}	1	FLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLYRVETMPG
ŀ			LGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECII
			PDVSRSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSL
			KKEAYEVEVHRLLSEABVLDHSKNPCEDSFLPDTEGHTYVAFIR
			MEKDDDFTTWTQLAKCLHIWDLDVRGNHRGLWRLFRKKNHFLVV
5879	3	981	GVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
3079	,	901	RLTEAAAAGSGSRAAGWAGSPPTLLPLSPTSPRCAATMASSDED GTNGGASEAGEDREAPGKRRRLGFLATAWLTFYDIAMTAGWLVL
1	1		
			AIAMVRFYMEKGTHRGLYKSIQKTLKFFQTFALLEIVHCLIGIV
1			PTSVIVTGVQVSSRIFMVWLITHSIKPIQNEESVVLFLVAWTVT EITRYSFYTFSLLDHLPYFIKWARYNFFIILYPVGVAGELLTIY
1	* .	•	AALPHVKKTGMFSIRLPNKYNVSFDYYYFLLITMASYIPLFPQL
ľ	,		YFHMLRQRRKVLHG\G*L*KRMIK*SLQTRCFFQNNQDYLSPSF
}	1		NNKNKQLCEISWIVWFLKI
5880	1138	1324	SLWCLVAGGLGLGPSSQNPLQRAGILARPREARGTFSALTACSA
3000	1130	1324	SVTSKGKSSSGMWPSAASDRDSPVPLRPPGPVOLPSGTGWVLSD
1	,	*	*KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARASDVL
1		•	CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP
			DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWORYN
1			ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC
			AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER
1			AQSRIQELEEKVASLLHOVSWRODSREPDAGRIHAGSKTAKYLA
1	,		ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH
1			CLOCFSDEQGEELLRHVAECCO
5881	26	441	GGIHPSPTEAPRAOHLTMDCTWRILFLVAAATGTHAOVOLLOSG
	20	227	SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD
]			LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV
			HHCATDTV
5882	2407	2216	L
""	2407	2210	SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*IHSGE
			RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER
			MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG
			ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE
			ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ
			IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF
1 (
			TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ĺ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			PRFELILEMNVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALV
			SINQTIPNERTMQLLGQLQVEVENFVLRVAAEFSSRKEQLVFLI
]			NNYDMMLGVLM\E*ERAADDSKEVESFQQLLNARTQEFIEELLS
			PPFGGLVAFVKEAEALIBRGQAERLRGEEARVTQLIRGFGSSWK
l		ļ	SSVESLSQDVMRSFTNFRNGTSIIQGALTQLIQ\LYHRFHRV\L
[SQPQLRALPARAELINIHHLMVELKKHKPNF
5883	2	1374	EFPGRRFRAVMEAGAGAGAGAGWSCPGPGPTVTTLGSYEASEG
			CERKKGQRWGSLERRGMQAMEGEVLLPALYEEBEEEEEEEEVE
1			EEEEQVQKGGSVGSLSVNKHRGLSLTETELEELRAQVLQLVAEL
1		į	EETRELAGQHEDDSLELQGLLEDERLASAQQAEVFTKQIQQLQG
			ELRSLREEISLLEHEKESELKEIEQELHLAQAEIQSLRQAAEDS
	1		ATEHESDIASLQEDLCRMQNELEDMERIRGDYEMEIASLRAEME
			MKSSEPSGSLGLSDYSGLQEELQELRERYHFLNEEYRALQESNS
1	1		SLTGQLADLESERTQRATERWLQSQTLSMTSAESQTSEMDFLEP
			DPEMQLLRQQLRDAEEQMHGMKNKCQELCCELEBLQHHRQVSEE
}	ļ	İ	EQRRLQRELKCAQNEVLRFQTSHS\SPSHPLPPIPPSSPCLL*A
			LVVISALLWCWWAETSS
5884	4261	2522	GVLARASARLRVPLTGVRACAEPEVGAEPAKVAGAAEPDEDGGR
	1	·	SRLRDCGDYTPSERLGPKGAMLWFQGAIPAAIATAKRSGAVFVV
1			FVAGDDEQSTQMAASWEDDKVTEASSNSFVAIKIDTKSEACLQF
			SQIYPVVCVPSSFFIGDSGIPLEVIAGSVSADELVTRIHKVRQM
ł			HLLKSETSVANGSQSESSVSTPSASFEPNNTCENSQSRNAELCE
i			IPSTSDTKSDTATGGESAGHATSSQEPSGCSDQRPAEDLNIRVE
			RLTKKLEERREEKRKEEEQREIKKEIERRKTGKEMLDYKRKQEE
1			ELTKRMLBERNREKAEDRAARERIKQQIALDRAERAARFAKTKE
1		j	EVEAAKAAALLAKQAEMEVKRESYARERSTVARIQFRLPDGSSF
ı			TNQFPSDAPLEEARQFAAQTVGNTYGNFSLATMFPRREFTKEDY
[KKKLLDLELAPSASVVLLP/ALFINF*AGRPTASIVHSSSGDIW
ł			TLLGTVLYPFLAIWRLISNFLFSNPPPTQTSVRVTSSEPPNPAS
			SSKSEKREPVRKRVLEKRGDDFKKEGKIYRLRTQDDGEDENNTW
1			NGNSTQQM
5885	900	467	AAGGGRRSRLSRSWPTGPSKSPSGVRCCG\RR\AWEDKDEFLDV
			IYWFRQIIAVVLGVIWGVLPLRGFLGIAGFCLINAGVLYLYFSN
1		1	YLQIDEEEYGGTWELTKEGFMTSFA/IVHGHLDHLLHCHPL*LM
1	,		VYSSQVLPIQSKGPS
5886	86	1341	PFRGRALTLKKQPRPGVAPPSLGTCHKSDPGRPAAQSQPPSPGS
1		1	GTFGLLSFRMVRTKTWTLKKHFVGYPTNSDFELKTSELPPLKNG
			EVLLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVESKNVAL
1		1 .	PKGTIVLASPGWTTHSISDGKDLEKLLTEWPDTIPLSLALGTVG
	1	1	MPGLTAYFGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGC
		1	KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLEETLKKASPDGY
		1	DCYFDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGPLPPGP
1		1	PPEIGIYQELRMEAFVVYRWQGDARQKALKDLLKWVLELPYFVI
		İ	D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE
		1	NMPAAFMGMLKGDNLGKTIVKA
5887	1937	104	APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE
			RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP
1		1	PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS
1		1	ACSVPVVTGDSOFCSQKAVIYSLNFTANPPQRVFELVDQINPSI
			FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNAESY
1		1	VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP
		1	AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK
1		1	KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV
1		1	LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ
	1	1	ENTOPVPLSGNPGYVVGLPLAAGFOPHKGSGIIOTTNRYGOLTI
1		Ī	LHSTTEODCLALEGVRTPVLFGYTMOSGCKLRLTGALPCQLVAQ
			KVKSLLWGQGFPDYVAPFGNSQGP/ADMLDWVPIHFITQSFNRK
1		1	DSCOLPGALVIEVKWTKYGSLLNPQAKIVNVTANLISSSFPEAN
		1	SGNERTILISTAVTFVDVSAPAEAGFRAPPAINARLPFNFFFPF
		1	V
I	<u> </u>	l	l *

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
I .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Joquanoc	\=possible nucleotide insertion)
5888	375	2302	LLCRTPGVAMQRADSEQPSKRPRCDDSPRTPSNTPSAEADWSPG
1 3000	373	2302	
		· ·	LELHPDYKTWGPEQVCSFLRRGGFEEPVLLKNIRENBITGALLP
	1		CLDESRFENLGVSSLGERKKLLSYIQRLVQIHVDTMKVINDPIH
	<u> </u>		GHIELHPLLVRIIDTPQFQRLRYIKQLGGGYYVFPGASHNRFEH
1			SLGVGYLAGCLVHALGEKQPELQISERDVLCVQIAGLCHDLGHG
	1		PFSHMFDGRFIPLARPEVKWTHEQGSVMMFEHLINSNGIKPVME
			QYGLIPEEDICFIKEQIVGPLESPVEDSLWPYKGRPENKSFLYE
ŀ	1		IVSNKRNGIDVDKWDYFARDCHHLGIQNNFDYKRFIKFARVCEV
ł	İ		DNELRICARDKEVGNLYDMFHTRNSLHRRAYQHKVGNIIDTMIT
Ţ	1		DAFLKADDYIEITGAGGKKYRISTAIDDMEAYTKLTDNIFLEIL
			YSTDPKLKDAREILKQIEYRNLFKYVGETQPTGQIKIKREDYES
			LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQEKNPIDHVS
l			FYCKTAPNRAIRITKNQVSQLLP\EKFAEQ\LIRVYCKKVDRKS
l .	į		LYA\ARQYFVQW\CADR\NFT\KPQDGRCY*PPTP*HPQKKGW\
į	İ		NDSTFSPKIPTRLPRRLPKSRV\QLFKDDPM
5889	1831		
3003	1031	731	LPAACGRPVTARPRQAPEGRSGRPRDLDPYPPQVFPPRPDRVAI
	i	•	VTGGTDGIGYSTAKHLARLGMHVIIAGNNDSKAKQVVSKIKEET
İ		•	LNDKET*VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLLK
1			FGIFIL\DLASMTSIRQFVQKFKMKKIPLHVLINNAGVMMVPQR
Į			KTRDGFEEHFGLNYLGHFLLTNLLLDTLKESGSPGHSARVVTVS
	ļ		SATHYVAELNMDDLQSSACYSPHAAYAQSKLALVLFTYHLQRLL
			AAEGSHVTANVVDPGVVNTDLYKHVFWATRLAKKLLGWLLFKTP
			DEGAWTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLQQQ
			LWSKSCEMTGVLDVTL
5890	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
			GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
1			LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
1			ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
	. 1		PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
		•	RMGÁFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
			KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
			AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
:			LVRQIP\NTAIMMATYELVVYLLNG
5891	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
1 : 1			GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
			LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
]			ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
			PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
			RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
1			KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
} J			AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
	.		
5892	1764	270	LVRQIP\NTAIMMATYELVVYLLNG
2092	1/04	379	VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMQRLQVVLGHLRGPA
	i		DSGWMPQAAPCLSGAPHASAADVVVVHGRRTAICRAGRGGFKDT
1 l			TPDELLSAVMTAVLKDVNLRPEQLGDICVGNVLQPGAGAIMARI
1 1	i		AQFLSDIPETVPLSTVNRQCSSGLQAVASIAGGIRNGSYDIGMA
[CGVESMSLADRGNPGNITSRLMEKEKARDCLIPMGITSENVAER
[]			FGISREKQDTFALASQQKAARAQSKGCFQAEIVPVTTTVHDDKG
[ŀ		TKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSQVS
[DGAAAILLARRSKAEELGLPILGVLRSYAVVGVPPDIMGIGPAY
{ l			AIPVALQKAGLTVSDVDIFEINE\AFASQAAYCVEKLRLPP*EG
	ļ		*TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC
			7 7
5893			PCAIGSWNGSPLPVFEYPWGT
2623	3	1653	ILSKRRCQKAKTKELMAKKVAVIGAGVSGLISLKCCVDEGLEPT
		•	CFERTEDIGGVWRFKENVEDGRASIYQSVVTNTSKEMSCFSDFP
[MPEDFPNFLHNSKLLEYFRIFAKKFDLLKYIQFQTTVLSVRKCP
ľ			DFSSSGQWKVVTQSNGKEQSAVFDAVMVCSGHHILPHIPLKSFP
			GMERFKGQYFHSRQYKHPDGFEGKRILVIGMGNLGSDIAVELSK
[NAAQVFISTRHGTWVMSRISEDGYPWDSVFHTRFRSMLRNVLPR
			TAVKWMIEQQMNRWFNHENYGLEPQNKYIMKEPVLNDDVPSRLL
		}	CGAIKVKSTVKELTETSAIFEDGTVEENIDVIIFATGYSFSFPF
LL			

Predicted Predicted en No: Incleotide No: Ocation Oc				
No. nucleotide corresponding to first amino acid residue of amino acid residue of amino acid sequence https://doi.org/10.0000/10.000000000000000000000000000	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
location coffeet main acid main ac				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first maino acid serious of serious colong colon	NO:			
to first smino acid seidus of smino acid sequence seque	1			
amino acid		corresponding	1	
residue of anino acid sequence (2000,)-possible nucleotide deletion, 2000, -possible nucleotide deletion, 2000, -possible nucleotide deletion, 2000, -possible nucleotide insertion, 2000, -possible nucleotide insertion, 2000, -possible nucleotide insertion, 2000, -possible nucleotide insertion, 2000, -possible nucleotide insertion, 2000, -possible nucleotide insertion, 2000, -possible nucleotide insertion, 2000, -possible nucleotide insertion, 2000, -possible nucleotide insertion, 2000, -possible nucleotide insertion, 2000, -possible nucleotide, 2000, -possible,		to first	amino acid	
amino acid sequence Codon, /=possible nucleotide deletion, possible nucleotide insertion		amino acid	residue of	
amino acid sequence Codon, /=possible nucleotide deletion, possible nucleotide insertion		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Appessible nucleotide insertion	Ì		sequence	Codon, /=possible nucleotide deletion,
LEDSLWKYENNWISLYKYIFPAILLOKSTIACIGLIQPIGSIFPT RELOARWYTRYKGICLSPERTMWINI IKRNEKRIDLIGFGENS OTLOTNYOVLOBILALEIGAKPOFCSILEKOPKLAVRLYFGICON SY*RILOPOGMEGRANIFTYOKRILLIKHAKKESJKWVRE SY*RILOPOGMEGRANIFTYOKRILLIKHAKKESJKWVRE PILKILIGILAWVARPY COLONS HERSCOGWILDPITTKERHILEIJULAGPILITEKRICARVORE HERSERDVVVVLBDIOLDIGISTOQVOPDOPKKOKILVEBMAPL KOVORGOVHBIEGUYKPERKIBERTERIOKLIVVVDSCORVES SCKISEPMEANINGSINLEHAGAKPKEKIEKUSFROKKILVEBMAPL LIEHASTITOKKICSSINCOSSISIORIKKUS-PRINKIVGCVHGV LICKAPGRSSHLVRHOKIHLIGBKYCGCECKYFGNAGLLEHIR, HTTEREPYLCHOKORVERRESHENTRERINKILVVTDSCORVES SCKISEPMEANINGSINLEHAGAKPKEKIEKUS-PROKAILGYHAK HTTEREPYLCHOKORVERRESHENTRENKILVTSTOCHOV LOKAPGRSSHLVRHOKIHLIGBKYCGCECKOKT SINDLIRHHIHTHO REPPKENTICKARAFINSHLAGHVITHBEKEYYCGCECKCKOKT FSOALLLITHIGRIHSHISKSHGCHECKASTSITSDLIRHHIHTHO REPPKENTICKARAFINSHLAGHVITHBEKEYYCGCECKCKOKT FSOALLLITHIGRIHSHISKSHGCHECKASTSITSDLIRHHIHTHO REPPKENTICKARAFINSHLAGHVITHBEKEYYCGCECKCKOKT FSOALLLITHIGRIHSHISKSHGCHECKASTSITSDLIRHHIHTHO REPPKENTICKARAFINSHLAGHVITHBEKEYYCGCECKCKOKT FSOALLLITHIGRIHSHISKSHGCHECKASTSITSDLIRHHIHTHO REPPKENTICKARAFINSHLAGHVITHBEKEYYCGCECKCKOKT FSOALLLITHIGRIHSHISKSHGCHECKASTSITSDLIRHHIHTHO REPPKENTICKARAFINSHLAGHVITHBEKEYYCGCECKCKOKT FSOALLLITHIGRIHSHISKSHGCHECKASTSITSDLIRHHIHTHO REPPKENTICKARAFINSHLAGHVITHAGHERYKUTSPOLITHOMALIS ROLOCHAPATERSHAMATINANIAGAGUALARAFINANI				
RELOARWITEVEKGLICSLESERTMAMDI I KENERRI ILLFGERSOS OTLICITYVOLLOBLALE IGARDPOESLE PROPILARATHYSPOCH 8 Y* TRILVOPOOMBGARNAI FTOKORI LIKELIKTRALKOBSNIFSVS FILKILI GLLAVVAPPFY COLOMS 174 1673 PYSEKEVLONKESSIKI GARTALVSAHISLAPIALKESLEVVER PRESENTAVICA BOLOLOGISTOS GORGODEL CALEPROLIKE PLANTESCHEVER RIBELCOGNICOPETETETETI LILLULGOPIA I LEVELGARVOBE HESERDIVAVUE BOLOLOGISTOS GORDODEO PRIKKEL LIVESMAPL KOVOGOOVAHEGEVI KERKEKSERTITENOKLI VYTDEGGRVES SCHISESPHEAINISORI RUEHDARVEKSTEV KYCERER SOR FOHLD LIEHASTITICKKI CESDVCOSSILIGHKKYLIS PERVIOC (HOV LIEHASTITICKKI CESDVCOSSILIGHKKYLIS PERVIOC (HOV LIEHASTITICKKI CESDVCOSSILIGHKKYLIS PERVIOC (HOV LIEHASTITICKKI CESDVCOSSILIGHKKYLIS PERVIOC (HOV LIEHASTITICKKI CESDVCOSSILIGHKKYLIS PERVIOC (HOV LIEHASTITICKKI CESDVCOSSILIGHKKYLIS PERVIOC (HOV LIEHASTITICKKI CESDVCOSSILIGHKKYLIS PERVIOC (HOV LIEHASTITICKKI CESDVCOSSILIGHKKYLIS PERVIOC (HOV LIEHASTITICKKI CESDVCOSSILIGHKKYLIS PERVIOC (HOV LIEHASTITICKKI CESDVCOSSILIGHKYLIS PERVIOC (HOV LIEHASTITICKKI CESDVCOSSILIGHKYLIS PERVIOC (HOV LIEHASTITICKKI CESDVCOSSILIGHKYLIS PERVIOC (HOV LIEHASTITICKKI CESDVCOSSILIGHKYLIS PERVIOC (HOV LIEHASTITICKKI CESDVCOSSILIGHKKYLIS PERVIOC (HOV LIEHASTITICKKI CESDVCOSSILIGHKYLIS PERVIOC (HOV REPPEKCI I COKARPELMSH HAGE SENDIC CECKTIC CHECKTOST REPPEKCI I COKARPELMSH HAGE SENDIC CHECKTOST REPPEKCI I COKARPELMSH HAGE SENDIC CHECKTOST REPPEKCI I COKARPELMSH HAGE SENDIC CHECKTOST REPPEKCI I COKARPELMSH HAGE SENDIC CHECKTOST REPPEKCI I COKARPELMSH HAGE SENDIC CHECKTOST REPPEKCI I COKARPELMSH HAGE SENDIC CHECKTOST REPEKTOLOGIS PERVES SENDIC CHECKTOST REPEKTOLOGIS PERVES SENDIC CHECKTOST REPEKTOLOGIS PERVES SENDIC CHECKTOST REPEKTOLOGIS PERVES SENDIC CHECKTOST REPEKTOLOGIS PERVES SENDIC CHECKTOST REPEKTOLOGIS PERVES SENDIC CONTROLLOM REPEKTOLOGIS PERVES SENDIC CHECKTOST REPEKTOLOGIS PERVES SENDIC CHECKTOST REPEKTOLOGIS PERVES SENDIC CONTROLLOM REPEKTOLOGIS PERVES SENDIC CONTROLLOM REPEKTOLOGIS PERVES SENDIC CONTROLLOM REPEKTOLOGIS PERVES SENDIC CONTROLLOM RE	<u> </u>	, sequence		LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIOPLGSIFPT
GTLQTNYDVLOBIALEICAEPPGSLLFKOPKLAVELYFOCOM SYSYELVOPOOMEGRANIFTOKORILKPATRIAVENSHEVS FILKILGILAVVARPY COLORS 174 1673 PYSPKRVIONESSIKUGARRALVSANSLAPANLKKEGLRVVRE PILKILGILAVVARPY COLORS REPERIOVAVVLEDLOLDIGSTOQVDOPKKKILVERMAPL KRVEDOQVENEGSUTYKERKILEILULAPATLEPHALLAV KRVEDOQVENEGSUTYKERKILEILULAPATLEPHALLAV KRVEDOQVENEGSUTYKERKILEILULAPATLEPHALLAV KRVEDOQVENEGSUTYKERKILEITAOKALVUTSEKAPL LIGHASTITIGKIKULGESDVOGSSLIONEKKILSPACKSERGORFICHLID LIGHASTITIGKIKULGESDVOGSSLIONEKKILSPACKSERGORFICHLID LIGHASTITIGKIKULGESDVOGSSLIONEKKILSPACHSKOSERGORFICHLID LIGHASTITIGKIKULGESDVOGSSLIONEKKILSPACHSKOSERGORFICHLID REPPKKINICOKARPRIASHLANDRIHAGRIPTIEMEKEVPOCSECCIONET SOALDLITHIGKIR HENKSHOCHEGGRAPSITEDLIRHRIHTG EXPPKKINICOKARPRIASHLANDRIKKILSPACHSCOLOCHAPROR RELPOSOOPHOLITHIGKIR HENKSHOCHEGGRAPSITEDLIRHRIHTG EXPPKKINICOKARPRIASHLANDRIKKILSPACHSCOLOCHAPROR RELPOSOOPHOLITHIGKIR HENKSHOCHEGGRAPSITEDLIRHRIHTG EXPPKKINICOKARPRIASHLANDRIVARIKKILSPACHSCOLOCHAPROR RELPOSOOPHOLITHIGKIR HENKSHOCHEGGRAPSITEDLIRHRIHTG EXPPKKINICOKARPRIASHLANDRIVARIKKILSPACHISTOCHEDOLOCHAPIT RENVPULGUBGRYLIPSTALIVILVOKOKKIR BUNGSUDLINOKIEKE PRINTINICOGTOSYOTATETKAL VEGGLIPSTOLISTICHILDISIS ROKALSPIEDPERELATLSEELIAMAVTARKEGEBIPPIREQO NOVLPVAGERNULTIANILVILVOKOKKIR BUNGSUDLIRHVILKOROPUPSI ROKALSPIEDPERELATLSEELIAMAVTARKEGEBIPPIREQO NOVLPVAGERNULTIANILVILVOKOKKIR BUNGSUDLIRHVILKOROPUPSI ROKALSPIEDREGERIATLSEELIAMAVTARKEGEBIPPIREQO TVEOLAKERHOCHERYTOPOLINKTI, OLDIVOKARVILLIANI LIVKHRISTSDIPERTYTPOLINKTI, OLDIVOKARVILLIANICOKARVILL				A FLOADWYTRYFKGLCSLPSERTMMMDI I KRNEKR I DLFGESOS
SY*RILYGEQMGARNALFTGKGRILKEFALKOSSISFSYS			}	
FILERIEGILAWVAPP\COLOMS		Į.		
174 1673 PRYSPERVLONESSIKLIOMYCAIVSAHSIAPIALKKEGIGWYGE DHYSTRROGFIGLOSKIKLOGUPTOLOGYROUNGETTOPERALS RLERICOGUPLOPETTYKERICETORPERALS RLERICOGUPLOPETTYKERICETTOPERALS RLERICOGUPLOPETTYKERICETTOPERALS RUSHERICHTOLOGUPTOLOGYROUNGETTOPERALS ROKISEFMEANINGUPLOLOGUPTOLOGYROUNGETTOPERALS ROKISEFMEANINGUPLOLOGUPTOLOGYROUNGETTOLOGYRUS SORKISEFMEANINGUPLOLOGUPTOLOGYROUNGETTOLOGYRUS SORKISEFMEANINGUPLOLOGUPTOLOGYRUS SUNGKLEYERIA LIEBASTHTOKKICESDVCQSSIJTGHKKVLS*PERVOLOC\HOV LOKAFORSSHUVANOKIHLGERPYCCHECOKYPSCANOGLEHIA I HITGERPYLCHOGUNFRASSILARRORI HAGBEE CEKEKOKY PSQALLITHEGRIPYCORECOKYPSCANOGLEHIA I HITGERPYLCHOGUNFRASSILARRORI HAGBEE CEKEKOKY PSQALLITHEGRIPYCHOGUNGOKAPSIJTGHLI RRHINGUPLOF ERPPKCNICOGARGYRINSHLAGUPYLINERERYCCSGCOAFFROR SOLLOGOKYHHKOKLA PSGALLATHEGRIPYSSPAPEPPSPYPHYLAMSHRESRHFINORGIHGE MELFYSDGYPGCLPYLAAAGRARGRABULISTYGPEDCVYPFTL RRHYPVLQLDSGYPGCLPYLAAAGRARGRABULISTYGPEDCVYPFTL RRHYPVLQLDSGYPGCLPYLAAAGRARGRABULISTYGPEDCVYPFTL RRHYPVLQLDSGYPGCTSPASALTYPLLQDAYTHYELDELSALHSW PGTILSTO\SPOCKARARUTHALDYTANUPHLGHI IGCULSADVPRAK ROKELSFIEPEELELATISEESILAMAVTAMKERIPPLEDELSPLIPROQ NVJLPVAGERBVLITTALPYVNVPHLGHI IGCULSADVPRAK ROKELSFIEPEELALTISEESILAMAVTAMKERIPPLEDRACO NVJLPVAGERBVLITTALPYVNVPHLGHI IGCULSADVPRAK ROKELSFIEPEELALTISEESILAMAVTAMKERIPPLEDRACO NVJLPVAGERBVLITTALPYVNVPHLGHI IGCULSADVPRAK ROKELSFIEPEELALTISEESILAMAVTAMKERIPPLEDRACO NVJLPVAGERBVLITTALPYVNVPHLGHI IGCULSADVPRAK ROKENTLILACTORYSTATUTHATUTAL SERVICATUT ROKENTISPOLOGUNGATATATATATATA SERVICATUT ROKENTISPOLOGUNGATATATATATATATATATATATATATATATATATATAT	1			
DHYSTWRGFKLGGNSKOLGOPPLCKOPROLEXEETTOPREAL RERELCQWLOPPDPEKRKHILELULEGE) LILIPEKELOARVOEN HPEGREDVVVLEDDLQLDLEGGQOVDPDPEKRKILVERMAN KOVQEQVENTEREKUTESETTERGKLLVVTDECGRVES SGKISEPMEANNGSNLERHQAKPEKIETYKCSERGEPICHLD LIERASTHTOKKLCSDVCGSSLTOHKKVLS*ERKVIQC/LIGU LIERASTHTOKKLCSDVCGASSLTOHKKVLS*ERKVIQC/LIGU LIERASTHTOKKLCSDVCGASSLTOHKKVLS*ERKVIQC/LIGU LIERASTHTOKKLCSDVCGASSLTOHKKVLS*ERKVIQC/LIGU LIGKAFQRSSHLVAHGKILGHENFYCCHCGKVSFSCANGALLEHLE THTGEKFYLC'HCGKNFRSSHLERHGRINGHENGEPCEKKEKYL FSQALLTHEIGH.HSHSKSNGCHGCKGAFSITSDLIRHKHINTG EKPPKCH.COCAPRINSHLAGUVIINERKFYCCSECGEAFRGR SGLFOGGYHHMIKKLA HEILGAIFFYPPGSPWPPPLLYHMSHKKSRHFINGGHEDCVYPFLT RERVPLOLDSGNYLFSTSALCRYFP_LLIGUSQDDLINGKHEN PREVPLOLDSGNYLFSTSALCRYFP_LLIGUSQDDLINGKHEN PREVPLOLDSGNYLFSTSALCRYFP_LLIGUSQDDLINGKHEN PREVPLOLDSGNYLFSTSALCRYFP_LLIGUSQDDLINGKHEN PREVPLOLDSGNYLFSTSALCRYFP_LLIGUSQDDLINGKHEN PROVID-PLAGETSLADIVLKGALYPILLOPATLPEELSALHHM FOTLSTOLDEFORARETHEN COGNAL BENDELWAG REGILSPIEPEEELATLSEELIAMATTAMKKGLESLPILPEQO NPULPVAGERRVLITSALPVANVPHLONIIGCVLSADVPARYS RIKGWATILLCETDBYCTATETKAL\EECITPGEICDRYHIIHA DIYARWISPISPITGRTTTPQQ\TKIT\QDIFQLLKGRECKGK NAVELKKEQCKVCRSCPVVQSSQHIFILDLPKLEKRLEBMIGHT PROSMITHAOPITTPGGTRWSFRROY-TEDLK\KNORPGTPE GFEKK\VFYVVFDATIGGLSTTANATOORERWN\KNEPQVDLTA PRAKANDVPFBSLUFPFSSALGABNYTL\VYLREGKGYPEM ANDENTANOPITTPGGTRWSFRROY-TEDLK\KNORPGTPE GFEKK\VFYVVFDATIGGLSLHTANTOORERWN\KNEPQVDLTA KYSKSRGVGVFROMAHDTGIPDISRFYL\UIRPEGK\DAA FRWTDLLLKNINS,BLINNLGNFINAAGGRAFVTLEAHALISVEL QPYMPTVSATIOAOLOLPPPACSILLITNICTLEAGHOITONA KYSKSRGVGVFROMAHDTGIPDISRFYL\UIRPEGK\DAA GROYL\QVSEMP\RIKKSRADRAATVYLVVQOKKOG BDVLGSVRRTJTHIDHORLEW LIPOLGERIDLISELELAPLEAGRAOTATEAGRAFTHEALISVEL QPYMPTVSATIOADCLAPPPLISTSALLTYTARCQIOA NELVESDVTGCNIVERIAARGARGRAFVLISTVGPBDLVVPPITARROQIOA NELVESDVTGCNIVERIAARGARGRAFVLISTVGPBDLVVPPITARROQIOA NELVESDVTGCNIVERIAAGRAAGRAFAREAULTTARLDAHALISVEL QPYTTYNATOORERWN\LIPOLGPATTARLOQIOA NELVESDVTGCNIVERSTALGTVFPLLISTENGLESLPPLRPQ NPULPVAGERNVLITASALGYPTLAAGRAFTHESLESPLLEPD REKVERPARFORKKKX REGREERASTANTILVEGELAPPLAGETTE REKVPLOLLDBOTTERTAALIS				
RIBELCOGNILOPETITISHILDILOTEGISTIC TITEMACLIA REPREDIVATIVA LEGIOLOLOLOGISTO CONTROLOGISTIC STATEMACH HPESERDAVATION CONTROLOCOME SIGNATUR SIGNATUR SIG	5894	174	1673	
HPSSRBUVVVLBELQLDLGETGQQVPDOPKKQKILVERMAPL KGVQEQQVMERGEVTKPRKEKGERTRIENKLYVDSCGRVES SGKISEPMBANNBGSBLRHGARPKEKKEYKCSBREQRFTQHLD LEHASHTHGEKKLCESDVCQSSLIGHKKVLKE LOKAFQRSSHLVPHQKILLGBLVQSSSLIGHKKVLKEKPYCQNSCGKVPSCNAGLLEHLR LOKAFQRSSHLVPHQKILHGRKEYCQNSCGKVPSCNAGLLEHLR HTTGEKPYLCILOCKNFRRSSHLARHQRIESCEGKECKKT PSQALLITHER HISHSKSHLAGHERGKINGCAFFGLRYGK SGLEQURGYRHKOKLA SGLEQURGYRHKOKLA 5895 2967 86 HPSLLGAIFFYPPPSSPWPPLYLFWNSHKKSRIFINGRGHGE RAFLQPTISAALYTILVVQGKKO\BDULGSKAFGING MELVYSGDYGCLEVLAAAGRARGRAEVLISTVGGEDCVVPPLT RRVYVLQLDGGNYLFSTAALCRYFF\LLSGMEGODLTNOMLEM BETLLQPTISAALYTILVVQGKKO\BDULGSVRRTLTHIDHSLS RQ\NCPPLAGETESLADIVLMGALFPLLQDPAYLPEELSALHSW FOTTLST\\SPCPANARRILVKQ\QQUALALYPYLQKDPQPSFA BGKGLSPIRPESELATLSEERIAMVTAWRKGLESLPPLRQQ NPULPVAGGRWNLTSALPYVANVPHLGNI LQYPLQKDPQSFA BGKGLSPIRPESELATLSEERIAMVTAWRKGLESLPPLRQQ NPULPVAGGRWNLTSALPYVANVPHLGNI LQYLKRGPVLDQ TVEQLRCERKCAFF\LLDGTPSTCTATTSTKAL\ESCLTPQCI COKKHI HA DIY\RWFNISPDIFGRTTTPQO\TKIT\QDIFQCLKKGPVLDQ TVEQLRCERKCAFF\LLDGTPSTCTATTSTKAL\ESCLTPQCI COKKHI HA DIY\RWFNISPDIFGRTTTPQO\TKIT\QDIFQCLKKGPVLDQ TVEQLRCERKCAFF\LLDGTFSFKYLDLKKGNFGTPS GFBK\VFYVWFDATIGYLSTLANYTDQWERW\NRPGTPS GFBK\VFYVWFDATIGYLSTLANYTDQWERW\NRPGTPS GFBK\VFYVWFDATIGYLSTLANYTDQWERW\NRPGTPS RYPSVLLLDRSHAMVS\LLNLGGGAARGARGAFTXLLTSTLANYTDQWERW\NRPGTPS RYPSVLLDRSHAMVS\LLNLGGGAARGARGAFTXLLTST\LYBCDCVVPLT TYPDQRELLA\BYVTLEGGIYYQ\LLFURAFTXRAQCAYFTULAYTARQOLDA LDDBYTYGANI VRELKAQKADKNEVAASEVAKLDLKKQLAVASG KPPRAPKGKKKX RRVPVLQLDESLAQRTGGGAKTSFKRAVVTAALGAUSAL LADBYTYQANI VRELKAQKADKNEVAASEVAKLDLKKQLAVASG KPPRAPKGKKXX RRVPVLQLDESLAGRTSGGAARGARGARGATYTLAYQCDCVPFLT RRVPVLQLDESLAGRTSGAARGARGARGARGAPTT\LYGKGDCDCVPFLT RRVPVLQLGGERVLLTTSALPYVNOPHLIGHI GCULSADVFARYS GKGLSFIEREERIAALTSELFIAMATVAMREGLEDPLRPQO NPVLPVAGERNULTTSALPYVNOPHLIGHI GCULSADVFARYS RRQWNTULTACTOTSYCTATTRIKALPESLOPLAYDCOCKYCKTI NAVELKKPQCKVCRSCPVVQSSCHLIDLPKLEKRLESDLPRLPQO GFBK\VFYVWPDATIGYSI TRANTYDQWERW\RNFGGDDLTNQALLBW PF\AKDDAVPFBLKVPSSALGAGADNTL\VSHLARPLESLPPLRPQO GFBKV\VFYVWPDATIGYSI TRANTYDQLKKWN\RNFGTPP-E GSDWTTNAGT TTPOPQOTKLTY,	İ	}		DHYSTWBQGFKLQGNSKGLGQEPLCKQFRQLRYEETTGPREALS
KOVQEQQVEHECEVTEPEKEKGEETITENGKLIVVTDSCGRVES SGKISEPMEANINGESKLERHORPEKELTEVTEOPERGFIGHIGH LIEHASTHTGKKLCESDVCQSSSLIGHKVILA* EEKVIQC/HGV LIGKAFQRSSHLVPRIQKIHLGEKEVQCNGCVGNGALLEHLE HTGERFYLCHCOKNFRRSSHLNRHQRIHSQEEPCBCKECGKT PSQALLITHERHIBIKSHQCHCGKAFSLTSDLINHHRHITG EKPFKCNICQRAFFELNSHLAGVRIHSEEPCSCCSCAFFQR SGLPQHQRYHKKOKLA 86 HPSLLGAIPPPPPSSPWPPPLYLFWNSHRKGRHFINQRGIHGE RPKYPVLQLGBGNYLSTSTALTGYPFLLSEWGODDLINQMLEN ERTELOPTISAALYYL/WYQGKKG\BDULGSVRRTUTHIBHSLS RQ\MCPPLAGETESLADIVINGALYPHLQDFSGODDLINQMLEN ERTELOPTISAALYYL/WYGKKG\BDULGSVRRTUTHIBHSLS RQ\MCPPLAGETESLADIVINGALYPHLQDFSGODDLINQMLEN ERTELOPTISAALYYL/WYGKKG\BDULGSVRRTUTHIBHSLS RQ\MCPPLAGETESLADIVINGALYPHLQDFSGODDLINQMLEN ERTELOPTISAALYYL/WYGKKG\BDULGSVRRTUTHIBHSLS RQ\MCPPLAGETESLADIVINGALYPHLQDFSGODDLINQMLEN ERTELOPTISAALYYL/WYGKKG\BDULGSVRRTUTHIBHSLS RQ\MCPPLAGETESLADIVINGALYPHICATORYDGODPSPA ERTELOPTISAALYYL/WYGKKG\BDULGSVRRTUTHIBHSLS RQ\MCPLAGETESLADIVINGALYPHICATORYDGODPSPA ERTELOPTISAALYYL/WYGKKG\BDULGSVRRTUTHIBHSLS RQ\MCPLAGETESLADIVINGALYPHICATORYDGAPAYS RHAGWNTLLIGGTBYGTATTERA\COMPARAYS RHAGWNTLLIGGTBYGTATTERA\COMPARAYS RHAGWNTLLIGGTBYGTATTERA\COMPARAYS RHAGWNTLLIGGTBYGTATTARATORYDGWEARAGODCHGGKGLI NAVELKKPQCKVCRSCPVVGSGOHLFLDLEKEKALEEWIGGRU RYAPKSRBGVGVFROM\AHDTIOTPDISRFYLLYRBGGC RYPSERBGKKKC RGCHSTBERGYRGTYTCHAVRIAALISVHL RGWYT\QVAEPPW\RITGHTPDISRFYLLYRBGGC RYPSERBGKKKK RGCHSTBERGARTUTTARAQCANTSYRAWALLDAWRALLSVHL RGWYT\QVAEPPW\RITGHTSPAGCANTSYRAWALLDAWRALLSVHL RCKLENDOLGSRRTTTTARAQCANTSYRAWALLDAWRALLSVHL RCKLENDOLGSRRTTTTARAQCANTSYRAWALLDAWRANS RCKGLSFIBERGETALBATTARAKLLESLEPDERQ RCKLENDOLGSRRTTTTARALLSVHL RCKLENDOLGSRRTTTTARALLSVHL RCKLENDOLGSRRTTTTARALLSVHL RCKLENDOLGSRRTTTTARALLSVHL RCKLENDOLGSRRTTTTARALLSVHL RCKLENDOLGSRRTTTTARALLSVHL RCKLENDOLGSRRTTTARALLSVHL RCKLENDOLGSRRTTTARALLSVHL RCKLENDOLGSRRTTTARALLSVHL RCKLENDOLGSRRTTTARALLSVHL RCKLENDOLGSRTTARATARALLSVHL RCKLENDOLGSRTTARATARARALLSVHL RCKLENDOLGSRTTARATARARALLSVHL RCKLENDOLGSRTTARATARARALLSVHL RCKLENDOLGSRTTARATARARARARARARALLSVHL RCKLENDOLGSRTTARATARARARARARARARARARARARARARARARAR				RLRELCQQWLQPETHTKEHILELLVLEQFLIILPKKLQARVQEH
SGKISSEMBANNEGSBLERHGARPEKKIEYKGSBREGRFICHLD LIEHASHTHIGKKICKSDWCGSSLICHKKWIE KRVIQCJBW LOKAFQRSSHLVRHOKILHGRKBYCONECKVPSCONGOLLEHLR HITGEKPYLCILGGKNFRRSSHLINRHORHSHSSCHECKECKST FSQALLITHOR HISHSKSHCHEGGKAFSLTSDLIRHRITHT EKPFKCNICQKAFKLINSHLAGHVRIHNSEKVPCCSEGGAFKQR SGLPGHQRYHKKOKLA 5895 2967 86 HESILGAIPFYFPFSSPWPPLYLFWNSHKKSRHFINQRGHGE RATSLOPTISAALYYLVVQGKKS\BDULGSVRRTITHIDHSLS RQ\MCPFLAGETESLADIVLMGALYPLLQDPAYLPEBLSALHSW ERTSLOPTISAALYYLVVQGKKS\BDULGSVRRTITHIDHSLS RQ\MCPFLAGETESLADIVLMGALYPLLQDPAYLPEBLSALHSW POTLSTU\SPCQR\ARRIVLTSALPYNNVPHLGNIGCUSVPHTITHIDHSLS RQ\MCPFLAGETESLADIVLMGALYPLLQDPAYLPEBLSALHSW POTLSTU\SPCQR\ARRIVLTSALPYNNVPHLGNIGCUSVPHTITHIDHSLS RQ\MCPFLAGETESLADIVLMGALYPLLQDPAYLPEBLSALHSW POTLSTU\SPCQR\ARRIVLTSALPYNNVPHLGNIGCUSVRATUS BLKQMNTLYLGCTDSVGATTSKAL\SEGSTLOPGTCHCWHIHTHA DIY\RWFNISPDIFGRTTTPQO\TKIT\QDIFQGLLKRGFVLQD TVEQLRCEHKARP\LAGRAFYLADRYSSVCYPCGVSEGOLDCKGKLI, DIY\RWFNISPDIFGRTTTPQO\TKIT\QDIFQGLLKRGFVLQD TVEQLRCEHKARP\LAGRAFYLADRYSSVCYPCGVSEGOLDCKGKLI, PGSDMTPHAQPITTPPROFERSYVCYPCGVSEGOLDCKGKLI, PGSDMTPHAQPITTPPROFERSYVCYPCGVSEGOLDCKGKLI, PGSDMTPHAQPITTPPROFERSYVCYPCGVSEGOLDCKGKLI, PGSBMTDHAQPITTPPROFERSYRCYPCGVSEGOLDCKGKLI, PGSBMTDHAQPITTPPROFERSYRCYPCGVSEGOLDCKGKGK, KYPSKSRGVGYRFRM\AHDYDLLGUPRSYRFGGGYYPGW LIPPDQRELLA,HVTLEQGGYAGLSFKSPRVVSFFFGGYYPGW LIPPDQRELLA,HVTLEQGGYAGLSFKSPRVVSFFGGYYPGW LIPPDQRELLA,HVTLEQGGYAGLSFLANTLAVGALGVALLSWLL QPYMPTWSATIQAOLOLPPPASILLANTLAUPALLSWLL QPYMPTWSATIQAOLOLPPASILLANTLAUPALLSWLL QPYMPTWSATIQAOLOLPPASILLANTLAUPALLSWLL QPYMPTWSATIQAOLOLPPASILLANTLAUPALLSWLL QPYMPTWSATIQAOLOLPPASILLANTLAUPALLSWLLOMARSH RETRIQPTILSAALYYLVQGGYALARAY REGRANGKKK RD\CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1			
LIEHASTHTOKKLCESDVCQSSLITGHKKVLS*ERKVJCQCKCKY LGAKAFORSSHLVPROKILHGEKPYJCCNCGKYROAGLLEHLE HTGEKRYJCCHCKKPKTYGKOKOKAGNAGLLEHLE HTGEKRYJCCHCKKPKTYGKOKOKAGNAGLEHLE EKPYKCNICQCAFPLINSHLAGHVRIHNEEKPYQCSECGEAFQR SGLPQHQRYHKKKALA 5895 2967 86 #BESLLGAIFPPPSSSPPPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGYPGCLFVLAAAGRAGRAEVLISTVGEDCVVPFLT RRKVPVLQLDGBNYLFSTSALTGYFPLLSGMEQDDLINQMLEW EATELQPTLSAALYYL,VVQGKKO\BDVLGSVRRTLTHIPHSLS RQ\MCPPLAGFTESLADYLVLAQAGRAGRAEVLISTVGEDCVVPFLT RRKVPVLQLDGBNYLFSTSALTGYFP\LLSGMEQDDLINQMLEW EATELQPTLSAALYYL,VVQGKKO\BDVLGSVRRTLTHIPHSLS RQ\MCPPLAGFTESLADYLVLAQALYPLLQDFAGEQDDLINQMLEW FOTLSTO\RPCQR\AARRIVLKQ\QQVLALR\PYLQKQPQPSPA BEKGLSPIREBEELATLSEELTMAYTDWESSQDDLINQMLEW FOTLSTO\RPCQR\AARRIVLKQ\QQVLALR\PYLQKQPQPSPA BEKGLSPIREBEELATLSEELTMAYTDWESSLDPDLRQQ NPVLPVAGERNVLITSALPYUNVPHLGNIGCTOPGLICKYHILHA DIY\RWMINISPIGFRTTPQQ\TKIT\QDICKGRGVLQ TYEQLRCEHCARP\LADRYSGVCPFCGYSEARGDQCTGKYHILHA DIY\RWMINISPIGFTTPQQ\TKIT\QDICKGRGVLQ NAVLEKKPQCCVCSCCVVQSSQHFLDLPLKEKRLEEWIGGRTL PGSSWTTNAQFITFFGFREWPSKRRW\CTDLLKWHGTPPE GFEDK\\FYYWPDATIGYLSTANYTQOMERW\KNPEQVDLVQ RP\AKDNVPHSLUPPSSALGABDNYTL\VSHLLATEVLHYEGG K\FSKSRGVGVPEDM\ALDTITPPDISRFTLYTPPGQ\TKIT\TRPEGK\DDICK K\FSKSRGVGVPEDM\ALDTITPPDISRFTLYTPREGK\DDICKTYSPE LTPDDQRLLA\HVVILELQHYHQ\LLEKVRIDALRSLITIS\MI GQYTYTVSATTQAGLQLPPACSTLITHFLCTLPAGHGIGTVSP LEQKLEMDQISELAGRAGGGAGTSTEKPAVTEVTRKPQQTIAS LMDEVTKQCNIVRELKAQKANKHEVAABVAKLLDLKKQLAVABG KYPRAPKJKKK SPRAPKJKKKK PSLGALFYLDAGPGLEVLAAAGRARGRAEVLISTGYBEDCVVPFLT RKVPVLQLDSGNYLTSTSATGYFFY\LLSGMERQDLAVARYS RCKGLSFIBEFEELATLSEELTMAYTAWRKLBELSFLPPERQQ NPULPVAGERNVLTTSALPYLVVQGKKS\GDVUPSRRTLTHIDHSLS RQ\MTYTLACTOTECTATTKALPSGLTYGDCVXHTITA DIY\RWMISFDIFGRTTTPQQ\TKIT\QDLKRGEBUGRYL DYNABRIKPQCKVCRSCVYQSSOHLFLDLPLEKRLEEBHGATL PGSDMTTNAQFTTPPGTPERFEXPRAPTARMELIESLEPERQC GFEDK\VPYVWPDATIGYLSTANLYQQCKKARWICVABRYLDDLYQCXARYS RCKGMTYLTACTOTECTATTKALPSGLTQCDKYHITHA DIY\RWMISFDIFGRTTTPQQ\TKIT\QDLKRGEBUGRTL PGSDMTTNAQFTTPPGTPERFEXPRAPTATHEDKLSGLOFNYHITHA PGGRCHAPTLANDTAWRCHARYLLDGUTYGLYBORDLYDLYG F\AKODRAPTSSATGTTPDISRFTYL\LYTRPGK\DAA KYFSKSK		· ·	,	
LGKAPQRSSHLVRNQKTHLGERPYQCXEGCKYFSONGLLEHLE HTTGERPYLCHICKORNFRSSHLRNGHTHSQEEPCECKCCKT FSQALLLTHHQRIHSHSKSHQCNECGKAPSLTSDLIRHERITG EKPPKCNICQKAPRIMSHLAQTVRINNEEKPYQCSECGBAFRQR SELPQHQRYHHOKLA MELPYSGOYGGLPULAAAGRARGRAPSLTSDLIRHERITG REKPYVLQLDSGNYLFSTSSAICRYFP\LLSGGEQDDLTNQMLEM RETSLQPTISAALYTL VYQKKKG BEDVARTRITHHDELS RONGPPLAGETESLADIVLWGALYPLLODPAYLPELISALHSW FQTLSTQ\EPCQR\ARRILVLKQ\QVULARLYPLLODPAYLPELISALHSW FQTLSTQ\EPCQR\ARRILVLSGUSYATTHTHDELSA BGKGLSPIEPESELATLSSEBIAMAYTAWEKGLESLPPLRPQQ NPVLPVAGERNVLLTSALPYVNNVPHAGNIGICCVLARGPVLQD TYEQLRCEHCARP\LADPYSTSTYCKTYCLYCOLYCULARGPVLQD TYEQLRCEHCARP\LADPYSTSTYCKTYCLYCOLYCULARGPVLQD TYEQLRCEHCARP\LADPYSTSTYCKTYCLYCOLYCULARGPVLQD TYEQLRCEHCARP\LADPYSTSTYCKTYCLYCULARGPVLQD TYEQLRCEHCARP\LADPYSTYCTCYCTYCTYCLYCULARGPVLQD TYEQLRCEHCARP\LADPYSTSTYCKTYCLYCULARGPVLQD TYEQLRCEHCARP\LADPYSTSTYCTCYCTYCTYCTYCLYCULARGPVLQD TYEQLRCEHCARP\LADPYSTSTYCTCYCTYCTYCTYCTYCTYCTYCTYCTYCTYCTYCTYC	1	(SGKISEPMEAHNEGSNLERHQAKPKEKIEYKCSEREQRFIQHLD
LGKAPQRSSHLVRNQKTHLGERPYQCXEGCKYFSONGLLEHLE HTTGERPYLCHICKORNFRSSHLRNGHTHSQEEPCECKCCKT FSQALLLTHHQRIHSHSKSHQCNECGKAPSLTSDLIRHERITG EKPPKCNICQKAPRIMSHLAQTVRINNEEKPYQCSECGBAFRQR SELPQHQRYHHOKLA MELPYSGOYGGLPULAAAGRARGRAPSLTSDLIRHERITG REKPYVLQLDSGNYLFSTSSAICRYFP\LLSGGEQDDLTNQMLEM RETSLQPTISAALYTL VYQKKKG BEDVARTRITHHDELS RONGPPLAGETESLADIVLWGALYPLLODPAYLPELISALHSW FQTLSTQ\EPCQR\ARRILVLKQ\QVULARLYPLLODPAYLPELISALHSW FQTLSTQ\EPCQR\ARRILVLSGUSYATTHTHDELSA BGKGLSPIEPESELATLSSEBIAMAYTAWEKGLESLPPLRPQQ NPVLPVAGERNVLLTSALPYVNNVPHAGNIGICCVLARGPVLQD TYEQLRCEHCARP\LADPYSTSTYCKTYCLYCOLYCULARGPVLQD TYEQLRCEHCARP\LADPYSTSTYCKTYCLYCOLYCULARGPVLQD TYEQLRCEHCARP\LADPYSTSTYCKTYCLYCOLYCULARGPVLQD TYEQLRCEHCARP\LADPYSTSTYCKTYCLYCULARGPVLQD TYEQLRCEHCARP\LADPYSTYCTCYCTYCTYCLYCULARGPVLQD TYEQLRCEHCARP\LADPYSTSTYCKTYCLYCULARGPVLQD TYEQLRCEHCARP\LADPYSTSTYCTCYCTYCTYCTYCLYCULARGPVLQD TYEQLRCEHCARP\LADPYSTSTYCTCYCTYCTYCTYCTYCTYCTYCTYCTYCTYCTYCTYC	1	1		
INTEGREYLCHICGENFRESSLINRHORTHSDEPCRECKECKY FSQALLITHQRIHHSKSHGCHSCGASKSHGOLISCASKSHGOLI	1	1		· · · · · · · · · · · · · · · · · ·
### ### ### ### ### ### ### ### ### ##		1		
### SEPPEKCHICOKAPRINSHLAQRYRINBEKPYQCSEGGAFRQR SCLPOMORYHHOKLA ### SELGAIPPYPPPSSPWPPPLYLPWNSHRKSRHFINQRGIHGE ### WILVSDGVYPGCLEVILAAAGRARGRAEVILSTVOPEBCVYPELI ### REVEVPLOUDSONTLETSTAICRYFF LLUSGMEQDDLTNQMLEM ### REVEVPLOUDSONTLETSTAICRYFF LLUSGMEQDDLTNQMLEM ### RETELQPTLSAALYYL\VVQGKKG\### BVALGSVRRTLTHIDHSLS ### ROKGLSPIEPEBELATLSEEIAMAVTAWEKGLESLPPLPPQO ### NEVLPVAGGERNLITSALPYVNNVPHIGNIIGCVLSADVPARYS ### RIRQWNTLYLCCTDEYGTATETKAL\EGGLTPQEICCHYHILHA ### DIY\RWNTLSPPIGRTTTPQO\TRIT\QDIPQOLLKRGFVLQD ### TVEQLRCEHCARF\LADRFYEGVCFFGSYBEARGDCDKGGKLI NAVELKRPQCKCVCRSCYVSSGNHFLD\LEKKRLEEWIGRTL PGSDWTPNAOFIIPPFGFRSWPSKPROO*TEDLK\WGNPGTPPE ### AKDNVPFHSLVPPSSALGAEDNYTL\SVSHLATFYLMYEDG ### AKDNVPFHSLVPPSSALGAEDNYTL\SVSHLATFYLMYEDG ### AKDNVPFHSLVPPSSALGAEDNYTL\SVSHLATFYLMYEDG ### AKDNVPFHSLVPPSSALGAEDNYTL\SVSHLATFYLMYEDG ### ROKGLSPJPPPPSSALGAEDNYTL\SVSHLATFYLMYEDG ### AKDNVPFHSLVPPSSALGAEDNYTL\SVSHLATFYLMYEDG ### AKDNVPFHSLVPPSSALGAEDNYTL\SVSHLATFYLMYEDG ### AKDNVPFHSLVPPSSALGAEDNYTL\SVSHLATFYLMYEDG ### AKDNVPFHSLVPPSSALGAEDNYTL\SVSHLATFYLMYEDG ### AKDNVPFHSLVPPSSALGAEDNYTL\SVSHLATFYLMYEDG ### AKDNVPFHSLVPPSSALGAEDNYTL\SVSHLATFYLMYEDG ### AKDNVPFHSLVPPSSALGAEDNYTL\SVSHLATFYLMYEDG ### AKDNVPFHSLVPPSSALGAEDNYTL\SVSHLATFYLMYEDG ### AKDNVPFHSLVPPSSALGAEDNYTL\SVSHLATFYLMYEDG ### AKDNVPFHSLVPPSSALGAEDNYTLLSTTSLATFYLMYEDG ### AKDNVPFNSALGAEDNYTLSTYTTAKPQOLOA ### LAPDEVTLGGINVERSALGAEDNYTLLSTYTTAKPQOLOA ### AKDNVPFNSALGAEDNYTLSTYTTAKPQOLOA ### AKDNVPFNSALGAEDNYTLSTYTTAKPQOLOA ### AKDNVPFNSALGAEDNYTLSTYTTAKPQOLOA ### AKDNVPFNSALGAEDNYTLLSGSBLOADNATANS ### AKDNVPFNSALGAEDNYTLSTYTTAKPQOLOA ### AKDNVPFNSALGAEDNYTLNAGAGRAEDAEDLATFYTTATATATATATATATATATATATATATATATATAT	1			
SSLFQHQRYHHKUKLA 1985 2967 86 HPSLLGAIPFYPPESPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGMYLFSTSAICRYFF\LLSGWEQDDLTNQMEW BATELQFTLSAALYYLVVQGKKG\LGSVRSTLTHIDHSLS RQ\NCPFLAGETSLADVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\LEPCQR\AARRLVLK\QCJKG\LGSVRSTLTHIDHSLS RQ\NCPFLAGETSLADVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\LEPCQR\AARRLVLK\QCJKG\LGSVRSTLTHIDHSLS RQKGLSPIEPEEELATLSEELAMAVTAMEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RIRQNMTLYLCCTDEVGTATETKAL\LEPCLTQSICCKYKIIHA DIY\RWFNISFDIFGRTTTPQO\TKIT\QDIFQGLKRGFVLQD TVGQLRCCHCARF\LABPYSSGVCPSERAGDQCDKGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTRNAGFITPFFGFREWPSKPRW*TRIK\MONPGTPS-L GFEDK\VPYVWFDATIGVISITANTVTQMERWN\KNBPGQVDLYQ FM\AKDNVPFHSLVFPSSALABENYTL\VSHLATEYLNYEDG K\FSKSRGVGVFPDM\ARDTGIPTSTQ\LLXFTYL\LYIPEGK\DSA FFWTDLLLKNNS\ELLNNLGSFINRA\GMFVSKFFGG\YYPEMV LITPDQRILLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GRQYI\QVNEPW\KRIKGSBADRGRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLITNFLCTLAPGHGIGTUSP LFQKLENDGIESLAGFFGGGGANTSFKPAVVETVTTAKPQGIQA LNDEVTKGGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPERPKGKKKK HFSLLGAIFFFPPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGREVLLISTVGPBCCVVPFIT RFKVFVLZDLOSGMYLFSTAACCHYFLGAGESLPPBCVQG MPVLFVAGERNVLITSTATCHTSTATCHYLGAGESLPPLRPQQ RO\NCPLFAGETSSLADIVLWGALYDDAPYLPESLSALHSW FGTLSTQ\EPCQR\AARRLVLKQ\QQVLALR\PYLQKQPQPSPA ESKGLSPIEPEEELATLSEEIAMAVTAWEKGLESLPPLRPQQ NPVLFVAGERNVLITSALPYNNNYHLGHIIGCVLSADVPARYS RLRQMNTLYLCGTDEVGTATETKAL\PECLFGCTCKHIIHA DIY\RWFMISFDIFGRFTPPQOFTENLX\WGNEGFVLOD TVEQLRCEHCARF\LADRFVEGVCPFCGYEERAGDQCDKGGKLI NAVBLKKPQCKVCRSCPVQSSCHLINDLPKLEKRLSEMGFTPE GEEDK\VFYWFDADFITGYFSALGAEDFYTLLVKHLGKFVLOD FM\AKDNYPHSLUFPSSALGAEDFYTLLVKHLGKFVLOD FKYSKSRGVGVFRDM\AHDTGIPDITRFYL\LYTRPEGK\DSA FFWTDLLLKNNS\ELLMILGNFINRA\GMFVSKFFGG\YVPSEMV LTPDDQRLLA\HVTLELGRYHIQLLEFNILGHTILDANIAALLSVML GRQYI\QVNEFW\KRIKGSEADRGRGGTTTGLANIAALLSVML OPYMPTVSATIGAQLDFPANCSILLTNFLCTLPARGRIGITUSP				
86 HPSLLGATPFYPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE RRLWYDGDYPGCLPVLAAARGRARAVLISTVGPEDCVYPFLT RPKYPVLQLDSGNYLFSTSALCRYFY_LLSGWEQDDLTNQMLEM RATELQFTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHTDHSLS RQ\MCPTLAGETESLADLYVLMGALYDDAPALPEELSALHSW FQTLSTO\EPCQR\AARRLULKG\QGVLALR\PYLGKQPQSSPA GKGKLSPIBPBEEELATLSEELAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYNNVPHLGNIIGCVLSADVFARYS RLRGWNTLYLCGTDEYGTATTKAL\EEGLTPQSICCKYHIIHA DIYYNWRWISFDIFGRTTPQO\TKT\DYLOKUKAGFVLQD TVEQLRCEHCARF\LADRFVSGVCPFCGYEBARGDQCDKGGKLI NAVELKKPQCKVCRSCPVVGSSQHLFLDLPKLEKKLEEWLGRTL PGSDNTNAOFIIPPTGGREWPSKPRWG*TRDLK\WRNPGCPUCH GFBDK\VFYWFDATIGYLSITANYTDQWERWR\KNPEQDYLCY K\PSKSRGVGFDM\AHDTIPPDISRFYL\LVHIPBEGK\DSA FSWTDLLLKHNIS\ELLNNLGNFINRA\GWYSKFFGG\YVPEMV LTPPDQRLLA\HTTLEDHYHQ\LLEWVIKDALRSILTIS\RH GNQYI\QVNEW\KRIKGSBADRGRAGTVTGLAVNIAALLSWL QPYMFYVAATIQAQLQLPPPACSILLINFLCTLPAGHGIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVETYTTAKPQGIDA LNDEVTKQGNIVELKAGKADKNEVAAEVAKLUKAQAADAG KPPEAPPKKKKK HPSLAFGATFYLVQKKK\EDVLGSVRTLTHTDHSLS RQ\MCPTLAGETSSLADIVLWGLKAGKADKNEVAAEVAKULKQQOTLAR RKVPVPUQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQMLEW EATELQFTLSAALYYL\VVQKKK\EDVLGSVRTLTHTDHSLS RQ\MCPTLAGETSSLADIVLMGALYFLLQDPAYLPEELSALHSW FOTLSTO\EPCQR\AARRLUKKQ\QGYLALR\PYLQKQPQPSSA GKGLSJPEPPEEELATLSEEILAMAVTAWKEGLESLPPLRQQ NPVLFVAGERNVLITSALPYVNVPHLGNIIGCVLSADVFARYS RLRGWNTLYLCGTDEVGTATETKAL\EEGLTPGICKYHIIHA DIY\RWFIISFDIFGRTTTOQO\TKT\QKITTLYBLCGTDEVGTATETKAL\EEGLTPGICKYHIIHA DIY\RWFIISFDIFGRTTTPQQ\TKT\QKITTLYBLGCKCHCARFYLAD NVLFVAGERNVLITSALPYVNVPHLGNIIGCVLSADVFARYS RLRGWNTLYLCGTDEVGTATETKAL\EEGLTPGICCKYHIIHA DIY\RWFIISFDIFGRTTTPQQ\TKT\QKITT\QDUCKGFVLQD TVQURCHCARFYLADRFVEGVCPFGGYEEBRGGCCKGKLII NAVBLKKPQCKVCRSCCVVGSSGLHADLFRLIKERGERGDCCKGKLII NAVBLKKPQCKVCRSCCVVGSSGLHADLFRLIKKERGFULQD FMAKDNVPFIISLTPSSALGAEDNTL\LVSHLIKMYKNFEGK\DAFYLLYTHYBGG K\PSKRSGVGVFRDM\AHDTIGTISTATAYTQQWERW\KNFEGQVDLYG FMAKDNVPFIISLTPSSALGAEDNTL\LVSHLIKTISTATYTQQGKYTGA K\PSKRSGVGVFRDM\AHDTIGTISTATATYTQQWERW\KNFEGGK\DAFA FSWTDLLLKNNS\ELLANLGNFINRA\GWFVKFFGGYVPDEM LTPDDQRLLA\HYTLELGRYIQ\LLEKVALFRGK\TLYYEBGK\DAFA LTPDDQRLLA\HYTLELGRYIQ\LLEK	1	i		1 · ·
MRLFYSGOVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQFTLSAALYYL\VVQGKKG\EDVLGSVRTLTHIDHSLS RQ\NCPPLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FOTLST\D\EPCQR\AARRIVLK\Q\QCVLALR\PYLQKQPQPSPA BGKGLSPIFPEBEELATLSEEEILAMVTAWEKGLESLPPLRQQ NPVLPVAGERNVLITSALPYVNNVPLLGIDLIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EBGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQ\TKTT\QDIPQLLKRGFVLQI TVEQLRCGHCARF\LABRYPSGVCPPCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSGHLFLDLPKLEKLEEWIGRTL PGSDWTRNAOFITPFEGTREFWFSKPATEDLK\WNOFTDFE GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ KM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLATEYLNYEDG K\PSKSRGVVFPDM\ARDITOIPPDISRFYL\LITSYLNYEDG K\PSKSRGVVFPDM\ARDITOIPPDISRFYL\LITSYLNYEDG K\PSKSRGVVFPDM\ARDITOIPPDISRFYL\LITSYLNYEDG K\PSKSRGVVFPDM\ARDITOIPPDISRFYL\LITSYLNYEDG K\PSKSRGVVFPDM\ARDITOIPPDISRFYL\LITSYLNYEDG K\PSKSRGVVFPDM\ARDITOIPPDISRFYL\LITSYLNYEDG K\PSKSRCVVFPDM\ARDITOIPPDISRFYL\LITSYLNYEDG K\PSKSRGVVFPDM\ARDITOIPPDISRFYL\LITSYLNYEDG K\PSKSRGVVFPDM\ARDITOIPPDISRFYL\LITSYLNYEDG K\PSKSRKKKK QPYMTVARITQAQLQLPPRGSILLTNFLCTLPAGHQIGTVSP LFQKLENDOIESLRGFGGGGAXTSKFRAVWETVTTAKPQQIQA LMDEVTKQGNIVELLAGKARAKNEVAAEVAKLLDLKKQLAVAEG KPPERAPKSKKKK FPSKLFVSGVVERGGGGAXTSFKFAVVETVTTAKPQQIQA LMDEVTKQGNIVELLAGKARAKNEVAAEVAKLLDLKKQLAVAEG KPPERAPKSKKKK FPSKLFVSGVVERGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RKVPVLQLDSGNYLESTSAICCXFF\LLSGWEGDDLTNQWLEW EATTELQPTLSAALYYL\VVQCKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPLSAALYYL\VVQCKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPLSAALYYL\VVQCKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPLSAALYYL\VVQCKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPLSAALYYL\VVQCKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPLSAALYYL\VVQCKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPLSAALYYL\VVQCKKG\EDVLGSVLRDLTRQQDLYQ NEVLEVAGERNVLITSALPYNNOWHGKICKGPLCD NVLLVAGERNVLITSALPYNNOWHGKICKGPULD TVEQLRCCARRYLADAPVSGVCPFCGVERAGROQCCKGGKLI NAVHKKRGERVLD TVEQLRCCARRYLADAPVSGVCPFCGVERAGROQCCKGGKLI NAVHKKKGEADQPTCPSAALAYALVANIAALLSVML FPMAKDNOPHSLUFPSSALGAEDNYL\SHLLKWRICRDAVRSTLYNYEGK FPMAKDNOPHSLUFPSSALGAEDNYL\SHLLKWRICRSULDYLYRYEGK YNFYVSATIGGRUFTANTAALLSVAL FPMTLLKNOWFRISHTFALLYNNIAALLSVML L			- 00	
RRYPVIQLDSGNYLFSTSAICRYFF\LLSGWEODDLTNOMLEW EATELQPTLSAALYYL\VVQKKG\EDVLGSVRRTITHIDHSLS RQ\MCPFLAGETESLADIVLMOALYPLLQDPAYLPEELSALHSW FQTLSTQ\BPQCR\AARRUVLKQ\\QGVLARL\PYLQKQPQBPAA BGKGLSPIEPBEEBLATLSEEBLAMAVTAWEKGLESLPPLRQQ MPVLPVAGERNVLLTSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EGCLTPQEICDKYHIIHA DIY\RWFNISPDIFGRTTTPQO\TKIT\\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFGCYSEBAGDQCDKCGKLI NAVELKKPQCKVCSCCVVQSSQHFLDLPKLEKRLEBULGRTL PGSDWTPNAQFITPFFGFREWFSKPRWO*TFDLK\WGNPGTP*E GFENK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ K\FSKSRGVGFFRM\AHDTGIPPDISRFYL\YIRPEGK\DSA K\FSKSRGVGFFRM\AHDTGIPPDISRFYL\YIRPEGK\DSA K\FSKSRGVGFFRM\AHDTGIPPDISRFYL\YIRPEGK\DSA K\FSKSRGVGFFRM\AHDTGIPPDISRFYL\YIRPEGK\DSA K\FSKSRGVGFFRM\AHDTGIPPDISRFYL\YIRPEGK\DSA CQYY\QVNBFW\KRIKGSBARQRAGTVTCLAVNITAALLSYML GRQYI\QVNBFW\KRIKGSBARQRAGTVTCLAVNITAALLSYML GRYY\QVNBFW\KRIKGSBARQRAGTVTCLAVNITAALLSYML GRYY\QVNBFW\KRIKGSBARQRAGTVTCLAVNITAALLSYML GRYYLQULDGINVTESLAQKAADKNEVAAEVAKLLDLKKGLAVABG LHDEVTKGGNIVRELKAQKAADKNEVAAEVAKLLDLKKGLAVABG KPPEAPKGKKKK RPPEAPKGKKKK RPPEAPKGKKKK RPPEAPKGKKKK RPPEAPKGKKKK RPPEAPKGKKKK RPPEAPKGKKKK RCNCPFLAGETESLADIVLNGQLGVPARYSHTLTIDLSLS RC\NCPFLAGETESLADIVLNGQLAFPLQDPATHPEELSALHSW FGTLSTQ\EPPCQR\AARRUVLKQ\GGULAFLYPLLGKDQPSFA GKGLSPIEPEEELATLSEESLATLSEESLAFLYPLETAALYPLLGKDQPSFA GKGLSPIEPEEELATLSEESLATLSEESLANLYPLLGKDQPSFA GKGLSPIEPEEELATLSEESLATLSEESLANLYPLLGKDQPSFA GKGLSPIEPEESLATLSEESLATLSEESLANLYPLLGKDQPSFA GKGLSPIEPEESLATLSEESLATLSEESLANLYPLLGKDQPSFA GKGLSPIEPERFOLTSTGTATETKAL\EBGLTPLFRQG TVEQLRCEHCARF\LADRYVNVPHILDNIIGCVLSADVPRAYS RLRQWNTLYLGGTDEYGTATETKAL\EBGLTPLFRQG TVEQLRCEHCARF\LADRYVNVPHILDNIIGCVLSADVPRAYS RLRQWNTLYLGGTDEYGTATETKAL\EBGLTPLFRQG TVEQLRCEHCARF\LADRYTDGFFFERERGDQCDKGGKLI NAVBLKKPQCKVCSGCPVQSSOHFFDLPRLEKKELSEWIGRTI GFEDK\VFYVWFDATIGYLSITANVTDQMERWN\KNEDGUDLYQ FMAKNDVPFHSLVFPSSALGAEDNYTL\VYSHLATATYLNYEDG K\FSKSRGGGVFRDM\AHDTGIPPISRFYL\VYSHLATATYLNYEDG K\FSKSRGGVFRDM\AHDTGIPPISRFYL\VYSHLATATYLNYEDG K\FSKSRGGVFRDM\AHDTGIPPISRFYL\VYSHLATATYLNYEDG K\FSKSRGGVFRDM\AHDTGIPPISRFYL\VYSHLATATYLNYEDG K\	5895	2967	86	
RATELQPTLSAALYYL\VVQGKKG\BDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALISW RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALISW BGKGLSPIEPPEERLATLSEBELMAUTAWKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISPDIFGRTTTPQQ\TKIT\QDIPQQLLKRGFVLQD TVEQLRCGHCARP\LADRYFSGVCPFCGYSEARGDQDCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWFSKPRWQ\TRDLK\NGNPGTP>E GFEDK\VPYWFDATIGYLSITANYTDQWERWN\KNPRQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VYBLGKKLESVLGRTL PGSDWTPNAQFITPFFGFREWFSKPRWQ\TRDLK\NGNPGTP>E KYSKRGVGVFRDM\AHDTGIPPDISRFYL\DYLNFBCG\VYPEMV LIPPDQRLLA\HVYLELQHYHQ\LLEKVRLDALRSILTIS\RH GRQYI\QVNEBW\KRIKGSBADRQRAGTVGLAVNIAALLSVML QPYMFTVSATIQAQLQLPPPACSILLTNFLCTLPAGHGIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIDA LMDEVTKQGNIVRELKAQRADRWARAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK SPEAPKGKKKK HSLLGATPFYPDPSSDWPPPLYLEWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGKAEVLLSTVQPEDCVVPFLT RRKVPVLQLDSGNVLFSTSAICRYFF\LLSEWGDDLTNQMLEW FQTLSTQ\PLFAGETESLADIVLWGALVPLLQDPAYLPEELSALHSW FQTLSTQ\PLFAGETESLADIVLWGALVPLLQDPAYLPEELSALHSW FQTLSTQ\PLFAGETESLADIVLWGALVPLLQDPAYLPEELSALHSW FQTLSTQ\PLFAGETESLADIVLWGALVPLLQDPAYLPEELSALHSW FQTLSTQ\PLFAGETESLADIVLWGALVPLLQDPAYLPSCKGKLI NAVBLKKPQCKVCRSCPVVQSSQHIFLDLPRLEKRLEEWLGRTL PGGDWTPNAQFITPPGGPTSTATETKAL\PEGLIFPGEICKHHI HAD DIY\RWFNISPDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCHCARF\LADRYSCPVGYCFCGYSERARGDCDKKGKLI NAVBLKKPQCKVCRSCPVVQSSQHIFLDLPRLEKRLEEWLGRTL PGGDWTPNAQFITPPFGPREWPSKPRW\KNPEQVVLYQ FMAKNDVPFHSLVFPSSALGAEDNYTL\VSHLIATFYLNYEGG K\PSKTSLUKKPQCKVCRSCPVVQSSQHIFLDLPRLEKRLEEWLGRTL PGGDWTPNAQFITPPFGPREWPSKPRW\KNPEQVVLYQ FMAKNDVPFHSLVFPSSALGAEDNYTL\VSHLIATFYLNYEGG K\PSKTSLUKLKNNS\SLELNNICHSTINRA\GMFVSKFFGG\YPPEW LTPDDQRLLA\HVTLELQHYQ\LLEKVRIRDALRSILTIS\RH GRQYI\QVNEW\KRIKGSBADRQRGRGTVTLANIAALLSVAL GPYMPVSATIQAGLQLDPPPACSILLITHFLCTLPAGRG\GTVPG	İ			MRLFVSDGVPGCDPVLAAAGRARGRAEVDISIVGFEDCVVFFDI
RQ\MCPFLAGETESLADIVLWGALYPLLQDPATLPEBLSALHSW FQTLSTQ\EPCQR\AARRIVLKQ\QQVPLAIR\PYLQKQPQPSPA BGKGLSPIEPEBEBLATLSEBEIAMAVTAMEKGLESLPPLRPQQ MPVLPVACERRVLITSALPYVNNVPHLGNIIGCVLSADVFARYS HLRQWNTLYLCGTDSVGTATETKALEGEITPPGEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIPQQLLKRGFVLQD TVEQLRCEHCARP\LADRFVEGVCPFCGYSERARGDQCDKCGKLI NAVELKKPQCKVCSGCVVQSSGUHFLDLEKLEKRLEEWLGRTL PGSDWTPMAOPITPFGFREWFSKPRQ*TTDLK\MGNPGTP*E GFEDK\VPYWFDATIGYLSITANTTOQWRRWW\KWPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGFFRM\AHDTGIPPDISRFT\LYIKPEGK\DSA FSWTDLLKNNNS\ELLANNIGNIBAA\GMPVSKFFGG\VPEXW LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSBADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILINNFLCTLPAGHOIGTVSP LFOKLENDOIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LADEVTKGQNIVRBLKAQKADKNEVAASVAKLLDLKKQLAVAEG KPPEAPKGKKKK 5896 1967 86 HPSLIGAIPFYPPPSSSPWPPPLYFWNSHRKSRHFINQRGIHGE MRLFYSDGVGCLEVLAAAGRARGRAEVLISTVGPBCVVPFLT RRKVPVLQLDSGNVLFSTSAICRYFF\LLSGWBQDDLTNQWLEW EATELQPTLSAALYTLVVQGGEDDVLGSVRRTTHTHDHSLS RQ\NCPFLAGETESLADIVLMGALYPLLQDPAYLPEELSALHSW FGTLSTQ\EPCQR\AARRULKQ\GGVLAR\PYLLKGQPSPA BCKGLSPIEPEBEIATLSEEILATLSEEILANAVTAWBKGLESLPPLRPQQ NPVLPVAGERRVLITSALBYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQGLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCFYEERAGDQCDKCGKLI NAVBLKKPQCKVCSCSCVVGSSOHFLDLPKLEKRLEEMIGRTL PGSDWTPNAQFITPPFGFREWPSKPRW\TTDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANTTOQWERW\KNPBQVDLYQ FMYMONPFFISLVFPSSALGAEDNYTL\VSHLIATEYLNYEDGE K\FSKSRGGGVFRDM\AHDTGIPPISRFYTL\JVIRPEGK\DSA FSWTDLLKKNNS\ELLKNNILGHTRA\GMFVSKFFGG\YVPEXW LTPDDQRLLA\HVTLELQHHQ\LLEKVRILDALRSILTIS\RH GRQYI\QVNEPW\KRIKGSBADRQRGGTVTLANIAALLSVAL GPYMPVSATIQAGLQLDFPPACSILLITHFLCTLBAGRGGLYTTSV	ŀ			
#GTLSTO\BPCOR\ABRRLVLKO\GSVLALR\PYILOKOQPOPSPA BGKGLSPIEPEEELATLSEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERRVLITSALPYVNNVPHLGRIIGCVLSADVFARYS RIKQNNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHITHA DIY\AWFMISPDIFGRTTTPQ\KIT\QDIFQCLKGRYLITHA DIY\AWFMISPDIFGRTTTPQ\KIT\QDIFQCLKGRYLITHA TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCEVVGSSGHLFLDLFKLEKRLEEMLGRTL PGSDMTPNAQPITTPFFGFRENFSKPRNQ*TRDLK\MGNFGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQMERWW\KNPEGVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGUGVFRDM\AHDTGIPPDISRFYL\LYIRPBGK\DSA FSWTDLLLKNNS\ELLNILGRFINRA\GBFVSKFFGG\YVPBMV LTPDDQRLLA\HVTLELDGHYHQ\LLEKVRIDALRSILTIS\RH GNQYI\QVNEFW\KRIKGSBADRQRGTVTGLAVNIAALLSVML QPYMFVSATIQAOLQDEPPACSILLITHLCTLPAGHOIGTVSP LFOKLENDOIBSLGRGFGGGGAKTSPKPAVVETVTTAKVQOIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKKKKK FSKTELGATFFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE RETELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLMGALYPLLOPPAYLPEELSALHSW FOTLSTQ\BEYGQCDK\ARRAUNOQGVLALR\PYLQKOPQDSED EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLMGALYPLLOPPAYLPEELSALHSW FOTLSTQ\BEYGQ\ARRAUNOQGVLALR\PYLQKOPQDSED BKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIGCULSADVFARYS RIRGWNTLYLCOTDEYGTATEKAL\SEGLIFQEICDKHITHA DIY\RWFNISFDIFGRTTPQQ\KKIT\ODIFGLICKKGFVLQD TVEQLRCCHCARF\LABAPFVEGVCFPCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCFVVQSSGHLFIDLPKLEKRLEEMLGRTL PGSDWTPNAQFITPFFGREFFSLRADO\TTL\KNRGPGTYDE GFEDK\VFYWWPDATIGYLSITANYTOWERWW\KMPEQVDLVQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLIATEYLLNYEDG K\FSKSRGGVPRDM\ARDTGIPPDISRFYL\LYNIEPEGK\DSA FFWTDLLLKNNS\ELLNILGRIFNTL\LYNIEDGKYTYGLKVNTERGKYTYGLKVNTERGKYTYGLKVNTERLISKH GRQYI\QVWEPW\KRIKGSEADRGRAGTVTGLKVNIAALLSVML GPMYTVASTIOAQGLQCLPFQFCGYEEARGDCAKFFGG\YYPBMV LTPDDQRLLA\HVTLELQHYQ\LLEKVRIRDALRSILTIS\RH GRQYI\QVWEPW\KRIKGSEADRGRAGTVTGLKVNIAALLSVML OPYMTYSATIOAQGLQDLPPPAGCSILLNTFLCTLTPAGHQIGTUSP			· ·	
BGKGLSPIEPEEELATLSEEEIAMAVTAWEKGLESLPPLRPOQ NPVLPVAGERNVLITSALPYUNNVPHLGNIIGCVLSADVPARYS RLRGWNTLYLCGTDEYGTATETKAL\EEGLTPQEIGDKYHLIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFGYBEARGDQCDKGKLI NAVELKKPQCKVCRSCPVVQSSGHLFLDLFKLEKELEBWLGRTL PGSDMTPMAQFITPFFGFREMPSKPRNQ*TRDLK\WGNFGTP*E GFEDK\VFYVWFDATIGYLSTATTVTQMERRWY\KNPEQVDLYQ K\FSKSRGWGVFRDM\AHDTGIPDISFYL\LYIRPBGK\DSA FSWTDLLKNNS FLLINILGNFINRA\GMFVSKFFGG\VYPMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\RRIKGSBADRGRAGTVGLAVNIAALLSVML LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\RRIKGSBADRGRAGTVGLAVNIAALLSVML LTDEVTKGGNIVRELKAQKADRNEVAAEVAKLDLKKQLAVBG K\FPSAPKGKKKK KPPEAPKGKKKK KPPEAPKGKKKK KPPEAPKGKKKK RPPEAPKGKKKK RPPEAPKGKKKK RPPEAPKGKKKK RQ\NCPFLAGETESLADIVLWGAUFDLGDPAYLPEELSALHSW FGTLSTO\BFPCQR\AARRLVLKQ\QGVLALR\PYLQKDPQSPS EGKGLSPIEPEEELATLSEEIAMAVTAMEKGLESLPLRPQQ NPVLPVAGERNVLITSALPYNNVPHLGNIIGCULSADVPARYS EGKGLSPIEPEEEELATLSEEIAMAVTAMEKGLESLPLRPQQ NPVLPVAGERNVLITSALPYNNVPHLGNIIGCULSADVPARYS RLRGWNTLYLCGTDEYGTATETKAL\EBGLTPQEICDKYHIHA DIY\RFFNISFDIFGRTTTPQQ\TKIT\QDIFQLLKKGFVLQD TVQQLRCBHGARF\LADRFVGCYPCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSOHLFLDLPKLRGFVLLQD TVQQLRCBHGARF\LADRFVGSTERFYLL\KNGNFGTIFE GFEDK\VFYVWFDATIGLISTANYTOWERW\KNFEGOYDDLYN FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGGVFRDM\AHDTGIPDISRFYLL\KNGNFGTIFE GFEDK\VFYVWFDATIGLISTANYTOWERW\KNFEGOYDPS FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGGVFRDM\AHDTGIPDISRFYLL\LYIRPEGK\DSA FFSHTDLLKNINS FLININGRFIFRA\GMFVSKFFGG\VYPSW LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\H GRQYI\QWEFW\KRIKGSEADRGRAGTYGLAVNITAALLSVML GRQYI\QWEFW\KRIKGSEADRGRAGTYGLAVNITAALLSVML GRQYI\QWEFW\KRIKGSEADRGRAGTYGLAVNITAALLSVML GRQYI\QWEFW\KRIKGSEADRGRAGTYGLAVNITAALLSVML GRQYI\QWEFW\KRIKGSEADRGRAGTYGLAVNITAALLSVML GRQYI\QWEFW\KRIKGSEADRGRAGTYGLAVNITAALLSVML GRQYI\QWEFW\KRIKGSEADRGRAGTYGLAVNITAALLSVML GRQYI\QWEFW\KRIKGSEADRGRAGTITTGAVNITAANLSVML GRQYI\QWEFW\KRIKGSEADRGRAGTYGLAVNITAALLSVML	1			RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RIRGWINTLYLCGTDBYGTATETKAL\EBGLTPQEICDKYHIIHA DIY\mwfhispiigrittptgycittit\ddipqclkkgfvlqd TVEQLRCBHCARF\LADRFVEGVCFCGYEBARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSGHLFLDLPKLEKRLEEWLGRTL GSDWTPNAQFITPFFGFREWPSKFRM0*TRDLK\WGMPGTP*E GFDR\VFVVWFDATIGYLSITANTTDWERRW\KNPBGVDLYQ K\FSKSRGVGVFDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLKNNS\BLINNLGNFINAS\GMFVSKFFGG\YVEBM\ LTPDDORLLA\HVTLELGHYHQ\LLEKVRIRDALRSITIS\RH LTPDDORLLA\HVTLELGHYHQ\LLEKVRIRDALRSITIS\RH GNQYI\QVNEPW\KRIKGSBADRQRAGTVTGLAVMIAALLSVML QPYMFVVSATIQAQLQLPPPACSILITNFLCTLPABGHQIGTVSP LFOKLENDOLISLRORFGGGQAKTSPKPAVVETVTTARPQQIQA LMDEVTKQGNIVELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK FSWTDLLGAIFFYPPPSSPWPPDLYLFWNSHRKSRHFINQRGIHGE MRLFYSDGVPGCLPVLAAAGRARGRAEVLLISTVGFEDCVVPFLT RPKVPVLQLDSGMYLFSTACTYFF\LLSGMEDDLTNOWLEW ANDEVLFVQGCTQPLJAAAGRARGRAEVLISTVGFEDCVVPFLT RPKVPVLQLDSGMYLFSTACTYFF\LLSGMEDDLTNOWLEW FGTLSTQAFECCQ\AARRICA\PYF\LGGMEDDLTNOWLEW GCKGLSPIEDEEELATLSEEIAMAVTAWEKGLESLPPLPQO NPVLPVAGERNVLITSALPYVNNVHEKALPYPLQCDPSPA GKGLSPIEDEEELATLSEEIAMAVTAWEKGLESLPPLPQO NPVLPVAGERNVLITSALPYVNNVHLUNIGCULSADVFARYS RIRGWMTLVLCGTDEVGTATETKAL\EBGLTPQEICDKYHITHA DIY\RWFNISPDIFGRTTTPQQ\TKIT\QDIFQOLLKRGFVLDD TVPQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCCPVVQSSOHLFILDLPKLEKRLEEMLGRTL PGSDWTPNAQFITPFGFREWPSKPRQW*TRDLK\WGNPGTF*E GFEDK\VFYVWFDATIGYLSITANYTOWERRW\KNPEQDDLYQ FM_AKNNVPFHSLVPFSSALGAEDNYTL\VSHLIATEYLNYEDG K\PSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FEWTDLLKKNNS\ELLNINGGFTFGREWVSKPGGVYPEMV LTPDDQRLLA\HVTLELQHYQ\LLEKVRIRDALRSILTIS\RH GRQYI\QVNEPW\KRIKGSEADRGRGTTTGLAVNIAALLSVML OPYMPTVSATIQAQLQIPPACSILLTNFLCTLPAGHGIGTVSP				
RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLCEHCAFF\LADAFYSEGVCFFCGYBERAGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEBWLGRTL PGSDWTPRAQFITPFFFFREWPSKPRWQ*TRDLK\WGNPGFP*E GFEDK\VFYVWFDATIGYLSITANTTDQWERW\KNPSQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFPDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLKRNS\ELLNILGNFINA\GMFVSKFFGG\YVEMV LIPDDQRLLA\HYTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSBADRQRAGTVTGLAVNIAALLSVML QPYMFTVSATIQAQLQLPPACSILLITMFLCTLPAGHGIGTVSP LFOKLENDQIESLRORFGGGQAKTSPKPAVVETVYTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLDLKKQLAVAEG KFPEAPKGKKKK FSHAPKGKKKK FSHAPKGKKKK RPEAPKGKKKK RPEAPKGKKKK RO\NCFFLAGEGTSLADIVJVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCFFLAGEGTSLADIVJV\VYQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCFFLAGEGTSLADIVJV\VYQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCFFLAGEGTSLADIVJV\VYQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCFFLAGEGTSLADIVJV\VYQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCFFLAGEGTSLADIVJV\VYQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCFFLAGEGTSLADIVJV\VYQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCFFLAGEGTSLADIVJV\VYQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCFFLAGEGTSLADIVJV\VYQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCFFLAGEGTSLADIVJV\VYQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCFFLAGEGTSLADIVJV\VYQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCFFLAGEGTSLADIVJV\VYQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCFFLAGEGTSLADIVJV\VYQGKKG\EDVLGSVRRTLTHIDHSLS RCKGLSPIEPEEELATLSEESIANAVTAWERGLESLPPLRPQQ NPULPVAGERUNLITSALPEYVNVPHLGMIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QCULBAVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QCULBAVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QCULBAVPARYS RCGGSDWTPNAQFIPPGFGYFGGYEGGERAGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFIPPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRYYL\VYRPBGK\DBS FSWTDLLLKNNS\SLLNNLGNFINRA\GMFVGKYTGBLKS\LSWL GRYYLQVMEPW\KRIKGSEADRGRGTTTGLAVINAALLSWL OPYMPTVSATIQAQLQPPAGSILLTNFLCTLPAGHGIGTVSP	1	Į		EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ
DIYRWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCAFF\LADRFVEGVCFGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKELEEMLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFBDK\VFYVWFDATIGYLSITANTTDQWERWM\KNPEQVDLYQ K\FSKSRGVGVFPDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINAS\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HYTLELQHYQ\LLEKVRIRPDLRSHITIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGAKTSPKPAVVETVTTAKPQGIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPRAPKGKKKK HPSLLGAIFFYPPPSSPWPPPLYLEWNSHRKSRHFINQRGIHGE RREVPVIQLDSGNYLFSTSAICRYFF\LLSGMEQDDLTNQWLEW RREFVSDGVFGCCP\LAAAGRARGRAEVLISTVGPEDCVVPFLT RREVPVIQLDSGNYLFSTSAICRYFF\LLSGMEQDDLTNQWLEW EATELQPTLSAALYYLVVQKKG\BDULGSVRRTLTHDHSLS RQ\NCFFLAGETTSLADIVLWGALYPLLQDPAYLPEELSALHSW FGTLSTQ\SFCQR\AARRUVLKQ\QGVLALR\PYLQKQPQSPSA EGKGLSPIEPEEELATLSEEIAMAVTAWEKGLESLPPLPPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIGCVLSADVFARYS RLRQWMTLVLCGTDEVGTATETKAL\EBGLTPQEICDKYHIHA DIY\RWFNISFDIFGRTTTPQQ'TKIT\QDLFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYERARGDQCXKCGKLI NAVBLKKPQCKVCRSCPVVQSSGHLFLDLPKLEKRLEEMLGRTL PGSDWTPNAQFITPFFGFREWPSKRPWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWPDATIGYLSITANVTDWERWW\KNPBCVDLYQ FM\AKDNVPPHSLUPPSSALGAEDMYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNINS\ELLNILGNFTNRA\GMFVSKFFGG\VPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYAG\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYAG\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYAG\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYAG\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYAG\LLEKVRIRDALRSILTIS\RH LTPDDQRLLA\HVTLELQHYAG	l		1	NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
TVEQLECHCARP\LADRFYEGVCPFGYSEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEMLGRTL PGSDMTPNAQFITPFFGFREWPSKPRQ*TRDLK\WGNPGTP*E GFBDK\VFYYWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\GMQYI\QVMEPW\KRIKGSBADRGRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLITNFLCTLPAGHGIGTVSP LFOKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK KHPEAPKGKKKK HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE RKLPVLQLDSGMYLFSTSATCRYFF\LLGGWEQDDLTNQWLEW RENTELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCFLAGETSSLADIVLWGALYPLLQDPAYLPEELSALHSW FOTLSTQ\EFCQR\AARRLVLKQ\QGVLALR\PYLQKDQPSPA EKKISPIEPEEELATLSEESIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWMTLYLCGTDEYCTATETKAL\EEGLTPQEICDKYHIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDLFQLLKRGFVLQD TVEQLECEHCARF\LADRFYVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSCHLFLDLPRLEKRLEEMLGRTL PGSDWTPNAQFITFFFTTTPQVTKIT\QDIFQLK\WGNPGTP*E GFEDK\\VFYWFDATIGYSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPFISRFYL\LYIRPEGK\DSA FSWTDLLLKKNNS\ELMINGRFINRA\GMFYSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDARSILTIS\RH GRQYI\QVNEPW\KRIKGSBADRRAGTVTGLAVNIAALLSVML OPYMFYVSATIQAQLQLPPPACSILLITNFLCTLPAGHQIGTVSP	}	ł	i	RLRQWNTLYLCGTDBYGTATETKAL\EEGLTPQEICDKYHIIHA
TVEQLECHCARP\LADRFYEGVCPFGYSEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEMLGRTL PGSDMTPNAQFITPFFGFREWPSKPRQ*TRDLK\WGNPGTP*E GFBDK\VFYYWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA K\GMQYI\QVMEPW\KRIKGSBADRGRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLITNFLCTLPAGHGIGTVSP LFOKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK KHPEAPKGKKKK HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE RKLPVLQLDSGMYLFSTSATCRYFF\LLGGWEQDDLTNQWLEW RENTELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCFLAGETSSLADIVLWGALYPLLQDPAYLPEELSALHSW FOTLSTQ\EFCQR\AARRLVLKQ\QGVLALR\PYLQKDQPSPA EKKISPIEPEEELATLSEESIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWMTLYLCGTDEYCTATETKAL\EEGLTPQEICDKYHIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDLFQLLKRGFVLQD TVEQLECEHCARF\LADRFYVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSCHLFLDLPRLEKRLEEMLGRTL PGSDWTPNAQFITFFFTTTPQVTKIT\QDIFQLK\WGNPGTP*E GFEDK\\VFYWFDATIGYSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPFISRFYL\LYIRPEGK\DSA FSWTDLLLKKNNS\ELMINGRFINRA\GMFYSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDARSILTIS\RH GRQYI\QVNEPW\KRIKGSBADRRAGTVTGLAVNIAALLSVML OPYMFYVSATIQAQLQLPPPACSILLITNFLCTLPAGHQIGTVSP	1	1		DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDMTPNAQFITPFFGFREPSKPRWQ*TRDLK\WGNPGFTP*E GFBCK\VFYWFDATIGSITANYTDUØRRWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPISFFT\L\YIRPEGK\DSA FSWTDLLLKNINS\BLINNICNFTNRA\GMFYSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSBARGRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLITHFLCTLPBAGIGTVSP LFOKLENDOIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK HESLGAIFPYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE RRKPVPUQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSAALHSW FOTLSTQ\EFCQR\AARRLVLKQ\GQVLALR\PYLQKQPQPSPA EKKGLSPIEPEEELATISEEIAMAVTAWKKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYCTATETKAL\EBGLIPGEICDKYHIHA DIY\RWFNISPDIFGFTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVQSSQHFLDLPKRKLEEWLGRTL PGSDWTPNAQFITPFFFFREWPSKPRWQ*TRDLK\WGNFGTP*E GFEDK\VFYWFDATIGYLSITANYTDOWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\BLLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLECQHYHQ\LLEKVRIRDALRSILTIS\RH GRQYI\QVNEPW\KRIKGSEADRQRAGTVYGLAVNIAALLSVML OPYMPTVSATIQAQLOLPPPACSILLITNFLCTLPAGHQIGTVSP				
PGSDWTPNAOF ITPFFGREWPSKPRWO*TRDLK\WGNPGTP*E GFEDK\VFYWWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGMFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\RKIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTWSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTWSP LFOKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK HPSLLGATPFYPPPSSDWPPPLYLFWNSHRKSRHFINQRGIHGE RKYPVLQLDSGNYLFSTSALGRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVOGKKG\BDVLGSVRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEBLSALHSW FOTLSTQ\EPCQR\AARRIVLKQ\QGVLALR\PYLQKQPQSPA EGKGLSPIEPEEELATLSEESIAMAVTAWEKGLESLPPLRPQQ NPULPVAGERNVLITSALPYVNNVPHLGHIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EBGLTPQBICDKYHIHA DIY\RWFNISPDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGQCOKKGKLI NAVBLKKPQCKVCRSCPVVQSSOHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAOFITPFFGREWPSKRRW*TRDLK\WGNPGTF*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVPFSSALGAEDNYTL\YSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISFFYLL\YIRPBGK\DSG FSWTDLLLKNNS\ELLNNIGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELGHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHGIGTVSP	•	1		
GFEDK\VFYWWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\PSKSEGVGYFRDM\AHDTGIPPDISRFYL\YIPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILITNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKKSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK 5896 2967 86 HPSLLGATPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRAGRAEVLIISTVGPBCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWSQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEBLSAHHSW FQTLSTQ\EPCQR\ARRELVLKQ\QGVLALR\PYLQKQPQPSPA ECKGLSPIEPEEELATLSEESIANAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCULSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRPVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSCHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQPITPFFGFREWPSKFRWQ*TRDLK\MGNFGTF*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\YSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIPEGK\DSA FSWTDLLLKNINS\ELLNNIGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML OPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHGIGTVSP				
FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNINS\ELINNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GMQYI\QVNEPW\KRIKGSBADRQRAGTVTGLAVNIAALLSVML LPOKLENDOIESLEROFFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK 5896 2967 86 HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVGCLPVLAAAGRARGRAEVLISTVGPEDCVVFFLT RPKVPVLQLDSGNYLFSTSALCRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPTLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FOTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEIAMAVTAWEKGLESLPPLEPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEVGTATETKAL\EBGLITPQEICDKYHIIHA DIY\RWFNISPDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLSEWLGRTL PGSDWTPNAQFITPFGFFREWPSKPRWO*TRDLK\MGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\PSKSRGVGVFRDM\AHDTGIPPDISRFYL\YSHLIATEYLNYEDG K\PSKSRGVGVFRDM\AHDTGIPPDISRFYL\YSHLIATEYLNYEDG K\PSKSRGVGVFRDM\AHDTGIPPDISRFYL\YSHLIATEYLNYEDG K\PSKSRGVGVFRDM\AHDTGIPPDISRFYL\YSHLIATEYLNYEDG K\PSKSRGVGVFRDM\AHDTGIPPDISRFYL\YSHLIATEYLNYEDG K\PSKSRGVGVFRDM\AHDTGIPPDISRFYL\YSHLIATEYLNYEDG K\PSKSRGVGVFRDM\AHDTGIPPDISRFYL\YSHLIATEYLNYEDG K\PSKSRGVGVFRDM\AHDTGIPPDISRFYL\YSHLIATEYLNYEDG K\PSKSRGVGVFRDM\AHDTGIPPDISRFYL\YSHLIATEYLNYEDG K\PSKSRGVGVFRDM\AHDTGIPPDISRFYL\YSHLIATEYLNYEDG GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML GPWPTVSATIQAQLQLPPPACSILLTTFLCTLPAGHQIGTVSP	1	1		
K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLIKNINS\ELLINNIGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFOKLENDO LESLRORFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK KPPEAPKGKKKK FPSAPKGKKKK HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTITHIDESLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FOTLSTO\EPCQR\AARRLVKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCCHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSOHLFLDLPKLEKRLSEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GRQYI\QVNEPW\KRKGSEADRQRAGTVTGLAVNIAALLSVML OPYMPTVSATIQAQLOLPPPACSILLTTFLCTLPAGHQIGTVSP		1		EM A PRINTER OF THE PERSON OF
FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\RVTLELQHYIQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK 5896 2967 86 HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVFFLT RPKVPVVQLDSGNYLFSTSAICRYFF\LLSGWBQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRUNLKQ\QGVLALR\PYLQKQPQPSPA BGKGLSPIEPBEEELATLSEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLKKRGFVUQD TVEQLRCEHCARF\LADRFVEGVCPPCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFIDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPPFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGTPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRILIA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML OPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1	1		to Baronarannow Ammarnantenery (I VIDDECK/ DCA
LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\RRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDOIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK 5896 2967 86 HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHGCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\PSKSRGGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVEIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLITNFLCTLPAGHQIGTVSP			1	
GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML OPYMPTVSATIQAQLQHPPACSILLTMFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKGGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK 5896 2967 86 HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLITHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFMISFDIEGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCFFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSCHLFLDLPKLRLEEWLGRTL PGSDWTPNAQFITPFFGREWPSKRRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML OPYMPTVSATIQAQLQLPPPACSILLITNFLCTLPRAGHQIGTVSP				
QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVBTVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK 5896 2967 86 HPSLLGATPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQDSGNYLFSTSATCRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPBEEELATLSEESIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALKSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP				LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\ARREVVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVGSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGPREWPSKPRW\TRDLK\WGNPGTP\E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML GPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1		1	GNQY1 \QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK 5896 2967 86 HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSALCRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FOTLSTQ\EPCOR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEULGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGBFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1	1	1	QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
KPPEAPKGKKKK 5896 2967 86 HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVILAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FOTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTPQQYIKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML GPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP			1	
### ### ##############################	1	1	1	LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRUVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDJFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNIS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML GPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1		İ	KPPEAPKGKKKK
MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FOTLSTO\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	5896	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHI IHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1	1		MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEXVRIRDALRSILTIS\RH GNQYI\QVMEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP				RPKVPVLOLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVMEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML OPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1	1		EATELOPTLSAALYYL\VVOGKKG\EDVLGSVRRTLTHIDHSLS
FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISFFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVMEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML OPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1			RO/NCPFLAGETESLADIVI.WGALYPLI.ODPAYI.PEELSALHSW
EGKGLSPIEPEEELATLSEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISFFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVMEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML OPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1			FOTT. GTO \ EDCOD \ ADDIT. WI. KO\ OCWI. AI.D\ DVI.OKODODQDA
NPVIPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVMEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1			
RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSDKPFVDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVMEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1	1		
DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRW\AHDTGIPPDISRFYLL\YIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP				
TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRM\AHDTGIPPDISRFYL\VIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1			REROWNTE VECCTOE Y GTATETRAE (EEGET POET CONVETTINA
NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVVFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	l			DIA/KMENIZEDIEGKILLЬŐŐ/LKIL/ŐDIEŐŐPPKKGEAPŐD
PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1			TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP				NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1			PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1			GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP	1	}		FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP				K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP				FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP				LTPDDORLLA\HVTLELOHYHO\LLEKVRIRDALRSILTIS\RH
OPYMPTVSATIOAOLQLPPPACSILLTNFLCTLPAGHQIGTVSP				GNOVI OWNERW KRIKGSEADRORAGTVTGLAVNIAALLSVML
LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA	1			ODVMDTVCATTOAOLOLDDDACCTLLTNFLCTLDACHOTCTVCD
LFQKLENDQ1ESLKQKFGGGQAK1SFAFAVVEIV11AKFQQ1QA	1			A TIME I ASWIT TOWN TO THE ENGINEER AS A TIME I ASWIT TOWN TO THE ENGINE I ASKIT TOWN TO THE ENGINE I ASKIT TO THE ENGINE I ASKIT TOWN TO THE ENGINE I ASKIT TOWN TO THE ENGINE I ASKIT TOWN TOWN TO THE ENGINE I ASKIT TOWN TO THE ENGINE I ASKIT TOWN TO THE ENGINE I ASKIT TOWN TO THE ENGINE I ASKIT TOWN TO THE ENGINE I ASKIT TOWN TO THE ENGINE I ASKIT TOWN TO THE ENGINE I ASKIT TOWN TO THE ENGINE I ASKIT TOWN TO THE ENGINE I ASKIT TOWN TO THE ENGINE I ASKIT TOWN TOWN TO THE ENGINE I ASKIT TOWN TOWN TO THE ENGINE I ASKIT TOWN TOWN TOWN TOWN TOWN TOWN TOWN TOW
	<u> </u>	<u> </u>	<u> </u>	PLÄVDVIDÄTE?PVÄVLGGGÄVVISLKAAAELAITAVGÄÄTÄY

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
10.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first		
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
i i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
			LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
1			KPPEAPKGKKKK
5897	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINORGIHGE
305.	2307		MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
			RPKVPVLOLDSGNYLFSTSAICRYFF\LLSGWEODDLTNOWLEW
1			EATELOPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
1			
			RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPBELSALHSW
1			FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
			EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ
1 .	ļ		NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
]			RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
			DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
			TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
1			PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
1			GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
I		,	FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
1			K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
	,		FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
	·		LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
			GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
	•		QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
			LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
		•	LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
j l			KPPEAPKGKKKK
5898	2967		
1 2020 1	290/	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
3030	2967	86	·-
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
3030	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
	2967	. 86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEBIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEBIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEBIAWVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCERLATLSEEIAMVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLKKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLKKGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
	2907	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEBIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
	2967	86	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCERELATLSEEIAMVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWBRWW\KNPEQVDLYQ FM\AKONVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNTAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCERLATLSEEIAMVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWBRWW\KNPEQVDLYQ FM\AKONVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNTAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
5899	326	1078	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKONVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK
			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ EANEKAEEIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE
			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEBIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP
			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFYSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQOIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVQKAI
			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFYSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVQKAI PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN
			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFYSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQOIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVQKAI
			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFYSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVQKAI PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN
5899	326	1078	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVQKAI PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN
5899	326	1078	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEBLATLSEEBIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLKKGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVQKAI PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALFGANTNRKFFI KAASRDSPCLEFCPLCGVSSHDLQHRMWYHRLSHLHSRLQDLLK GGVIYPALPQPNFKSLLPLAVHWHHTASKSLTCAWQQHEDHFEL
5899	326	1078	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEBLATLSEEEIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLKKGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNTAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVQKAI PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALFGANTNRKFFI KAASRDSPCLEFCPLCGVSSHDLQHRMWYHRLSHLHSRLQDLLK GGVIYPALPQPNFKSLLPLAVHWHHTASKSLTCAWQQHEDHFEL KYANTVMRFDYVWLRDHCRSASCYNSKTHQRSLDTASVDLCIKP
5899	326	1078	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEBIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDOWBRWW\KNPEQVDLYQ FM\AKONVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNTAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVQKAI PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALFGANTNRKFFI KAASRDSPCLEFCPLCGVSSHDLQHRWWYHRLSHLHSRLQDLLK KYANTVMRFDYVWLRDHCRSASCYNSKTHQRSLDTASVDLCIKP KTIRLDETTLFFTWPDGHVTKYDLNWLVKNSYEGQKQKVIQPRI
5899	326	1078	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEBIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKONVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVQKAI PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALFGANTNRKFFI KAASRDSPCLEFCPLCGVSSHDLQHRWWYHRLSHLHSRLQDLLK KYANTVMRFDYVWLRDHCRSASCYNSKTHQRSLDTASVDLCIKP KTIRLDETTLFFTWPDGHVTKYDLNWLVKNSYEGQKQKVIQPRI LWNAEIYQQAQVPSVDCQSFLETNEGLKKFLQNFLLYGIAFVEN
5899	326	1078	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEELATLSEEBIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDOWBRWW\KNPEQVDLYQ FM\AKONVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNTAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVQKAI PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALFGANTNRKFFI KAASRDSPCLEFCPLCGVSSHDLQHRWWYHRLSHLHSRLQDLLK KYANTVMRFDYVWLRDHCRSASCYNSKTHQRSLDTASVDLCIKP KTIRLDETTLFFTWPDGHVTKYDLNWLVKNSYEGQKQKVIQPRI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
IĎ	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bequence	\=possible nucleotide insertion)
	Bequence		OKAPEEFELLSKSAI\KHEYIEDVGECHQPHDWDWAQS*ISTHG
	Ì		/YKELYLIRYNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPE
j	1.		,
]	1		NEFWVKLKPGRVLFIDNWRVLHGRECFTGYRQLCGCYLTRDDVL
		<u> </u>	NTARLLGLQA
5901	1	2121	VAIEQTSLKMMQAVGGAPARPTGEYICNQCGAKYTSLDSFQTHL
ĺ	1		KTHLDTVLPKLTCPQCNKEFPNQESLLKHVTIHFMITSTYYICE
i		1	SCDKQFTSVDDLQKHLLDMHTFVFFRCTLCQEVFDSKVSIQLHL
	}		\AVKHSNEKKVYRCTSCNWDFRNETDLQLHVKHNHLENQGKVHK
		1	CIFCGESFGTEVELQCHITTHSKKYNCKFCSKAFHAIILLEKHL
	1		REKHCVFETKTPNCGTNGASEQVQKEEVELQTLLTNSQESHNSH
ļ.			
1			DGSEEDVDTSEPMYGCDICGAAYTMETLLQNHQLRDHNIRPGES
1			AIVKKKAELIKGNYKCNVCSRTFFSENGLREHMQTHLGPVKHYM
1			CPICGERFPSLLTLTEHKVTHSKSLDTGNCRICKMPLQSEEEFL
1			EHCQMHPDLRNSLTGFRCVVCMQTVTSTLELKIHGTFHMQKTGN
			GSAVQTTGRGQHVQKLYKCASCLKEFRSKQDLVKLDINGLPYGL
	,	1	CAGCVNLSKSASPGINVPPGTNRPGLGQNENLSAIEGKGKVGGL
1			KTRCS*LATFKF*VLKVELPEPHPKPFHRGVSRPDSNSTQLKTP
			QVSPMPRISPSQSDEKKTYQCIKCQMVFYNEWDIQVHVANHMID
İ	j	j	EGLNHECKLCSOTFDSPAKLOCHLIEHSFEGMGGTFKCPVCFTV
[1		FVOANKLOOHIFSAHGOEDKIYDCTQCPQKFFFQTELQNHTMTQ
1			HSS
<u></u>	<u> </u>	<u> </u>	
5902	712	209	LKNRRRSRPSIRQSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF
	į		IPLKPRQ*ED*MFQSWLHAWGDTLEEAFEQCAMAMFGYMTDTGT
1	į.	1	VEPLQTVEVETQGDDLQSLLFHFLDEWLYKFSADEFFIP\GWGE
	1	1	EFSLSKHPQGTEVKAITYSAMQVYNEENPEVFVIIDI
5903	2106	735	DTPGPSLPSTTAPFSLRSLSFPSRPSYLLPGDPQPLQGRGLPTT
	1	1	PALFALSAVPGGAASPMPPSGLRLLPLLLPLLWLLVLTPGRPAA
	1		GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP
I	1	1	LPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVET
1.	ł	İ	HNEIYDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
1	1	İ .	KLKVEOHVELYOKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV
			ROWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGR\RGDL
}	1 .	1	ROWLSRGGE I EGERLSANCS COSKON I LOVO DINGE I TOR (RODL
L	1	l .	ATIHGMNRPFLLLMATPLERAQHLQS\SRHRQAL\DTNY\CFSF
İ	1	1	HGGRNCLRC/VHC+HLIFRKDL\GW\KWI\HE\PKGYHANFC\L
1		1	GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\
1		1	LPIVYY\VGRKPKVEQLSNMIVRSCKCS
5904	3	1126	MMEEIENAINTFKEEQRLIYEELIKEEKTTNNELSAISRKIDTW
		1	ALGNSETEKAFRAISSKVPVDKVTPSTLPEEVLDFEKFLQQTGG
		1	RQGAWDDYDHQNFVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ
1	1	1	HEKWYOKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP
		1	VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL
	1		KEEEEKEKKHOKEROROFKLKLLLESYTOOKKEQEEFLRLEKEI
1			
1			REKAEKAEKRKNAADEISRFQERDLHKLELKILDRQAKEDEKSQ
1			KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW
			ATSTYPT*GYSNLETRNTEKSMR
5905	287	2912	MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP
1			DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR
1		1	QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIEWH
			RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL
1			TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\
			SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS
1			WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF
i			
			SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI
			WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK
			KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS*
1			LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMVKF*FIEM
			*LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A
			QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK
	1		REGGL*YLTLFISVYFS*LVFGINGFQYSFVVKLHCLYFMFRLI
ł:			
			EKT.TEMPNI*NDICMSALINI, KTOFNI, TMTLSIFFKLI, I TYNA*
			FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA* YNLN*I*QF*YKMCHFVLCMSE*SYNICLFIAGF\LWNMDKYTM

070	1 - 1/ - 1	<u> </u>	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
	204.0	<u> </u>	(-possible indefedence insertion) IRKLEGHHHDVVACDFSPDGALLATASYDTRVYIWDPHNGDILM
•			TRADEGRANDVACDFSPDGALLATASYDTRVYIWDPHNGDILM
ł	•		EFGHLFPPPTPIFAGGANDRWVRSVSFSHDGLHVASLADDKMVR
i		·	FWRIDEDYPVQVAPLSNGLCCAFSTDGSVLAAGTHDGSVYFWAT
	<u> </u>		PRQVPSLQHLCRMSIRRVMPTQEVQELPIPSKLLEFLSYRI
5906	146	2038	REGAGSGRMASGA\YNPYIEIIEQPRQRGMRFRYKCEGRSAGSI
	}		PGEHSTDNNRTYPSIQIMNYYGKGKV\RITLVTK\NDPYKPHPH
1			DLVGKDCRD\GYYEAEFGQE\RRP\LFFQN\LGIRCVKKKEVKE
l			A\IITR\IKAGINPFDVP*KQLNDIEDCDLDVVRLWFRVFLPDG
j]		HGNL\TTALPPV\VSSPIYDNRAPNTAELRVCRVNKNCGSVRGG
i	i		DEIFLLCDKVQKDDIEVRFVLNDWEAKGIFSQADVHRQVAIVFK
			TPPYCKAITEPVTVKMQLRRPSDQEVSESMDFRYLPDEKDTYGN
1			KAKKQKTTLLFQKLCQDHVETGFRHVDQDGLELLTSGDPPTLAS
i			
1	1		QSAGITVNFPERPRPGLLGSIGEGRYFKKEPNLFSHDAVVREMP
1	1 .		TGVSSQAESYYPSPGPISSGLSHHASMAPLPSSSWSSVAHPTPR
1	1		SGNTNPLSSFSTRTLPSNSQGIPPFLRIPVGNDLNASNACIYNN
1		•	ADDIVGMEASSMPSADLYGISDPNMLSNCSVNMMTTSSDSMGET
			DNPRLLSMNLENPSCNSVLDPRDLRQLHQMSSSSMSAGANSNTT
			VFVSQSDAFEGSDFSCADNSMINESGPSNSTNPNSHVFVQDSQY
L			SGIGSMQNEQLSDSFPYEFFQV
5907	99	1873	TYLLSSWSS**NLDTKIKSQVKV/RKGHKKISWPYPQPAKQNGK
i			KATSKVPSAPHFVHPNDHANREAELKKKWVBEMREKQQAAREQE
	1		RQKRRTIESYCQDVLRRQEEFEHKEEVLQELNMFPQLDDEATRK
			AYYKEFRKVVEYSDVILEVLDARDPLGCRCFQMEEAVLRAQGNK
			KLVLVLNKIDLVPKEVVEKWLDYLRNELPTVAFKASTQHQVKNL
1		•	NRCSVPVDQASESLLKSKACFGABNLMRVLGNYCRLGEVRTHIR
1	ļ i		VGVVGLPNVGKSSLINSLKRSRACSVGAVPGITKFMQEVYLDKF
			THE LD DOTTING DISCRIPTION AND PROPERTY OF COLUMN AND PROPERTY OF CO
		<u> </u>	IRLLDAPGIVPGPNSEVGTILRNCVHVQKLADPVTPVETILQRC
		*	NLBEISNYYGVSGFQTTEHFLTAVAHRLGKKKKGGLYSQEQAAK
]			AVLADWVSGKISFYIPPPATHTLPTHLSAEIVKEMTEVFDIEDT
1		•	EQANEDTMECLATGESDELLGDTDPLEMEIKLLHSPMTKIADAI
			ENKTTVYKIGDLTGYCTNPNRHQMGWAKRNVDHRPKSNSMVDVC
	'		SVDRRSVLQRIMETDPLQQGQALASALKNKKKMQKRADKIASKL
	· .		SDSMMSALDLSGNADDGVGD
5908	247	975	HCGIKKRGEGSGSPSPASGGFQLGCQIPEPSLPSEEETHPHTRA
			HTRTLRATLTRRPPRSHSTRLRFPMPLDGDGGLASWK/PMRER*
			GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI
			VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKIEERSQT
]			VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK
			VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK VLPDRKGWSCSSGNKVKTTRVTH
5909	1	5002	
-:	-	5002	PAIPGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP
	1		SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR
			CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR
	i		STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS
			ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV
	ĺ		SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS
	į.		DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK
1	ł.		IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL
l	İ		GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI
l			TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE
		}	CCECHADEOL CECCADDEDONOCALI CEDAESTA STATES CONTRACTOR CECCADDEDONOCALI CEDAESTA CONTRACTOR CONTRACTOR CEDAESTA CONTRACTOR CEDAESTA CONTRACTOR CEDAESTA CONTRACTOR CEDAESTA CONTRACTOR CEDAESTA CONTRACTOR CEDAESTA CONTRACTOR CONTRACTOR CEDAESTA CONTRACTOR CONTRACTOR CEDAESTA CONTRACTOR C
į		ļ	SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM
i			VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE
I			DGEAPASTKEEPLEEEATTQSRAGREEEEKEQEEEGDVSTLEQG
	ļ		EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR
ŀ			IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV
- 1			AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT
1			HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS
	1		SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD
1			EEEENSAFESVPDSMQSPELDPESTNGAGPWODELAAPSGHVER
			SPEGLES PVAGPSNRREGECPILHNSOPVSOLPSLRPEHHHYPT
		·	IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR
		ļ	RSGSIQQMEQLNRRYQNIQRTIATERSEEDSGSQSCEQAPAGGG

Predicted Pred				
NO: location corresponding to first amino acid residue of maino acid residue of amino acid residue of amino acid sequence Peroline Q-edutamine, R-Argargine, Peroline, Gentlement, Peroline, Verbaline, Reading of amino acid sequence Peroline, Territorine, Verbaline, Reading of amino acid sequence Peroline, Verbaline, Reading of amino acid sequence GGGGSDERESGSSILLARREGELSFVSSGNITHLIGSPAVET THE PEROLINE, Verbaline, Reading of the Verbaline, Reading of the Verbaline, Reading of the Verbaline, Verbaline, Verbaline, Verbaline, Verbaline, Verbaline, Verbaline, Reading of the Verbaline, Ver	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cortesponding to first anino acid anino acid residue of anino acid sequence Colon	ID			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
to first maino acid residue of amino acid sequence sequen	NO:			
to first anino acid residue of anino acid sequence sequ	1			
amino acid residue of amino acid sequence Sequence GGGGSDEPESSGSIDLERGSLEFVANSCHILKOWN, **Stop Codon, /-possible nucleotide deletion, /-possible nucleotide				
residue of amino acid sequence amino acid sequence Codon, /=possible nucleotide deletion, /=				P=Proline, Q=Glutamine, R=Arginine,
### squence Sequence Codom, /~possible nucleotide deletion, /~possible nucleotide insertion)				S=Serine, T=Threonine, V=Valine,
Sequence Sequence	1			
GGGSDSENSSSSSSLDERESSLSPYNOSKITLLLGSPANKET TNEEPFVLHANYSARVFISSTCLKEMILLGVERDANNERSKOR NEDLWIFINNFADTRIELPROME KETDOGGES FYDEINSRATTE TDERTIPLONGRIPHILITREHUNGLIRSSYSAGEASSUSWINGASI. LARPGHSLVARA TRSGGGGES LPLAVNDKTVAFLRGPNI FEMILOS ROPSLARMHILESETH TYETENMIGH KISCADALVILLISLFEE EIMSYVPLQAARHOCKSFSPRCSCSSSPONSFOLGRASARAPSP VREDPFAKLRYPYRKLEAGFGGGGFKKLSCADALVILLISLFEE EIMSYVPLQAARHOCKSFSPRCSCSSSPONSFOLGRASARAPSP VREDPFAKLRYPYRKLEAGFGGGGFKKLSCADALVILLISLFEE EIMSYVPLQAARHOCKSFSPRCSCSSSPONSFOLGRASARAPSP VREDPFAKLRYPYRKLEAGFGGGGFKKLSCADALVILLISLFEE EIMSYVPLOARHOCKSFSPRCSCSSSPONSFOLGRASARAPSP VREDPFAKLRYPYRTALLIKURGYTSGKTLG LALLI HQVLLDAPF7\PPYRALLIKLECTOLLEWFRSGKTLG LALLI HQVLLDAPF7\PPYRALLIKLECTOLLEWFRSGKTLG LALLI HQVLLDAPF7\PPYRALLIKLECTOLLEWFRSGKTLG LALLI HQVLLDAPF7\PPYRALLIKURGYTSGKTLGVLFUNGFYFUNDSKLSVVPDARELE VLERMVKRWSGRVVCQTFALLWFSCHLSWFSTASKTGVALGT BURLAGLUGVTGTSSVVPGGFAAPPREPMGLRRFLP*KKRGKTTSS VREDPFACTOLENDERVSTRATLESCHLSTENSTLSVVPDARELE UNIAGRASITENSTLATILLALGSSLATFLEDAVILVTRITCSTVAVC FRENCHLARDSTSSLATFLEDAVILVTRITCSTVAVC FRENCHLARDSTSSLATFLEDAVILVTRITCSTVAVC FRENCHLARDSTSSLATFLEDAVILVTRITCSTVAVC FRENCHLARDSTSSLATFLEDAVILVTRITCSTVAVC FRENCHLARDSTSSLATFLEDAVILVTRITCSTVAVC FRENCHLARDSTSSLATFLEDAVILVTRITCSTVAVC FRENCHCALLESSSNSPARAS LADIT TOWERRAGLIFVFILVET BROAD FRENCHLARDSTSLATFLEDAVILVTRITCSTVAVC FRENCHCORGANETICTPORTERSTLATICLOCATION FRENCHLARDSTSSLATFLEDAVILVTRITCSTVAVC GERMANGCCTI LAULININIATIVTRISCHSTVATION FRENCHLARDSTVALUTRICTSTVANDERFORDITTYSTVAVC GERMANGCCTI LAULININIATIVTRISCHSTANDAVETTYFORGENTIAGRITTYSTVAVC GERMANGCCTI LAULINIANITYTRISCHSTANDAVETTYFORGENTIAGRITTYSTVAVC GERMANGCGGESTAVAAALAULINITSTVANDAVCHALDAVA FREDERFORMATOR FRENCHLARDSTVANDAVCHALDAVATISTVANDAVCHALDAVA FREDERFORM FRENCHLARDSTVANDAVETTISTVANDAVCHALDAVA FRENCHLARDSSPIPMTLIANIANA FRENCHLARDSTVANDAVATISTVANDAVCHALDAVA GGGSSELDPERVOLUTURERSTRASSFRONDAVATISTVANDAVCHALDAVA FRENCHLARDSSPIPMTLIANIANA FRANCHALDAVATISTVANDAVCHALDAVE GGGSSELDAVATOR FRENSINANS GERERFORMATARAMINGCLIADA FRENCHLARDSTVANDAVATOR FRANCHALDAVATISTVANDAVCHALDAVE G	1	amino acid	sequence	
TIMESPETULHANYSAURUFISSTICLEMILLAVERANFERKOR NEDLAWTINMFADURELPROME LENDOGRES FUGINSRATT IDRIPLOMORLIPHILITROHLOGIRS SYSAGRASSE LAPPORISUVALIS REGURES LIPANORU TVAFIROPHI PIPEMIOR ROPSILARIMILERIHYTETERIMIGEKISCOADLYILLISLFEE EIMSYVPLOARHIGUSTENOKU TVAFIROPHI PIPEMIOR ROPSILARIMILERIHYTETERIMIGEKISCOADLYILLISLFEE EIMSYVPLOARHIGUSTENOKU TVAFURGEBULDYSCOLINITY VARYSKELORIKU VITVEUSEBULDYSGREEFFELLOGULNIT UPAYSKELORIKU VITVEUSEBULDYSGREEFFELLOGULNIT VYGLPEYSANDTYTVOLIS PMARAVENILLEWFFISGRIIG LIALLI ROYLLDAPFTY NEPTVOQUES MARAVENILLEWFFISGRIIG LIALLI ROYLLDAPFTY NEPTVOQUES MARAVENILLEWFFISGRIIG LIALLI ROYLLDAPFTY NEPTVOQUES MARAVENILLEWFFISGRIIG LIALLI ROYLLDAPFTY NEPTVOQUES MARAVENILLEWFFISGRIIG LIALLI ROYLLDAPFTY NEPTVOQUES MARAVENILLEWFFINATER FOR THE ROYLLOGULD THE STATEMING THE ROYLLOGULD THE STATEMING OF THE		sequence ·		
NRILANDINGADTRILLERGMEILTCDOCKSFFVDENSRATE TORRIPLONGRIPHILTROHILGRESSTAGRASSIVSRRGASI LARROHSLWARTSCHOHESSIPLAYNDELVAFIROPHIPENDEL RICHARDHSLWARTSCHOHESSIPLAYNDELVAFIROPHIPENDEL RICHARDHSLWARTSCHOHESSIPLAYNDELVAFIROPHIPENDEL RICHARDHSLWARTSCHOHESSIPLAYNDELVAFIROPHIPENDEL RICHARDHSLWARTSCHOHESSIPLAYNDELVAFIROPHIPENDEL VIRTUP VIGUARSH VIRTUP				
TDRRIPLONGLENHITHROHLORIRSYSAGRASEVSRINGSEL LARPORISLARINFLERKIHY IETSONIGLEKLSCDADLVZILLSFEE BURSYVPLQARPOYS FPRES CSS PONS POLYGOLAGAFFEE BURSYVPLQARPOYS FPRES CSS PONS POLYGOLAGAFFEE BURSYVPLQARPOYS FPRES CSS PONS POLYGOLAGAFFEE BURSYVPLQARPOYS FPRES CSS PONS POLYGOLAGAFFEE BURSYVPLQARPOYS FPRES CSS PONS POLYGOLAGAFFEE BURSYVPLQARPOYS FPRES CSS PONS POLYGOLAGAFFEE BURSYVPLQARPOYS FRANCE CSS PONS POLYGOLAGAFFEE BURSYVPLQARPOYS FRANCE CSS POLYGOLAGAFFEE BURSY FRANCE COLOR FRANCE FROM FRANCE CLICACY FOLYGOLAGAFFEE BURSY FRANCE COLOR FRANCE FROM FRANCE CLICACY FOLYGOLAGAFFEE BURSY FRANCE COLOR FRANCE FROM FRANCE FROM FRANCE FRANCE FROM FRANCE	j		·	
LARROHSLWAIRSCHOHESLPLAYNDKIVAFIROPHITEMUS ROPSIARNHITLEKKHIVIETESONIGEKLSCODIUVILISIFEE BIMSYPIQAAPHOYSYSPRCSSCOSSONIGHLORASKARJEY YREDPERALENPYRICEAROFGOSKIKUITEROHLEKOFTON VMAYSRKELORMKILVYFYGEBGLDYSGGEREFFILISORLIFTON VMAYSRKELORMKILVYFYGEBGLDYSGGEREFFILISORLIFTON VMAYSRKELORMKILVYFYGEBGLDYSGGEREFFILISORLIFTON WANDENTITUILDIPTYMEBUYGGUTERLISSORJATOVHEKNEK EYIEMWKREVERGVVQOTFALVUGSTEUVOSRLVSUPCRARES EYIEMWKREVERGVVQOTFALVUGSTEUVOSRLVSUPCRARES EYIEMWKREVERGVVQOTFALVUGSTEUVOSRLVSUPCRARES EYIEMWKREVERGVVQOTFALVUGSTEUVOSRLVSUPCRARES EYIEMWKREVERGVVQOTFALVUGSTEUVOSRLVSUPCRARES EYIEMWKREVERGVVQOTFALVUGSTEUVOSRLVSUPCRARES EYIEMWKREVERGVVQOTFALVUGSTEUTOSRLVSUPCRARES EYIEMWKREVERGVVQOTFALVUGSTEUTOSRLVSUPCRARES EYIEMWKREVERGVVQOTFALVUGSTEUTOSRLVSUPCRARES EYIEMWKREVERGVVQOTFALVUGSTEUTOSRLVSUPCRARES TERMYKREVERGVVQOTFALVUGSTEUTOSRLVSUPCRARES EYIEMWKREVERGVVQOTFALVUGSTEUTOSRLSVENSTEUTOSRCVSTEUTOSRLVSUPCRARES EYIEMWKREVERGVVQOTFALVUGSTEUTOSRCVSUPCRARES LUTAGTASIOLASSIPSSIPSE PEWWAGCESS PTASMYQOTFIL LLIKKELQ\R*CALASSIPSSIPSE PEWWAGCESS PTASMYQOTFIL RGAQLVGSTILSSAJCSSTUSTANSTANTUGSTEUTOSRCVSUPCRARES ELLILITETHITUTUTUTUTYTRYTYRROHKVGYETTSSPDLOLIALKALKENN AMTMKGCCTH ELLILITETHITUTUTUTYTYTRYTYRROHKVGYETTSSPDLOLIALKALKENN AMTMKGCCTH S911 109 591 591 924 277 MILIKALMILGALALFTVARECGGBDLVABHVASYAVRILVGSYGP GHRIVQOGALGILIAVUTILIPSPRVILIGALITYVULYET GHRIVQOGALGILIAVUTILIPSPRVILIGALITYVULYET GHRIVQOGALGILIAVUTILIPSPRVILIGALITYVULYET GHRIVQOGALGILIAVUTILIPSPRVILIGALITYVULYET GHRIVQOGALGILIAVUTILIPSPRVILIGALITYVULYET SQQYSHBFDCDEFTYVDLERKETVAQDALPHASYAVRILVGSYGP SQQYSHBFDCDEFTYVDLERKETVAQDALPHASYAVRILVGSYGP SQQYSHBFDCDEFTYVDLERKETVAQDALPHASYAVRILVGSYGP SQQYSHBFDCDEFTYVDLERKETVAQDALPHASYAVRILVGSYGP SQQYSHBFDCDEFTYVDLERKETVAGARATAGUTYTAGA SQCYSHBFDCDEFTYVDLERKETVAGARATAGUTYTAGA FYGERSPPPERALGGERGARATAGUTARESPELIKMGALITYLDFYTAGA SQCYSHBFDCDEFTYVDLERKETVAGARATAGUTYTAGATAGUTARAGATAGATAGATAGATAGATAGATAGATAGATAGATA	ļ ·	1		
RQPSLARMYLREXTHY INTEGNIGLEKISCOADLUTILISTER BIMSYVPLQAREPOYS PPROSES SORONS OLD SARAPSE YREDPEAKLEN PYRKLEA KORGOGOPCK KILL IRROHLLEGTEN WAYSRKELORNKLYVPT VERBEDLDY SOGPREE PPLISOBLEND YYGLFEYSANDTYTYOJS PMSAF VENHLEWFRYSGRILD (LALI HQVLLDAFF \ RPFYRALIA KLEC\D\ LISIDET LDEEFINGOLEND YYGLFEYSANDTYTY VIS SMSAF VENHLEWFRYSGRILD \ LALI HQVLLDAFF \ RPFYRALIA KLEC\D\ LISIDET LDEEFINGOLEND MKONNIT DILDIT PURBEV SEGOTY TERRISOGS ANTOTYTEOKK EYTERMYKKEVERGY VQQTEAL VROEFTEN VYDSRLVSVEPAREE LVIAGTAS I LISIDEMENTEYS ROCHOGISLIVIRE PROTECTION ORLELLOF VTGTSS VPYEOF PAPPWED PROTECTION AND THE PROTECTION GRIELLOF VTGTSS VPYEOF PAPPWED PROTECTION AND THE PROTECTION FYLLIM VWEOF SEGOT SEGOT AND THE PROTECTION AND THE PROTECTION FYLLIM VWEOF SEGOT SEGOT AND THE PROTECTION AND THE PR	1		1.	
EIMSYPIQAAPHOYS FSPRCSS PONSPOLDRASARAPS VREPPRALENS PYRLEAR PROGREK KLI I TROUBLEST FIND VMAYSEKELORMKL, VYT FYGERGLDY SGERREF FYLLSOELTH VMAYSEKELORMKL, VYT FYGERGLDY SGERREF FYLLSOELTH VMAYSEKELORMKL, VYT FYGERGLDY SGERREF FYLLSOELTH VMAYSEKELORMKL, VYT FYGERGLDY SGERREF FYLLSOELTH VMAYSEKELORMKL, VYT FYGERGLDY SGERREF FYLLSOELTH VMAYSEKELORMKL, VYT FYGERGLDY SGERREF FYLLSOELTH VMAYSEKELORMKL, VYT FYGERGLDY SGERREF FYLLSOELTH VMAYSEKELORMKL, VALUE FY STENDEN WARD FYLLSOELTH VMAYSE FY STENDEN WARD FYLLSOELTH VMAYSE FY STENDEN WARD FYLLSOELTH VMAYSE FY STENDEN WARD FYLLSOELTH VMAYSE FY STENDEN WARD FYLLSOELTH VMAYSE FY STENDEN WARD FYLLSOELTH VMAYSE FYLLSOELTH VMAYSE FYLLSOELTH VMAYSE FYLLSOELTH VMAYSE FYLLSOELTH VMAYSE FYLLSOELTH VMAYSE FYLLSOELTH FASHLVE WARD FYLLSOELTH FYLLSOELTH FASHLVE WARD FYLLSOELTH FYLLSOELTH FASHLVE WARD FYLLSOELTH FYLL	İ			
YRRDPSALENNYFYRILEAKGFOQGESILLITRIDHILEGOFFNO VMAYSKRELGRINKILVYTVEGEIDLYSGERSPFFILSGELPYN YVGLPSYSANDTTTVOLSPMSAFVENHLEWFFSGRILO; JALI HQYLDAPFT PEYKALL VELOCYOLSPLOSPLOSPERSPFFICIAL MONDITDILDLTFTVNBEVFGQVTERELKSGGANTQVTERKK EYIERWIKWRVERGWUQTSALURGPYEVDSRILVSVFDARRELE LVIAGTASIOLNOMENNTETRGYSTWOLGVYBLVSVFDARRELE LVIAGTASIOLNOMENNTETRGYSTWOLGVYBLVSVFDARRELE LVIAGTASIOLNOMENNTETRGYSTWOLGVYBLVSVFDARRELE LVIAGTASIOLNOMENNTETRGYSTWOLGVYBLVSVFDARRELE LVIAGTASIOLNOMENNTETRGYSTWOLGVYBLVSVFDARRELE SPIO 1526 446 VABERAMBEGRTOIKLDBRYTADLLEVLKTNYGFSSCFSOPT AQCILRALGPUNGLAUSTHILLAGSIATIFEDDAVLYKNYTLCG FYLLMINWWSGFGKSAVLUKHTIDTPMWVITTGCCCCCCCCPRI IKRRILLAGSASTVUSVLCCFGLMIPSSLVLJENTTTSTAVC FYLLMINWWSGFGKSAVLUKHTIGTSGANGLAGS FYLLMINWWSGFGKSAVLUKHTIGTSGANGLAGS RAGOLVGSTLSSA/CSTLLAIMINGISTGACGCCCCCCCCRI LLITRKLOQR CKALLAGSA/CSTLLAIMINGISTGACGSOPTYSSKTTSGVYNCH LLITRKLOQR CKALLAGSA/CSTLLAIMINGISTGACGSOPTYSSKTTSGVYNCH LLITRHLOQRS FSVLANGGALGASPPYSSKTTSGVYNCH LLITRHLOQRS FSVLANGGALGASPPYSSKTTSGVYNCH LLITRHLOQRS FSVLANGGALGASPPYSSKTTSGVYNCH LLITRHLOQRS FSVLANGGALGASPPYSSKTTSGVYNCH LLITRHLOQRS FSVLANGGALGASPPYSSKTTSGVYNCH LLITRHLOQRS FSVLANGGALGASPPYSSKTTSGVYNCH LLITRHLOQRS FSVLANGGALGASPPYSSKTTSGVYNCH LLITRHLOQRS FSVLANGGARGASPLAYLOGS GGFHVQGACELL/MVVILHIPSPPRVUGLIGA AMTMIGCCTH SPI1 109 595 GLFLAPCTQGKSGLENYNGPSPROGRANGGVSLLSPULPGSYGF GGHTVQGACELL/MVVILHIPSPRPVUGLIGA- FSVLANGGACHAPPSCAGASPPROPROGRANGGVSLLSPULPGSPROPPLICT GCHROGAAPRAYTYTVASPCGGEDIVADIVASYGVSULYQSYGF SCOSSIBPOGEPPYVOLEKERVNQLDLEFRERFRFPOPFALTN LAVLKHININIVIRSSNSTAATNSVEGVTVFSSSPYKLOGPTLI CLVDNIFPPVIVITINISNSHSVTGGVSETRPSFRSSPKSHFILLQU VYSSSPPFF****OL**TAKVEGLGAMFERPLICHMGASIFTYTUS LAVLKHININIVIRSSNSTAANSVEGVTVFSSSPKSHFILLQU VYSSSPPFF****OL**TAKVEGLGAMFERRIGATICAGSYCHGG HLUFFLYTHTRIPRFCQCGGSRVANLOCALTORYTGSPKSHFILLGAGSPERFRCPOPGALTA S913 46 1198 DERCSVSGSVRQALVACSTCTPPGBERAGICLAGSYCHGG HLUFFLYTHTRIPRFCQCGGSRVANGALVACSTCTPGBERAGICAGGACGAGS GGRANGGACTAPSSACAGGAGSPERFRUNGGALDAGAA KARTAGAGACTAPSSACAGAGAA AQATDSSDPLHTRENGRAGAATAGATTAGABANGSCLOLD S914 960 124 NIGGSSLPFS	[
VMYSKELQRNILYTVTOGENGAPVENILEARFFFSGRILG\LALL HQYLLDAFFT\RPFYKALL\RLDC\D\LSDLSYLDREFFSGRILG\LALL HQYLLDAFFT\RPFYKALL\RLDC\D\LSDLSYLDREFFSGRILG\LALL HQYLLDAFFT\RPFYKALL\RLDC\D\LSDLSYLDREFFSGLIG\M MKDNITDIDLDTYNBEVGOYTERLKSGANTOVTEKHKK EYIERMYKKWYERGVVQQTEALVRGYTEVVDSRIVSVFDARELE LVIAGTASIDLINDKRINTERTGGYHDGHLVIRKWAAVERFINE QRERLIQFVTSTSVYYEGFAAPPBBMENGERFIP-YKRGKITS LPFRG\HTCLQPHWCLQPHWCLAPPBWENGHERFIP-YKRGKITS LPFRG\HTCLQPHWCLAPPBWENGHERFIP-YKRGKITS LPFRG\HTCLQPHWCLAPPBWENGHERFIP-YKRGKITSTFGT AQLLAR-GPVELALTSILTLLALGSIAIFLEDAVYLYKTNTLCP KRAFLLAWSASPTVSVLCCFGLAIF PRSILVAGIFSGPFT AQLLAR-GPVELALTSILTLLALGSIAIFLEDAVYLYKTNTLCP YLIMLWAWEGFGKKAAVLETLRDTPHWVHTGPCCCCCCCCPGRL LLTKKLQ\RCALLARTICAITSICTLLALGSIAIFLEDAVYLYKTNTLCP FYLLMLWAWEGFGKKAAVLETLRDTPHWVHTGPCCCCCCCCPCRL LLTKKLQ\RCALLARTICAITSICTLLARGAITSICTLARGAINTGFSANTOGTAT RAQLVGSTLSSA/CSTLLALWTLGIISRGALLKOONMAKP ALPQVLLILTALQPSIFSULANGGGIACSPPTSSKTSQVMNCH LLLISTFLINTVITRMYYRKTOKIKVGYETTSSPDLDINLKRALRWM AWTMKGCTH LLISTFLINTVITRMYYRKTOKIKVGYETTSSPDLDINLKRALRWM AWTMKGCTH CGHHROGGASFKYRPTDVOGEORPTOKAHRGGVSLLSPRLCS GTISAHCHILRJSSSNSPAPAS-LAGITGGYCHLIFTVFLUST GFHHVQGAGLELL/NVYHHLPSPRKVLGLQA 5912 924 277 MILKKALMIKALVIKRSSNSPAPAS-LAGITGGYCHLIFTVFLUST LAVKLIMIALVIKRSSNSPAPAS-LAGITGGYCHLIFTVFLUST LAVKLIMIALVIKRSSNSPAPAS-LAGITGGYCHLIFTVFLUST LAVKLIMIALVIKRSSNSPAPAS-LAGITGGYCHLIFTVFLOGNTLI CLVDNIFPPVVNITULSNGHSYTEGGSBIVAGULTVFLOGNTLI CLVDNIFPPVVNITULSNGHSYTEGGSBIVAGULTVFLOGNTLI CLVDNIFPPVVNITULSNGHSYTEGGSBIVAGULTVFLOGNTLI CLVDNIFPPVVNITULSNGHSYTEGGSBIVAGULTVFLOGNTLI CLVDNIFPPVVNITULSNGHSYTEGGBEPAGICLACGYBCHGG HKLFELYTKRHFRCQCGNSKFKKALSCKLLEPKGNOMMCGTH DSEKCSYSGGSVKRQALVACSTCTPDGBEPAGICLACGYBCHGG HKLFELYTKRHFRCQCGNSKFKKALSCKLLEPKGNOMMCGTH PFGLYCICKRPYPDPBBIPDENICQVVCEDMFHGRHAGAIPPE SGDPGMVCQACMKGSFLHARASKSGCVLLD PFGGSSSSBLICTCDCMKMYGDLDVLFITDEVDTVLAYENKGKI AQATRSBDUHDTLSSMRVQOVELLC/GJOVCADMFHGRHAGAI TYGAVURGHTGAPATS S915 960 124 NLGGSELPPERALPTQOVASHNORRVDFYLASIEDMLVAIJGGRN RGALSSVETTSPKTDSWSVAGLRRFTYGHAGTTKKKKI AQATRSBDUHDTLSSMRVQOVALVAGGSTGGRPCPGGSPCSCANDH RICHARDAGAIPP	ł		1	
YYGLFEYSANDTTTYQISPNSAFVENILEWFETSGRIED/ALLI HQYLDAPFT YRPKALALYLDCY ALDE YLDEEFFIGION MKONNITDILDLFTYNREVFGQYTERLKSGGANTGYTEKKK EYIERWYKWRVERGVYQTEALVRGYFEVVYDFARELE LVIAGTASIOLNDWANNTEWRGYFEVVYDFARELE LVIAGTASIOLNDWANNTEWRGYHDGHLVIRWFAAAFERPINE QRIRLLQFYNGTSSVPYRGFAAFPWBPMGLRRFLP*KKMGKITS LPPRG\HTCLALAGSTAFTHALEKLITA\VEETSTFGT \$910 1526 446 446 VABFAAMBEGRTOIKLDFRYTHALEKLITA\VEETSTFGT IKRRILAKSSAFTVYSUCCGGLAIPGBLVKINNGIPSAGSPDFT AAGLERAGSPUFLLIALAGSTAFTHALDGYLVYRNTLCG FYLLMLWWBGFGGKEAVLETHATDYPMWVITHOFCCCCCCCCCPL LLTRKKLQ\R*CMALSNTPS*R*R*PSPPASMTQOTFL RGAGLIGGTISSA, VCSTLLALWTLGIISRQARLHGENMGAKF ALFQVLLILTALQPSIFSVLANGGJACSPPYSSKTRSQVNNCT RGAGLIGGTISSA, VCSTLLALWTLGIISRQARLHGENMGAKF ALFQVLLILTALQPSIFSVLANGGJACSPPYSSKTRSQVNNCT RGAGLIGGTISSA, VCSTLLALWTLGIISRQARLHGENMGAKF ALFQVLLILTALQPSIFSVLANGGJACSPPYSSKTRSQVNNCT RGAGLIGGTISSA, VCSTLLALWTLGIISRQARLHGENMGAKF ALFQVLLILTALQPSIFSVLANGGJACSPPYSSKTRSQVNNCT RGAGLIGGTISSA, VCSTLLALWTLGIISRQARLHGENMGAKF ALFQVLLILTALQPSIFSVLANGGJACSPPYSSKTRSQVNNCT RGAGLIGGTISSAFTARAGTIGCCHHAQLIFVULFT GFHVQGAGLILLALLAYUVLHLPPSPYSTLAGGIACSPPYSSKTRSQVNNCT AWTHKCCCTH GFHVQGAGLILLALLAYUVLHLPPPPVLGLGAL 5911 109 595 QLPIABPCTGRGGLEMSFKPQSFIRSKHRGVSVLLSPRLECS GTISALCULRPSSNSDAPAS*LAGITGCCHHAQLIFVULFT GFHVQGAGLILLALLAVULTHAPPPRVLGLGAL TYPULKENLANUTYLRSSNSDAPAS*LAGITGCCHHAQLIFVULFT GFHVQGAGLILLALLAVULTHAPPPRVLGULGAL CLIVANITPPVVNITHISSGRISVTEGVSSTRPSSFKSDHFILLDO VTSSSPFE**DI-TALVEGLGAWFEDLLANGSPTLTQGPNTLI LCLIVANITPPVVNITHISSGRISVTEGVSSTRPSSFKSDHFILLDO VTSSSPFE**DI-TALVEGLGAWFEDLLANGSRITTL CLIVANITPPVVNITHISSGRISVTEGVSSTRPSSFKSDHFILLDO VTSSSPFE**DI-TALVEGLGAWFEDLLANGSRITTL CLIVANITPPVVNITHISSGRISVTEGVSSTRPSSFKSDHFILLDO VTSSSPFE**DI-TALVEGLGAWFEDLLANGSRITTL FPLYFRKTHAPCCCCCCONSKRNLSCKLLPDRAKVNSGNKYNDN FPGLYCICCRPYPDPDPEDEIPDERLERCAVVLGSS BERCSYSGSVRQALVACTCTPGEEBERLERCAVLGSS CAGSSESSLICTVYSTROSSKYNDANTAVTSTTYROPYTYSG GROWNEGSVITHAPSSTCACAVULTSTTARGHSMCCLIACSSC SGREGENGAFTAPSSTCACAVULTSTTARGHSMCCLIACSSC GROWNEGSVITHAPSSTCACAVULTSTTARGHSMCCLIACSSC TYSGVANDEGSVITHARGATARGATTARGABNSKACULLDS				
HOYLLDAFFT.RFFYKALLVRLDCVD_LISDLEYLDBEEFGSLOW MKDNNITOILDLIFTYURBEVEGVQUTEALKSGSLOW MKDNITOILDLIFTYURBEVEGVQUTEALKSGTUTGERINGSTUTGERINGKE BY IERNYKMRVERGVUQOTEALVRGFYEVVDSRLVSVFDARELE LVIAGTAEIDLIDNDRINGTETSGGYHDGHLUTHEWRAAVERFNNE QRERLLQFVTGTSSVPYEGFAAPPWEPMGERRPLP+KKWGKITS LPFRG_HTCLQPMBULPTVSPRTPMLITEK_LLITA\VEETSTFOT 5910 1526 446 VAEFAAMEEGRITOILDRINGTSLEKSLITALLESSLATIEBDYVIKYNTICE KARTLLMKSSAFTVVSVLCCGCIMI PRSILVUSMITTSFYAVC FYLLMLWAVEGFGKKAVLKTILRDTPMWVHTGPCCCCCCPRL LLITKKKLQ\RK CANLSINTSS + R* P\$WARGSFSTASMTQOTFL LLITKKKLQ\RK CANLSINTSS + R* P\$WARGSFSTASMTQOTFL LLITKKKLQ\RK CANLSINTSS + R* P\$WARGSFSTASMTQOTFL RGAQLVGSTLSSA/CSTLLALWTLGI ISRQARLHLGSQNMGGKP ALFQVLLILLAHQES IFSVLANGGGIACSPSTSTSGVNNCS LLILETPLMTVLTRMYYRROHKVGYETFSSPDLDLINLKALRWM AWTMKGCCTH LLILETPLMTVLTRMYYRROHKVGYETFSSPDLDLINLKALRWM AWTMKGCCTH CGHRRGGAFKYRPTPVVGDEGRPTGGKHRRGGVSLLSFRLGCS GTISARCHLRJFSSINSDAPS-LAGITGGYCHHQLIFVFLVET GFHHVGQAGLELL/NVV1HLPRPPKVLJCQA 5912 924 277 MILKKALMIGALALTTVARSPGGGDI VADHVASYGVNLVQSYGP SQOYSHEPGGDEPTYVDJERKFTVNQJELGKHRRGVSVLLSFYLLGGPALTI LCLVDTH PPVVNITTHLSNGHSVTEGVSETRFSSFKSDHFLLGDQ VTSPSPPF*E*DL*TAKVEQLGAMFEDLLLAHRALIFTLDQ VTSPSPPF*E*DL*TAKVEQLGAMFEDLLHARALIFTLDQ VTSPSPPF*E*DL*TAKVEQLGAMFEDLLHARALIFTLDQ VTSPSPPF*E*DL*TAKVEQLGAMFEDLHARAKIFTTL CLVDTH PPVVNITTHLSNGHSVTEGGSEDLAVANGKKYNDM FFGLYCICKRPYDDEBBIPDEMIQCVVCEDMFHGRILGALFPE SGDPGMVCQACMKRGSTLANAAQLAVTLTGMMDMGTIM B*/DDGGVIKPENBENDSTLKEDVPEGGEDDVRAVSVEGNBEP CASSSESSLOTVYNKISKSINGLSCLLLPKMDMCGTIM B*/DDGGVIKPENBENDSTLKEDVPEGGEDDVRAVSVEGNBEP CASSSESSLOTVYNKISKSINGLSCLLLPKMDMCGTIM B*/DDGGVIKPENBENDSTLKBDVPEGGEDDVRAVSVEGNBEP CASSSESSLOTVYNKISKSINGLSCLLLPKMDMCGTIM B*/DDGGVIKPENBENDSTLKBDVPEGGEDDVRAVSVEGNBEP CASSSESSLOTVYNKISKSINGLSCLLLPKMDMCGTIM B*/DDGMVIKPENBENDSTLKBDVPEGGEDDVRAVSVEGNBEP CASSSESSLOTVYNKISKSSGCCLLGRAMMDMGTIM B*/DDGMVIKPENBENDSTLGVANGLCCHTTAKANHAGNISKSCCLLGBANDH B*/DDGMVIKPENBENDSTLGVANGLCCHTTAKANHAGNITTHAKHGHMANGLGLDBA S915 1604 703 PGGPFPALGGPCPPANDSSTSSTSSTSCCNSTCASASADBA PASRABEDVAVVVGGTBEGBAPRASAPACHTAGHPBPPACASAPCH P	1			VMAYSRKELQRNKLYVTFVGEEGLDYSGPSREFFFLLSQELFNP
MKONNITOILDLIFTYNBEVEGGUTERELKSGGANTOTENKK BY1ERBYKRWERGVUQCTEALWEFYEVUSSLIVSVEDAELE LV11GTAEIDLINDWINNTEYRGGYHDGHLVIRWFWAAVERFYNBE QRLRLLQFVTGTSSVEYEGFAAPPBWBBMERLP*KKKGLTS LPPRG\HTCLQPDWLPTVSPRTPMLYEK\LLTA\VEETSTGT 5910 1526 446 VAEFAAMEGGRTGIKLDERYTADLLEVLKTRYGIFSACSOFFT AAQLLARLGPVELLAISTLITLALGS IAIFLEDAVYLYKNTLCP IKRRTLINKSSAPTVVSVLCCFGIM PRSLVLVEWTISFTYAVC FYLIMLVWEGFGKESAUVERTRIRDTPMWHTGPCCCCCCCCCPRI. LLTKKKLQNR*CWALSNTES*R*PWWACCSSFTASWTQOTFL RGAQLVGSTLSSA/CSTLLAWTIGIISAGALLVKOMGAKP AALFQVLLILTALQPSIFSVLANGGGIACSPPYSSKTRSGVNNCH LLLTALAWTGIISAGAGLLAWTGIISAGAGLLVKNPSTFVF GOLPLAPCTGGKGLEMRSPKPOSFTIRSSHSGAGLLVKNPSTFVF GOLPLAPCTGGKGLEMRSPKPOSFTIRSSHSGAGLLVKNPSTFVF GOHNGGAGLELL/NVVIHLPPPKVLGTHAGOLIFVFUVET GFHWGGAGLELL/NVVIHLPPPKVLGHLAFTFVFSKSFVTLGQPKTL CGHRWGGAGLELL/NVVIHLPPPKVLGHLAFTFVFSKSFVTLGQPKTLI CLVDNIFPFVVNIHLNFPPKVLGDLFLFRFRRFDPOFALTN IAVLKINLINIVIKSSISTAATIEVPEVTYPSKSFVTLGQPKTLI CLVDNIFPFVVNIHLSRNGSVSTRPSSFKSBHLLQD SGQYSHEPGDGEFFYVDLERKETVWQLPLFRRFRRFDPOFALTN IAVLKINLINIVIKSSISTAATIEVPEVTYPSKSFVTLGQPKTLI CLVDNIFPFVNIHLSRNGSTATREVPEXTYPSKSFVTLGQPKTLI CLVDNIFPFVNIHLSRNGSTATREVPEXTYPSKSFVTLGQPKTLI CLVDNIFPFVNIHLSRNGSTATREVPEXTYPSKSFVTLGQPKTLI CLVDNIFPFVNIHLSRNGSTATREVPEXTYPSKSFVTLGQPKTLI CLVDNIFPFVNIHLSRNGSTATREVPEXTYPSKSFVTLGQPKTLI CLVDNIFPFVNIHLSRNGSTATREVPEXTYPSKSFVTLGQPKTLI CLVDNIFPFVNIHLSRNGSTATREVPEXTYPSKSFVTLGQPKTLI CLVDNIFPFVNIHLSRNGSTATREVPEXTYPSKSFVTLGQPKTLI CLVDNIFPFVNIHLSRNGSTATREVPEXTYPSKSFVTLGQPKTLL CLVDNIFPFVNIHLSRNGSTATREVPEXTYPSKSFVTLGQPKTLL CLVDNIFPFVNIHLSRNGSTATREVPEXTYPSKSFVTLGQPKTLLAGSFECHGS IKLFELYTRRIPRCDCGNSKYKNLLGCLLPDRACVLXGSTE SSGQYSKGGAGAAGRAGSELPVVSLUVDLEEDEELARCAVLGGS IKLFELYTRRIPRCDCGNSKYKNLLGCLLPDRACVLXGSKYKGHLAGA IKLFELYTRRIPRCDCGNSKYKNLLGCTLEPDRACCVCCCCCCCCOCCHMINGGAGAAAA PPOGLYCICCREPPTPERSTEDEMTGCACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC				YYGLFEYSANDTYTVQISPMSAFVENHLEWPRFSGRILG\LALI
BYTERMYKMRUERGUVQCTEALURGFYEVUSELUSYDARELE LVIAGTA ELDINDWRNITEYRGCYMGHULVIRHWWAAVERFNNE QRLRLLQFVTGTSSVPYEGFAAPBWEPMGLRELP_KKKGKITTS LPRGQHTCLQPVWBLATSLITTLAALQETSTFGT 446 446 446 446 446 446 446 4		ŀ	i	HQYLLDAFFT\RPFYKALL\RLPC\D\LSDLEYLDEEFHQSLQW
IVITAGRAEIDLINDWINNTEYRGGYHDGHLVIRMFWAAVERTNIE ORLRILIGPVICTSSUPVERGAAPDWEEDRIPLP*KKKRITS LPPRG\HTCLQPDWDLPTVSPRTPMLYEK\LLTA\VEETSTFGT	1			
ORLELLOPVICTSSUPYEGFAAPWEPMELMRILPK-KKGKITTS LPPRO\HTCLOPDMDLPTYSPRTPMINEK\LITA\VEETSTFGT 5910 1526 446 VAEFAAMEGRTQIKLDFYTSPRTPMINEK\LITA\VEETSTFGT VAEFAMEGRTQIKLDFYTSDLLEVLKYNTYGIFSACFSQFFT AAQLLRALGPVELALTSILTILLALGSIAIFLEDWYYKNTLCF IKRRILIMSSAPTVYSULCCFGIM PRESULVLEMMITSFTAVC FYLLMLVMWEGFGSKEAVLRTIRRITPMMVHTGPCCCCCCCPR. LLITKKKQAR-CWALSHTSF**s**P**P**PWAMCPSSFTASMTQOTFL RGAQLVGSTLSSA\CSTLLAUWTIGIISRQARLHLGEDMMGAKF ALFQVLLILTALQPSIFSVLANGGQIACSPPYSKKTRGQVMNCH LLILEFTIMTVITMMYYRKDHKVGVETFSSPDLDIMLKALRIM AWTMKGCCTH 5911 109 595 QLPLAFCIGGKGLEMRSPKPOSFTIRSSHSGAGLLVKNESTPVF CGHRRGGAAFKYKPTPVVOPBCRFTTGKHMRGGSGLLSPRLECS GTSAHCHURLPSSNSNSPARS**LGAITVCHHAQLIFVFLVET GFHNVCQAGLELL\NVVIHLRPPKVLGLQA 5912 5912 5914 277 MILKKALMIGALAITVMSFCGGEDIVADHVASYGVNLYQSYG SGQYSHEPDOEBETYVDLERKETVWQLIPFRFFRFDPGFALTH IAVLKHNLMIVIKSNSTAATNEVPEVTVFSKSFVTLGGPNTLI CLVNNIFPVVNITWLSNSHSYSGVSETBSKSDHLLQDQ VTSPSFPF**DL*TAKVSQLGAMFEFLLKHKGABIPTLL CLVNNIFPVVNITWLSNSHSYSGVSETBSKSDHLLQDD VTSPSFPF**DL*TAKVSQLGAMFEFLLKHKGABIPTLL GDRMAGGAARGSELEPVSLDVULCEBLERERCAVLGGS SBKCSYSGSVKRQALYACSTCTPBGEEPAGICLACSYECHGS HKLPELYTRKNFRCDCGNSKYRIDLECKLLPDRAVVINGKKTNDM FFGLYCICKRYPOPBEBETPDEMIQCVCDEDWFIGKRILGALPPE SGDPGBWCQACMRCSFLMAYAAQLAVTKIST\GMDWCGTLM B**/DOGBY KYEPNGHGDBSTLKEDVPBGCKDDVREVKVXONSEP CAGSSSSIDLOTVFKNSLINABSKSGCKLQELKAKQLIKKDTAT YWPLNWSKLCTCDCMKWYGDLDULETDVTULAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED 5914 960 124 MLGGSLPPERLPTQVSSMNRRVPFYLASIEDMUVAI/GGRN RGALLSSVETYSPTDSWSVVAGLPRTYCHABTIYKDFVYLSG GHDYQIGPYRKHLLCYDHKTDWBERRPMTTARGWHSMCSLDS SGVAMWGRIYILGGYSWNTAFSKTOVQNDREADKWSGVULD KAIAGGSACFILAP*SLGQRTRKRKAARARGTGABCSCAWDLD KAIAGGSACFILAP*SLGQRTRKRKAARARGTGABCSCAWDLD KAIAGGSACFILAP*SLGQRTRKRKAARARGTGABCAGABCSAWDLD KAIAGGSACFILAP*SLGQRTRKRKAARARGTGABCAGABCSAWDLD KAIAGGSACFILAP*SLGQRTRKRKAARARGTGABCAGABCSAWDLD KAIAGGSACFILAP*SLGGRTRKRKAARARGTGABCAGABCS SGVAMWGRIYILGGYSWNTAFSKTOVYDREADKWSGVULD KAIAGGSACFILAP*SLGGRTRKRKAARARGTGABCAGABCS SGVAMWGRUNDSTROVYDONTRAPELLHAPAPCHLAPAP PARABCPVAVVNOHTBEGAPARSASPKEPFGLPRPLGSFPCPT POEBPALGGP	1	}	I	
LPPRQHTCLQDWDLETUSPRTDMLYEK, LLITA, VERTSTFOT				
S910 1526				QRLRLLQFVTGTSSVPYEGFAAPPWEPMGLRRFLP*KKWGKITS
AQQLRALGPVELALTSILTLLAMGSIAIFLEDAYVLVKNTICP IKRRTILMKSSAPTVVSVLCCFGLMIPRSLVLVEMTITSPYAVC FYLLMLVMVGGFGKEAVLRTIRDTPMAVHTGPCCCCCCPCPAL LLITKKLQ\R*CWALISTIPS***R*PMWACFSPTASMTQCTFL RGAQLVSSTLSAI/CSTLLALMTLGTGARAHLIGEOMMAKF ALFQVLLILTALQPSIFSVLANGGGIACSPYSSTRSGVWNCH LLILETPLMTVLTRMYYRKDHKVGYETFSSPDLDILKALRWM AWTMKGCCTH 5911 109 595 QLPLAPCTGGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF GGHRGGAAFKYKPTPVVGPGRPTGGKHMEGGVSLLSPRLECS GTISAHCHURLSSSNSPAPA**LAGITGVCHHAQLIFVFLVET GFHHVGQAGLELI/MVUHLPRPPPKULGLQA 5912 924 277 MILKKALMIGALALTTVMSPCGGEDIVADHVASYGVNLYQSYGP SGQYSHEPPGDEEFFYVDLERKETVVQLPLFRRFRPDQFALTM LAVLKHNLNIVIKRSHSTATMEVPEVTVFSKSPVLLGQFMTLI CLIVDNIFPPVVNITHLSNGHSVTEGVSTTRSSSPSDHFLLQDQ VTSSSPPF**DL**ATAVBCLGAWFBFLLKHWGABITPTL CLIVDNIFPPVVNITHLSNGHSVTEGVSTRTRSSPSDHFLLQDG VTSSSPPF**DL**ATAVBCLGAWFBFLLKHWGABITPTL 5913 46 1198 QLRMAGAEGAAGRQSELEPVVSLVDVLEEDELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPFGGEPAICLACSYBCHGS HKLFELTYKRNFRCDCORSKFKNLESKLLPPKAKVNSGNKYNDN FFGLYCICKRPYPDFEDSIPDEMIQCVVCEDMFHGHLGAIPPE GAGSSSSDLGVFVKNRSLARBSKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTQCDCORSKFKNLESKLLPPKAKVNSGNKYNDN FFGLYCICKRPYPDFEDSIPDEMIQCVVCEDMFHGHLGAIPPE GAGSSSSSDLGVFVFKNRSLARBSKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTQCDCMSKYMOLDLVHITDSYDTVLAYENKGKI AQATDRSDPLMDTLSSMRVQVELIC/GIQ**FED 124 MLGGSELPFPEALFTQVASNNGRVDLLFIDDSYDTVLAYENKGKI AQATDRSDPLMDTLSSMRVQVELIC/GIQ**FED 15914 960 124 MLGGSELPFPEALFTQVASNNGRVDLHTDSEYDTVLAYENKGKI AQATDRSDPLMDTLSSMRVQVELIC/GIQ**FED SGRAPGBEPFEALFTQVASNNGRVDLATSGETTRAGSDPSCASWOH PHRHLPGLCRPAATS 5915 1604 703 FFGFFTFFLKLGRRRKARIIQAPHCHISPRPTTGPGALQAPEA PASRAGGPVAVVNGHTEGPAPARSAPKEPPGDFRLGSFCPF PQEDFPALGGPCPPRMPSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSHPHPYPSPPGFAVVGFREADSWSGVDLD PRELIGGSEPSAHPVHQCLPPARRSPLLGFPPPALGSFCPP PQEDFPALGGPCPPRMPSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSHPHPYPSPAPAPPPPGALQPALPGLPPPPGALQAPEA PASRAGGPUAVVNNHTEGPAPARSAPKEPPGGFPPDGLVPPIS RPEPGGEPSAHPVHQCLPPARRSPLORVGPRERGPTGGSFCPT PQEDFPALGGPCPPRMPSPGFSAVVLLKGTPPPPFGLVPPIS RPEPGEBPSAHPVHQCLPPARRSPLORVGPREBRDFTGGSFCGCT TUTGAVHRHLMHVAGIIPWVTTLA	•		·	
TKRRTILIMKSSAPTVVSULCFGLMIPRSLIVLENTITSPYAVC FYLLMLVMVEGFGGKEAVLRTLRDTPMWATGGCCCCCPCCPRL LLTEKKLQ\R*CMALSNTPS*R**P*PWMACFSSPTASMTQQTF! RGAGLYGSTLSSA/CSTLLALWTLGIISRQARLHLGEQNMGAKF ALFQVLLITTALQPSIFSVLANGGOLACSPPYSSKTRSQVMCH LLILETPLMTVLTRMYYRKDHKVGYETFSSPDLDLNLKALRWM AWTWKGCTH: 5911 109 595 OLPLAPCIQGKGLEMRSPKPQSFIIRSSHSGGGLLVKNPSTPVF CGHRRGGARKYKPTPTVVGPBQRPTGQKMMRGGVSLLSPRLECS GTISAHCNIRLPSSSNSPAPAS*LGTGYCHHAQLIFVFLVET GFHHVQAGLELL/NVVIHLPRPPKVLGLQA 5912 924 277 MILKKALMLGALALTTVASPGGGEDIVADHVASYGVNLYQSYGP SGQYSHBPPDGEBETPVDLERKETVWQLPLFRRFRFDPQFALTM IAVLKHNLINLVIKRSNSTAATINEVPETVTVSSPVTLGQPHTLI CLVDNIIPPPVNLTHUSSNGHSYTEGVSETRPSSPKSDHFLLQQD VTSPSFPFF**DL*TAKVEQLGAMFEPLLKHWGABIPTTL CLVDNIIPPPVNLTHUSSNGHSYTEGVSETRPSSPKSDHFLLQDQ VTSPSFPFF**DL*TAKVEQLGAMFEPLLKHWGABIPTTL 5913 46 1198 OLRMAGAEGAAGRQSELSPVSLUDVLEEDBELENEACAVLGGS DSEKCSYSGGSVKRQALVACSTCYBEGSPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN PFGLYCICKRPYPDPEDBIPDEMIQCVCDDMFRGHLGAIPPF SGDPCENVCQACMKRCSFLMBYAAQLAVTKIST\GMMDWCGTLM B*/DDGEVIKPENGBHQDSTLKEDVPBCGKDDVREVKVEQNSEP CAGSSSSDLQTVFKNESLNARSKSGCKLQELKAKQLIKKDTAT YMPLNMRSKLCTCQDCMKMYGDLDVLFLTDEDTVLAVENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*PSDHTUSHTVLAVENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*PSTPULAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*PSTPULAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*PSTPULAYENKGKI SGVAVWGGRIYILGGYSWENTAFSKTVQVYDREADKWSGVDLP KALAGGSACTIAP*SLGQRTRKRKARGTTGASDPSCASWDH PHRHLPGLCRPAATS SGVAVWGGRIYILGGYSWENTAFSKTVQVYDREADKWSGVDLP KALAGGSACTIAP*SLGQRTRKRKARGTTGASDPSCASWDH PHRHLPGLCRPAATS PFGRFTPRLKLGRRRKRARIIQAPHRTGPPPPPCLVPPIS KAPGGSACPIAP*SLGQRTRKRKARGTTGASDPSCASWDH PHRHLPGLCRPAATS PFGRFTPRLKLGRRRKRARIIQAPHRTGPPPPPCLVPPIS KAPGGSACPIAP*SLGQRTRKRKARGTTGASDPSCASWOH PHRHLPGLCRPAATS PFGRFTPRLKLGRRRKRARIIQAPHRTGPPPPPCLVPPIS KAPGGSACPIAP*SLGQRTRKRKARGTTGASDPSCASWOH PHRHLPGLCRPAATS PFGRFTPRLKLGRRRKARIIQAPHRTGPPPPPPCLVPPIS KAPGGSACPIAP*SLGGRFFREDIA*APADQAGTSQQYPDH PPGDFPALGGGCPPRNPPSPGFSAVVLLKCTPPPPPPCLVPPIS KAPGGSACPAAH PPGDFFGALLPSPHPPVNSAPAPPPPPCKARAADQAGATSQQYPDH PTGLLUONAGATAGQAG	5910	1526	446	, ··
FYLIMLVMVEGFGGKEAULRTLRDTPMMVHTGGCCCCPCCPRL LLTRKKLQ/R* CWALSNTPS*R*R* PWACFSSPTASMTQQTFL RGAQLYQSTLSSA/CSTLLALWTLGI ISRQARLHLGEQNMGAKR ALFQVLLILTALQPSIFSVLANGGQIACSPPYSSKTRSQVWNCH LLILETFLMTVLTRMYYRKDHKVGYSTFSSPDLDLNLKALRWM AWTMKGCTH 5911 109 595 QLPLAPCTGGKGLEMRSPKPQSFIIRSSHSGGLLVKNPSTPVF CGHRRGGARFKKTPTVVGPBGRFTGGKHMRGGVSLLSPRLECS GTISAHCNLRLPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GFHWQAGLELL/NVVIHLPPRPKVLQLQA 5912 924 277 MILKKALMIGALALTTVMSPCGGBDIVADHVASYGVNLYQSYGP SQCYSHBPDGDEFYYDLERRETWQLPLFRRFRRFDPGFALTN LAVLKHNLNIVIKRSNSTAATNEVTVSSPSVTTVSGSPBTLTG LCVNDIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFLLQDQ VTSPSFFFF**DL*TAKVBGLGAWFEFLLKHWGABIPTTL CLVNDIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFLLQDQ VTSPSFFFF**DL*TAKVBGLGAWFEFLLKHWGABIPTTL CLVNDIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFLLQDQ VTSPSFFFF**DL*TAKVBGLGAWFEFLLKHWGABIPTTL SPHOMAGEGAARGSSLEPVVSLUDVLEEDEELENBCAVLGGS DSEKCSYSGGSVKRQALVACSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKYNLECKLLPPKAKVNSNKYNDN FFGLYCICKRPYVPDEBBIPDEMIQCVVCEDWFHGRHLGAIPPF SGDFPEVVCACKRCSFLMAYAAQLAVTSITS\CMMDWCSTLM FFGLYCICKRPYVPDEBBIPDEMIQCVVCEDWFHGRHLGAIPPF SGDFPEVVCACKRCSFLMAYAAQLAVTSITS\CMMDWCSTLM FFGLYCICKRPYVPDEBBIPDEMIQCVVCEDWFHGRHLGAIPPF SGDFPEVVCACKRCSFLMAYAAQLAVTSITS\CMMDWCSTLM FFGLYCICKRPYVPDEBBIPDEMIQCVVCEDWFHGRHLGAIPPT GAGSSESDLQTVFKNESLNASKSGCKLQELKAKQLIKKDTAT YWPLNMSSKLCTCQDCMKNYGDLDVLB/LIDFDYTVLAYENKGKI AQATDRSDPLMDTLSSMMRVQQVEYLLC/GIQ**FBD CAGSSSESDLQTVFKNESLNASKSGCKLQELKAKQLIKKDTAT YWPLNMSSKLCTCQDCMKNYGDLDVLB/LTDFDYTVLAYENKGKI AQATDRSDPLMDTLSSMMRVQQVEYLLC/GIQ**FBD INSIGGSDDNIESMERFDVLGYBAYSPCCNOWTRVAPLLHANSE SGVAWWEGRIYILGGSWBNTAFSKTVQVVDREADKWSGVDLD KAIAGGSACPIAP*SLGQRTRKRKAKARGTTGASDPSCASWDH PHRHLDCLCRPAATS PAGREGPVAVVNGHTEGPAPARASPREPPPPPQLVPPIS KAIAGGSACPIAP*SLGGWSRMTVLLKGTPPPPPPPLVIPPIS REPLEGGEPSAHPVNGLDABRRGFLQVEDLRGVQTCPPLRS PPLQEDPPALGGPCPPRMPPSPFGSAVVLLKGTPPPPPPLVPPIS REPLEGGEPSAHPVNGLDABRRGFLQVEDLRGVQTCPPLRS PPLQEDPPALGGPCPPRMPSFFLEGEPRPSTPFDFLYGGCT TVTGAVHRHLNHVAGIIPVLHSGLKPTXATAQDQATSGQYYDH PPRLLICHONATAQDQATSGQYPDH PPRLLICHONATAQDQATSGQYPDH	1			1
LLTRKKLQN*C*CHALSNTPG*S*P*****P*PWWACFSSPTASMTQQTFL RGQQLYGSTLSAA/CSTLLALWTLGIISRQARLHGEQNMGAKF ALFQVLLILTALQPSIFSVLANGGQIACGPPYSSRTRSQVMNCH LLILETPLMTVLTRMYYRRKDHKVGYETFSSPDLDLNLKALRMM AWTMKGCTH 5911 109 595 QLPLAPCIQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF CGHRRGGAAFKVKPTFVVGPBQRFTGQKHMRGGVSLLSPRLECS GTISAHCNILELSSSNSPAPAS*LAGITGVCHHAQLIFVTLVET GFHHVGQAGLELL/NVV1HLPRPPKVLGLQA 5912 924 277 MILNKALMCALALTVVMPFCGBTUADHVASYGVNLYQSYGP SQQVSHBFDGDEEFYVDLERKETVWQLPLFRRFRRFDPQFALTN LAVLKHALNIVIKRSNSTAATNEVPEVTVFSSPVTLGQPNTLI CLVNNIPPPVNNTHWISSNHSVTSBGVETRPSSPKSDHTLQDQ VTSSFPFE**DL*TAKVBGLGAMFEPLLKHMGABIPTTL CLVNNIPPPVNNTHWISSNHSVTSBGVETRPSSPKSDHFLLQDQ VTSSFPFE**DL*TAKVBGLGAMFEPLLKHMGABIPTTL 5913 46 1198 QLRMGAGAGGAGRQSELEPVVSLVDVLEEDEELENBEACAVLGGS DSEKCSYSQSVKRQALVACSTCTPRGBEPAGICLACSYBCHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN PFGLYCICKRPYPDPBDEIPDEMTQCVVCDBMFERGHLGATPFE SGDPOMVCQACMKRCSFLMAYAAQLAVTRIST\CAMBWCGTLM B*/DDQRVVKPGACKKRCSFLMAYAAQLAVTRIST\CAMBWCGTLM B*/DDQRVVKPGACKKRCSFLMAYAAQLAVTRIST\CAMBWCGTLM B*/DDQRVVKPGACKKRCSFLMAYAAQLAVTRIST\CAMBWCGTLM B*/DDQRVVKPGACKKRCSFLMAYAAQLAVTRIST\CAMBWCCTLM B*/DDQRVVKPGACKKRCSFLMAYAAQLAVTRIST\CAMBWCCTLM B*/DDQRVVKPGACKKRCSFLMAYAAQLAVTRIST\CAMBWCKLGMSP CAGSSSSDLQTVFKNESLNARSSGCKLQELKARQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEDVTULAYENGKI AQATDRSDPLMDTLSSMRVCQVQUELLC/G1Q*PED CAGSSSSSDLQTVFKNESLNARSSGCKLQELKARQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEDVTULAYENGKI AQATDRSDPLMDTLSSMRVCQVQUELLC/G1Q*PEDT USGGSDDNIESMBEFPDULGVEAYSPQCNOWTRVAPLIHANSE SGVAVWEGYIYILGGYSWENTAFSKTVQVTDREABAWCSIGDLS 1YSIGGSDDNIESMBEFPDULGVEAYSPQCNOWTRVAPLIHANSE SGVAVWEGYIYILGGYSWENTAFSKTVQVTDREABAWCSIGDLS VXIGGSDDNIESMERFDULGVEAYSPQCNOWTRVAPLIHANSE SGVAVWEGYIYILGGTPRFRICATBADCHSRGVULD PHRHLDGLCRPAATS PGRPTFRPLKIGGRRKRARITQAPCHTRADCHSPPPPPPPPPCK,RPLLPAPPPPPPPPPPPPCK,RPLLPAPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	[
RGAQLYGSTLSSA/CSTLLALWTLGIISRQARLHLGEQNMGAKF ALFQVLLILTALQPSIFSVLANGGQIACSPPYSSKTRSQWNCH LLILETTIMTVLTRMYTRKDIKVGYETFSSPDLDLMLKALRWM AWTMKGCCTH 5911 109 595 QLPLAPCIQGGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF CGHRRGGAFKYRFTPVUGPEQRPTGQKHMRGGVSLLSPRLECS GTISAHCHLEFSSSNSPAPAS*LAGITGVCHHAQLIFVTLVET GFHHVQAGLELL/NVVILHLPRPFKVLGLQA 5912 924 277 MILNKALMLGALALTTVMSPCGGEDIVADHVASYGVRLYQSYGP SGQYSHBFDGDEFTYDLERKETVWQLPLFRFRFRFDPQFALTM LAVLKHNINIVIKSNSTAATHEVPSVTVFSKSEVTLGQDYNTLI CLVDNIFPPVNTTWLSNGHSVTEGGSETFSSPKSDHFLLQDQ VTSPSFPFE*DL-TAKVBGLGMFEPLLKHKGABIPTL CLVDNIFPPVNTTWLSNGHSVTEGGSETPSSPKSDHFLLQDQ VTSPSFPFE*DL-TAKVBGLGMFEPLLKHKGABIPTL S913 46 1198 QLRMGAEGAAGRQSELEPVSLVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPGBEBPAGICLACSYECHGS HKLFSLTYKKNFRCDCONSKFKNLECKLLPDKAKVNSGNKYNDN PFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFCENVCQACMKRGSFLMAYAQLAVTKIST\CMMDWCGTLM BY-JODGEVIKPENGEHQDSTLKEDVPEQGKDDVREVKYCGNSEP CAGSSSSBDLQTVFKWESLNABSKSGCKLGELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVFLTDEDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELLC/GIQ*FED AQATDRSDPLMDTLSSMNRVQQVELLC/GIQ*FED S914 960 124 NLGGSELPPEBALFIQVASNNQRRVDFYLASIEDMLVAI/GGRN NLGGSELPPEBALFIQVASNNQRRVDFYLASIEDMLVAI/GGRN SGLASSVETYSPFTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERPDVLGWSAYSPQCNQHTRVAPLLHANSE SGVAVWEGRIYILGGSYBENTBSKTVQVYREADKWSGYDLD KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS SGPTFFPELKIGGRRKKARITQAPHCHSPRPRTCPPGALQAPEA PASRAGGSVAVVNGHTGGPAPARSAPKEPPGLPRPLGSFPCDL*SFPCPPPPGCKPPTSCLLSFPCPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	1			
ALFQVLLILTALQPS I FSVLANGGQIACSPPYSSKTRSQVMNCH LLILETFLMTVLTRMTYTRKDIKVGYETFSSPDLDLNLKALRWM AWTMKGCCTH 5911 109 595 QLPLAPCIQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF CGHRRGGAAFKYRPTPVVGPEQRPTGQKHMRGGVSLLSPRLCS GTISAHCNLELPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GFHHVGQAGLELL/NVVIHLPRPPKVLGLQA 5912 924 277 MILNKALMILGALALTTVMSPCGGEDIVADHVASYGVNLYQSYGP SGQVSHBPDGDEEPYVDLEEKETVWQLPLFRRFRFFDQFALTN LAVLKHNLNIVIKRSNSTAATMEVPEVYTYFSKSPVTLAGQNTLI CLVDNIPPPVVNITWLSNGHSTVTGSVSETRSSPKSDHFLLQD VTSSSFPFE*DL*TAKVEQLGAMFEPLLKHWGABIPTTL 5913 46 1198 QLRMAGAEGAAGRGSELEPVVSLVDVLEEDEELEMEACAVLGGS DSEKGSYSQGSVKRQALYACSTCTPFBGEPAGLCLAGSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCICKRPYPDPEBEIPDEMIQCVVCEDWFHGRHLGAIPPE GGDPGWVQACWKRGSFLMAYAQLAVTKIST/GMMDWGSTLM B*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVRSVKVEQNSEP CAGSSSSBLQTVFKNESINAESKSGCKLQELKAKQLIKKDTAT TWPLNWRSKLCTCQDCMKWYGDLDVLFLTDEDTVTLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED 5914 960 124 NLGSSELPPEBALFIQVASMNRVGDVFLICGIQ*FED GHDYQIGPYRNLLCYDHRTDVWEERRPMTTARGHHSNCSIGDS IYSIGGSDDNIESMERFDVLGVERSYPQCYCMWTVAPLLHANSE SGVAWWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLD KAIAGGSACFIAP*SLQQRTRKRKAKARGTRTGASDPSCASWDH DHRHLPGLCRPAATS 5915 1604 703 FFGRFTRFLKIGRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGFVAVVVNGHTEGFAPARSAFKEPFGLPRPLSFFCCPT PQEDFPALGGCPPRMPPSFGSFAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPQK/RPRLLPAP/PGLPS PRELIGGEEPSAHPVHQCLPAERRGDLZQVQEPLRGVQTGPDLRS KPPPGFSGLLPSPHP\PVSPAPPPPPQK/RPRLLPAP/PGLPS PRELIGGEEPSAHPVHQCLPAERRGDLZQVQEPLRGVQTGPDLRS 5916 256 633 SPRMWEIWGFWHRWESFSLEGEWFSRIPEPSPSTKTGSGKGCR TVTGAVHRHLMHVAGIIPWVHSQLKPTAATAQDQWTSQQYDDL	1			
LLILETPLMTVLTRMYYRRKDHKVGYETFSSPDLDLNLKALRWM AWTMKGCTH S911 109 595 QLPIHAPCIQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF CGHRRGGABFKYRPTPVVGPEGRPTIGGKHRGGVSLLSPRIECS GTISAHCNLRLPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GFHHVQAGLELL/NVVIHLPRPPKVLGLQA 5912 924 277 MILNKALMLGALALITTWASPCGGEDIVADHVASYGVNLYQSYGP SGQYSHBPGGBEFYVDLERKETVWQLDLFRRFRFDPQFALTN IAVLKHHLNIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTLI CLVDNIFPPVNNTTWLSNGHSVTEGVSBETRSSPKSDHFLLQDQ VTSSFFPFE**DL*TAKVEGLGAWFEPLLKHWGABIPTTL CLVDNIFPPVNNTTWLSNGHSVTEGVSBETRSSPKSDHFLLQDQ VTSSFFPFE**DL*TAKVEGLGAWFEPLLKHWGABIPTTL S913 46 1198 QLRMAGAEGAAGRQSELEPVVSLVDVLEEDBELRNEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGBEPAGICLACSYECHGS MKLFELTYKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FPGLVCICKRPYPDPEDBIPDENIQCVVCEDWFHGRHLGAIPPE SGDPCMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEGNSEP CAGSSSSBDLQTVFKNESLNABSKSGCKLQELKAKQLIKKDTAT TYPPLMRSKLCTCDCCMKWGDDLDVLFLTDEVDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED S914 960 124 NLGGSELPPEBALPIQVASNNQRVDFYLMSIEDMLVAI/GGRN RNGALSSVETYSPKTDSWSYADLPFTTGHAGTYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQMTRVAPLLHANSE SGVAVWEGRIVILGGSYBENTAFSKTVQVYDREADKWSRGVDLP KALAGGSACFIAP*SLOQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS SGVAVWEGRIVILGGSYBENTAFSKTVQVYDREADKWSRGVDLP KALAGGSACFIAP*SLOQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS SFRREGVAVVVNGHTEGPAPARSAPKEPGLPRPLGSFPCDYPLG KPPGFSGLLDSPHPPPPPGLVPPIS KPPGFSGLLDSPHPPPPPPGLVPPIS KPPGFSGLLDSPHPPPPPPPPCLVPPIS KPPGFSGLLDSPHPPPPPPPPCLVPPIS KPPGFSGLLDSPHPPPPPPPPPPPCLVPPIS KPPGFSGLLDSPHPPPPPPPPCLVPPIS KPPGFSGLLDSPHPPPSPPPPPPPPCLVPPIS KPPGFSGLLDSPHPPPPSPPPPPPPPPCLVPPIS KPPGFSGLLDSPHPPPPPPPCLVPPIS KPPGFSGLLDSPHPPPSPPSPPSTKGTSGKGCR TTTGAVHRHUMVAGIIPWVHSQLKPTAATAQDQWTSTGQVTPDH PTRLILO*NOATAKNA*TALLQPHGRL\SPRMAEA				,
S911 109 595 QLPLAPCIQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF CHRRGGAFKYKPTPVVGPBQRPTGKHMRGGVSLLSPRLECS GTISAHCNLRLPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GFHHVGQAGLELL/NVVIHLPRPPKVLGLQA 5912 924 277 MILINAIMIGALAITTVMSFGGBDIVADHVASYGVNLYQSYGP SCQVSHBPDGDEEPYVDLERKETWQDLPKRFRERFDQPALIN IAVLKHNLNIVIKRSNTAATNEVPEVTVFSKSPVTLGQPNTLI CLVDNIFPPVNITWLENGHSVTEGVESTRSSPKSDHFLLQDQ VTSPSFPPE**PDL*TAKVEQLGAMFEPILLKHWGABIPTTL 5913 46 1198 QLRMAGAEGAAGRQSELEPVVSLDVLEEDEELENEACAVLGGS DSEKCSYSGGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLFFLYTKRFRCDCCMSKFKNLEFKLLPPKAKVNGGNKYNDN PFGLYCICKRPYPDPEDEIPDEMIQCVVCEDMFHGRHLGAIPPE SGDFCMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWGTIM B*/DDQEVIKPENGGHQDSTLKEDVPEGGKDDVERVKVEQNSEP CAGSSSESDLQTVFKNSLALVELKKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATRRSDPLMDTLSSMRVQQVELIKAKQLIKKLDIAT YWPLNWRSKLCTCQDCMKMYGDLDVLFTDEYDTVLAYENKGKI AQATRSDPLMDTLSSMRVQQVELJKAKQLIKAKQLIKKLDIAT SQHDYQIGPYRKNLLCYDHRTDVHEERRFMTTARGWHSMCSLGDD GHDYQIGPYRKNLLCYDHRTDVHEERRFMTTARGWHSMCSLGDD SGRGSSESTISPKSLLGGYRKKAKARGTRTGASDBSCASWDH HRH.DGLCRPAATS SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDBSCASWDH PHRH.DGLCRPAATS 5915 1604 703 FFGRPTRFLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGFVAVVVNOHTEGPAPARSAPKEPPGLBRPLGSFPCCPF PQEDFPALGGCPPFRMPSPGFSAVVLLKGTPPPPPFQLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPPLPFGSPPCPPPPPFSCHPPPF	1]		
Total	ł		ļ	LLILETFLMTVLTRMYYRRKDHKVGYETFSSPDLDLNLKALRWM
CGHRRGGAPKYKPTPVVGPBGRPTIGKHMRGGVSLLSPRLECS GTISAHCHRLPSSNSNPAPAS+LAGITGVCHHAQLIFVFLVET GFHHVGQAGLELL/MVVHLPRPPKVLGLQA 5912 924 277 MILNKALMLGALALTTVMSPCGGEDIVADHVASYGVBLYGSYGP SGQYSHEPDGDEFFYVDLERKETVWQLPLFRRFRRPDQFALTN LAVLKHNLNIVYKRSNSTAATMEVPEVTVFSKSPVTLGQPNTLI CLVDNIFPPVNHITMLSNGHSVTEGVSETRPSSPKSDHFLLQDQ VTSPSFFFF*+DL*TAKVEQLGAWFEPLLKHWGABIPTTL 198 QLRMAGABGAAGRGSELEPVSLVDVLEEDEELENEACAVLGGS DSEKCSYSGGSVKRQALYACSTCTPBGBEPDGICLACSYECHGS HKLFELYYKRNFCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCICKRPYPDPEDBITDEMIQCVVCEDWFHGRRLGAIPPE SGDPOEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*\DDQEVIKPENGEHQDSTLKEDVPPQKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNABSXSGCKLQELAKQLIKKDTAT YWPLMWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQVELIC/GIQ*FED 124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMUVAI/GGRN ENGALSSVETYSPKTDSWSVVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIBSMERFDVLGWEAYSPQCNQWTKVAPLLHANSE SGVAVWEGRIYLLGGYSWENTAFSKTVQVVDREADKKSRGVDLP KAIAGGSACFIAP*SLGQRTRKKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FFGRPTRPLKLGRRRKRARIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQGBFFALGGCPPRNPPSGFSSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPGLRQVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPGLRQVPPIGLPPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPGLRQVPFDLRS PVLQELPFGAGGCFPERNPSGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPGLRRQVTGPDLRS PVLQELPFGAGGCFPERNPSGFSAVVLLKGTPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPGLRRQVTGPDLRS PVLQELPFGAGGFPERNFATFATAQQYEDPLRGVCTGPDLRS PVLQELPFGAGGFFPERLS+*AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPESPDSTKGTSGKGCR TUTGAVHRILINHVAGIIPWLHAOGLIPPATATAQQQYEDH	1			
GTISHCULRLESSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GFHHVGQAGLELL/NVVIHLPRPPKVLGLQA 5912 924 277 MILNKALMIGALALTTVMSPCGGEDIVADHVASYGVNLYQSYGP SCQYSHBPDGDEFYVDLERKETVWQLPLFRRFRRFDPQFALTN LAVLKHNINIVIKRSNSTAATHBEVEVTYFSKSPVTLGQPNTLI CLVDNIFPPVVNITHLISNGHSVTEGVSETTPSSPKSDHFILLQDQ VTSPSFPFE*+DL*TAKVEQLGAWFEPLLKHWGABIPTTL 5913 46 1198 QLRMAGAEGAAGRQSELEPVVSLLVD/LEEDEBLENERCAVLGGS DSEKCSYSQGSVKRQALYACSTCTPPEGBEPAGICLACSYECHGS HKLFELYTKRWFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCICKRPYPDPEDEITPDENIQCVVCEDWFHGRRIGAIPPE SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWGGTLM E*/DDQEVIKPENGEHQDSTLKEDVEQGKDDVREVKVEQNSEP CAGSSSESDLOTVFKNESLNASSKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKWYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNSVQQVELIC/GIQ*PED AQATDRSDPLMDTLSSMNSVQQVELIC/GIQ*PED S914 960 124 NLGGSELPPERALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVGLPRFTYGHAGTIYKDFVYISG GHDYQIGFYKNLLCYDHTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVERAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTQVVDREADKWSRGVDLP KALAGGSACFIAP*SLGQRTRKKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FFGRFTPFLKLGGRRKRARIIQAGPKGRAPKGRAPKGPBALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGDALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGDALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGDALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGDALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGDALQAPEA PRELPGEEPSAHPVHQGLPARRRGPLQVQEPLRGVQTGPDLRS PUQELPGFAGGEFPSGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRTPESPDSTKGTSGKGCR TVTGAVHRILINHVAGIIPWLHAGIIPWLKAGAVGPDH	5911	109	595	QLPLAPCIQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF
SPHHVQQAGLELL/NVVIHLPRPPKVLGLQA	1			
S912 924 277				
SGQYSHEPDGDEEFYVDLERKETVWQLPLFRRFRRFDPQFALTN IAVLKHNLNIVIKRSNSTAAATNEVPBEVTVFSKSPVTLGQPNTLI CLVDNIFPPVVNITWLSNGHSVTEGVSETRSSPKSDHFLLQDQ VTSPSFPFF**DL*TAKVEQLGAWFEPLLKHWGABIPTTL 5913 46 1198 QLRMAGAEGAAGRGSELEPVVSLVDVLEEDBELENEACAVLGGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYKNDN PFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\CMMDWCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPPQKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNABSKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLITDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED 124 NLGSSELPPBEALFIQVASMNQRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDWEERRPMTTARGMHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRSCVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FPGRPTRFLKLGRRKRARIIQAPHCHSPRPTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVNQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGFPPGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIFEPSFDTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVHSQLKPTAATAQQWTSQQYPDH PTRLILO*NOATADKNN*TTAALLQPHQRL/VSPRNAEA	1			GFHHVGQAGLELL/NVVIHLPRPPKVLGLQA
IAVLKHNLNIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTLI CLVDNIFPPVVNITWLSNGHSVTEGGVESTRPSSPKSDHFILQDQ VTSPSFPFF*DL*TAKVEQLGAWFEPLLKHWGABIPTTL 5913 46 1198 QLRMAGAEGAAGRGSELEPVVSLVDVLEEDEELENEACAVLGGS DSEKCSYSQGVKRQALYACSTCTPEGBEPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN PFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNARSKSGCKLQBLKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMMRVQQVELIC/GIQ*FED 5914 960 124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPRTDSMSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHPGLCRPAATS PRENPGLCRPAATS PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQGDFPALGGPCPPRMPPSPFGSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRWBEIWGPWHRWESFSLEGEWPSRTFEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILD*NOATADKNN*TTAALQPHGRLVSSPRMAEA	5912	924	277	
CLVDNIFPPVVNITWLSNGHSYTEGVSETRPSSPKSDHFLLQDQ VTSPSFFFF**DL*TAKVEQLGAMFEPILKHWGABIPTTL 5913 46 1198 QLRMAGAEGAAGRQSELEPVVSLVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEBPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYKDN FFGLYCICKRPYPDPEDEITDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIRPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLMWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED 124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSVVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLIGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKKRAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKKRAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS PFGRPTRPLKLIGRTRKRARTIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PCBLPGEEPSAHPVHGGLPAERRGPLQRVQEPLRGVQTGPDLRS PPELPGEEPSAHPVHGGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWEEFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NOATADKNN*TTALLQPHQRL\VSPRMAEA				
VTSPSFPF***DL*TAKVEQLGAWFEPLLKHWGAEIPTTL 5913 46 1198 QLRMAGAEGAAGRQSELEPVVSLVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRMFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNABSKSGCKLQELKAKQLIKKDTAT YWPLNNRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED 5914 960 124 NLGGSELPPEEALFIQVASMNQRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILLGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH ENGHLPGLCRPAATS 5915 1604 703 FFGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLSFPCT PQEDFPALGGPCPPRMPSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGGEPSAHPVHQCLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGFSFLGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN**TTALLQPHQRL\VSPRMAEA				
5913 46 1198 QLRMAGAEGAAGRQSELEPVVSLVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGBEPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNARSKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED 124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIG9YRKNLLCYDHRTDVMEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLQQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FFGRPTRPLKLGRRRKRARIIQAPHCHSFRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPEPPEGLVPPIGSFPCT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLDSPSPHP\PVSPAFPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPECL**AAGPAAH 5916 256 633 SFRWWEIWGPWHRWESFSLEGEWPSRIPEFSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQQQWTSQQYPDH PTRLILO*NQATADKNN**TTALLQPHQRL\VSPRMAEA			Ì	
DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHOS HKLFELYTKRNPRCDCGNSKFKNLECKLLPPKAKVNSGNKYNDN PFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQENVCQACKKRCSFLWAYAAQLAVTKIST\GMMDWCGTIM E*/DDGEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNNRSKLCTCQDCMKNYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED 124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGFVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCDT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFLVPPIS KPPPGFSGLLPSPHP\PVSFAPPPPPPQK/RRRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEPPEGL**AAGPAAH 5916 256 633 SPRMWETWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NOATADKNN*TTALLQPHQRLVSPRMAEA	1			
HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEMVCQACMKRCSFLMAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNABSKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED 5914 960 124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMBRFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FFGRPTRFLKLGRRRKRARITQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGBAGGEFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTTALLQPHQRLVYSPRMAEA	5913	46	1198	
FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED 124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 1604 703 FFGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPPFDGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGFFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGFHRWESFSLGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NOATADKNN*TTALLQPHQRL\VSPRMAEA				
SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED 5914 960 124 NLGGSEPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHVVQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGFFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHGRL\VSPRMAEA] ,	HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN
E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNABSKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED 5914 960 124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNOWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA	1	1		FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE
CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED 5914 960 124 NLGGSELPPEEALFIQVASMNQRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDFSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQCLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA	1	1		SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM
YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED 5914 960 124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA			· ·	E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP
AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED 5914 960 124 NLGGSELPPERALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAFPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA				CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT
5914 960 124 NLGGSELPPERALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA			1	
ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA		I		AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED
GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH . 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA	5914	960	124	NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN
IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FPGRPTRPLKLGRRRKRARITQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA		,		
SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLPSPHP\PVSPAPPPPPPQK/RPRLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA				GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS
KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS 5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA				IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE
PHRHLPGLCRPAATS 5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSFGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA				SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP
5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL*+AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA				
PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL*+AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA				
PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL*+AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA	5915	1604	703	FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA
KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL*+AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA				PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT
PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA				PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS
PVLQELPGPAGGEFPEGL**AAGPAAH 5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA				KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS
5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA	Ţ			PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS
TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILO*NQATADKNN*TTALLQPHQRL\VSPRMAEA	ĺ			PVLQELPGPAGGEFPEGL**AAGPAAH
PTRLILO+NQATADKNN+TTALLQPHQRL\VSPRMAEA	. 5916	256	633	SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR
PTRLILQ+NQATADKNN+TTALLQPHQRL\VSPRMAEA 5917 1343 827 AHQILTYLEP/ICLVVNYNKILTVFLTKSVLEI*KFIHTPQTYR				TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH
5917 1343 827 AHQILTYLEP/ICLVVNYNKILTVFLTKSVLEI*KFIHTPQTYR				PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA
	5917	1343	827	AHQILTYLEP/ICLVVNYNKILTVFLTKSVLEI*KFIHTPQTYR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Godge / manadala muslandia di seleta
	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence	<u> </u>	\=possible nucleotide insertion)
Į			F*NDFFGIKEVYVSRRLRKTSF/RLAVTFLEQAVVSKECVPVDQ
1			FMEHLLPSLLSLASDPVPNVRVLLAKALRQMLLEKAYFRNAGNP
			HLEVIEETILALQSDRDQDVSFFAALEPKRRNIIDTAVLEKQN
5918	13	1247	EGAQVARRRSRRQWRAGRCGRGRGGRRAERTGGRGPPGRPRPLP
	1		PGPARRGRRMETPFYGDEALSGLGGGASGSGGTFASPGRLFPG
1	1		APPTAAAGSMMKKDALTLSLSEQVAAALKPAPAPASYPPA\ADG
i	1		APSAAPPDGLLASPDLGLLKLASPELERLIIQSNGLVTTTPTSS
		}	QFLYPKVAASEEQEFAEGFVKALEDLHKQNQLGAGRAAAAAAA
			ACCDCCTATION DOCT ADARA A DEL DITARA LA COMA A COMA
			AGGPSGTATGSAPPGELAPAAAAPEAPVYA\NLSSY\AGGCRGL
1	1		RGGAAT\VAFAAEPVPFPPPPPPPGALGPRRP/RLALQGRRPQTV
1	İ]	PDVP\SFGESP\PLSPIET\DTPRRI\KAKRKRL\RNPQIRAPK
1	1	1	PASRKLGAQSRALERESEDPS*SPEHGSLASTASLLREQVAQLK
		<u></u>	QKVLSHVNSGCQLLPQHQVPAY
5919	1	4254	TSVQGDSQGTPTSSQGSINMEHWISQAIHGSTTSTTSSSSTQSG
1	1		GSGAAHRLADVMAQTHIENHSAPPDVTTYTSEHSIQVERPQGST
1	1		GSRTAPKYGNAELMETGDGVPVSSRVSAKIQQLVNTLKRPKRPP
1			LREFFVDDFEELLEVQQPDPNQPKPEGAQMLAMRGEQLGVVTNW
1	1		PPSLEAALQRWGTISPKAPCLTTMDTNGKPLYILTYGKLWTRSM
1	İ	•	KVAYSILHKLGTKQEPMVRPGDRVALVFPNNDPAAFMAAFYGCL
1			LAEVVPVPIEVPLTRKDAGSQQIGFLLGSCGVTVALTSDACHKG
ļ	1		LPKSPTGEIPQFKGWPKLLWFVTESKHLSKPPRDWF\PHIKDAN
1			NDTAYIEYKTCK\DGSVLGVTVTRTALLTHCQALTQACGYTEAE
			MINIM DRIVENICA MICH TOURS AND THE THEORY TEAM
1			TIVNVLDFKKDVGLWHGILTSVMNMMHVISIPYSLMKVNPLSWI
			QKVCQYKAKVACVKSRDMHWALVAHRDQRDINLSSLRMLIVADG
į			ANPWSISSCDAFLNVFQSKGLRQEVICPCASSPEALTVAIRRPT
1			DDSNQPPGRGVLSMHGLTYGVIRVDSEEKLSVLTVQDVGLVMPG
	!		AIMCSVKPDGVPQLCRTDEIGELCVCAVATGTSYYGLSGMTKNT
	i		FEVFAMTSSGAPISEYPFIRTGLLGFVGPGGLVFVVGKMDGLMV
1	1		VSGRRHNADDIVATALAVEPMKFVYRGRIAVFSVTVLHDERIVI
			VAEQRPDSTEEDSFQWMSRVLQAIDSIHQVGVYCLALVPANTLP
			KTPLGGIHLSETKQLFLEGSLHPCNVLMCPHTCVTNLPKPRQKQ
			PEIGPASVMVGNLVSGKRIAQASGRDLGQIEDNDQARKFLFLSE
	1		VLQWRAQTTPDHILYTLLNCRGAIANSLTCVQLHKRARKIAVML
1.] :		MERGHLQDGDHVALVYPPGIDLIAAFYGCLYAGCVPITVRPPHP
-	'		
	j : j		QNIATTLPTVKMIVEVSRSACLMTTQLICKLLRSREAAAAVDVR
	ļ		TWPLILDTDD*PKKRPAQICKPCNPDTLAYLDFSVSTTGMLAGV
1.			KMSHAATSAFCRSIKLQCELYPSREVAICLDPYCGLGFVLWCLC
1]		SVYSGHQSILIPPSELETNPALWLLAVSQYKVRDTFCSYSVMEL
	į		CTKGLGSQTESLKARGLDLSRVRTCVVVAEERPRIALTQSFSKL
1			FKDLGLHPRAVSTSFGCRVNLAICLQGTSGPDPTTVYVDMRALR
1			HDRVRLVERGSPHSLPLMESGKILPGVRIIIANPETKGPLGDSH
1	}	•	LGEIWVHSAHNASGYFTIYGDESLQSDHFNSRLSFGDTQTIWAR
1			TGYLGFLRRTELTDANGERHDALYVVGALDEAMELRGMRYHPID
1 .			IETSVIRAHKSVTECAVFTWTNLLVVVVELDGSEQEALDLVPLV
ĺ			TNVVLEEHYLIVGVVVVVDIGVIPINSRGEKQRMHLRDGFLADO
1			LDPIYVAYNM .
5920	1381	1499	QLGAVAHAGVSRIPP*LFPPLHPTFLSLWCLHHKLP/HPPGASM
		4477	
			VRPPVVPRRPPAHISSVRQASTQVPRTVPHTQRVANIGTQTTGP
			SGVGCCTPGRPLLPCKCSSAAHSTYRVQEPAVHIPGQEPLTASM
			LAAAPLHEQKQMIGERLYPLIHDVHTQLAGKITGMLLEIDNSEL
			LLMLESPESLHAKIDEAVAVLQAHQAMEQPKAYMH
5921	727	157	VCPGTGGE*GLWGQLGGLPKETPLKPMDAFTGSGLKRKFDDVDV
	İ		GSSVSNSDDEISSSDSADSCDSLNPPTTASFTPTSILKROKOLR
l i			RKNVRFDQVTVYYFARRQGFTSVPSQGGSSLGMAQRHNSVRSYT
			LCEFAQEQEVNHREILREHLKEEKLHAKKMKLTKNGTVESVEAD
		,	GLTLDDVSDEDIDVENVEVDDYFFLQPLPTKRRRALLRASGVHR
	İ		
			IDAEEKQELRAIRLSREECGCDCRLYCDPEACACSQAGIKCQVD
'			RMSFPCGCSRDGCGNMAGRIEFNPIRVRTHYLHTIMKLELESKR
	1		Q\GAAQQPQ*GALPDCQLQPDRSTGL*DPSWIGSKGLSFTGKG
	i		
5922	2475	495	AAATHLIILRVIENRGAEGKRK SYSNWGLFPSVFIQVPRSRTGNLKPIFLFYSYYE\CMETLKG\T

		- 17 - 1 - 1	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Actu, b=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		Bequence	\=possible nucleotide insertion)
	sequence		CLYNATQYKVCSPRNDRPDACYNPSEPAATTVFEIRTGLLLGDT
	İ	1	SKIITRTEEKEIPKQITLRFDACAAINSKKLEIGCGSLN*ERS*
			SKITTKTEEKETPAQITEKFDACAAINSKEETGCGSDN BKS
		1	RVENKYVCHESGVCKNCAYWPCVI*AT*KKNKNDSVYLQKGEAN
	ļ	1	PSCAAGHCNPLELIITNPLDPHWKKGERVTLGINRTGLKPQVVI
			LIKGEVHKCSPKPVFQTFYEELNLPAPELLKKTKNLFLQLAENV
	i	i	IFLLNGTSCYVRGGTTIGDRWPWEA*ELVPTDPAPDIIPI*KAE
		1	ASNF*VLKTSIIRQYCIAREGKDFIIPVGKPNCIGQKLYNSTTK
			TIT**DLNHTEKNPFSKFSKLKTA*AHAESH*DWTVPSGLY*IC
	1		RHRAYFRLPNKWADSCVIGTIKPSFFLLPIKMGELLGFSVYASR
			EKKGIVIGNWKDNEWPRERIIQYYGPATWAQDGSWGYR/TP/VY
			MLNWIIRLQAILEIISNETGRALTVLAWQETQMRNAIYQNRLAL
ĺ	1		MDNWITKLQAIDETISNETGKADIVDAMQETQRKMATIQNKDAD
			DYLLVAEGGVCRKFNLTNCCLQINDQGQVVKNIVRDMTKLAHVP
İ	1		IQVWHKFDPESLFGKWFPAIGGFKTLIVGVLLVIRTCLLLPCVL
	1		PLLFQMIKGIVATLVHQKTSAHVNYMNHYRSISQRDSKSEDESE
		1	NSH
5923	137	638	QLCGRRGQRFRTSIKRMHPI*RTCPNTNL/IILLSQENTQIRDL
1			OOENRELWISLEEHQDALELIMSKYRKQMLQLMVAKKAVDAEPV
}	1		LKAHQSHSAEIESQIDRICEMGEVMRKAVQVDDDQFCKIQEKLA
		ļ	QLELENKELRELLSISSESLQARKENSMDTASQAIK
		2746	EKGKVKDAGAEQWISLSLSCKGSWETQFSNHLNSLTPPTSVRRM
5924	274	2146	PLITTVTLLKMVARHHMKLLCSKAFSTQLQQKIFLHSQMGIHHQ
			PETTTYTELKMYAKHMKEECSKAFSTQEQQXIFEHSQUGITHIQ
		1	SVCMKLKPNTSHIISILMGQPMALVQLETLAPLTIIIQKFQTQD
į.		1	HMKFWKNLPLHSHHLTPSVPQTVIPKKTGSPEIKLKITKTIQNG
		1	RELFESSLCGDLLNEVQASE\Q*NQSIESRKEKRKKSNKHDSSR
1		· I	SEERKSHKIPKLEPEEQNRPNERVDTVSEKPREEPVLKEGSPSS
ļ		1	ANTIFCSNNGSVHW\FKFQVGDLVWSKVGTYPWWPCMVSSDPQL
ł		1	EVHTKINTRGAREYHVQFFSNQPERAWVHEKRVREYKGHKQYEE
Ì	1	1	LLAEATKQASNHSEKQKIRKPRPQRERAQWDIGIAHAEKALKMT
ł	1		REERIEQYTFIYIDKQPERALSQAKKSVASKTEVKKTRRPRSVL
ļ		i	NTQPEQTNAGEVASSLSSTEIRRHSQRRHTSAEEEEPPPVKIAW
1			NTOPEOTRAGEVASSISSIE IKKNSUKKIISABEBBFFFVKIM
Ì	1 .		KTAAARKSLPASITMHKGSLDLQKCNMSPVVKIEQVFALQNATG
-	l .		DGKFIDQFVYSTKGIGNKTEISVRGQDRLIISTPNQRNEKPTQS
}	1		VSSPEATSGSTGSVEKKQQRRSIRTRSESEKSTEVVPKKKIKKE
İ	ļ	,	QVGFLHVES
5925	216	1911	MMTAESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL
	}		QDTPPPDPEIFRQRFRRFCYQNTFGPREALSRLKELCHQWLRPE
ľ	1		INTKEQILELLVLEQFLSILPKELQVWLQEYRPDSGEEAVTLLE
	1		DLELDLSGQQVPGQVHGPEMLARGMVPLDPVQESSSFDLHHEAT
Į.	1		QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALFT
1			ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAF
1	İ		POGGENRNENEESTSKAETSEDSASRGETTGRSQKEFGEKRDQE
,			GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK
j		1	GRIGERQUANFEERIKAEKRUSGFALGAURALIIGERGEGET TRUV
1	1		GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK
1		}	IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE
1		Ì	CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ
	Į.		RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK
1			\AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV
5926	 2	233	DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPBPPGAHEP
3320		1	SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS
FASE	4146	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA
5927	4146	1240	YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR
		1	YKKYGDKKLHEKKPLQKHQAHQIPEKKVKIGEBKKKIDEBAAK KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG
1	1		KKKLET I BREKKUNDU I I SEGGET A ROCKER BEGOVERNING TERO
1			WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ
1			MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR
1			KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV
İ	}		YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
	1		RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV
			AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS
i			SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN
			LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL
	1		DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE
i	1	·	DISESTIEMITAGEATUTGAMORELISO ITTO

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
			AIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLETEILQEPS
1		İ	GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG
			VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE
1		ļ	HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
			LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI
			EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS
			EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
1			GEIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE
			DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
5928	4146	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA
			YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR
			KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG
1			WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ
			MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR
			KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV
			YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
			RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV
1			AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS
			SLTDTRETSBEMQKTNNAISSKREILRRLNENLKAQEDBKGKQN
			LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE
ł			LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
	·		AIVDSPVETKSPEFSEASPOMSLKLEGNLEEPDDLETEILOEPS
1			GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG
1			VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE
	,		HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
1			LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI
1			EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGERYS
1 1			EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
			GEIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE
1 .			DEDENIEICSKIVONILGNEHOHLYAKILHLVMADGAYOEDNDE
5929	3	1558	LDFSMTTQLPAYVAILLFYVSRASCQDTFTAAVYEHAAILPNAT
•			LTPVSREEALALMNRNLDILEGAITSAADQGAHIIVTPEDAIYG
			WNFNRDSLYPYLEDIPDPEVNWIPCNNRNRFGQTPVQERLSCL\
	'		AKNNSIYVVANIGDKKPCDTSDPQCPPDGRYQYNTDVVF\DSQG
1 - 1	İ		KLVARYHKQNLFMGENQFNVPKEPEIVTFNTTFGSFGIFTCFDI
}			LFHDPAVTLVKDFHVDTIVFPTAWMNVLPHLSAVEFHSAWAMGM
. 1			RVNFLASNIHYPSKKMTGSGIYAPNSSRAFHYDMKTEEGKLLLS
1 1	1		QLDSHPSHSAVVNWTSYASSIEALSSGNKEFKGTVFFDEFTFVK
1			LTGVAGNYTVCQKDLCCHLSYKMSENIPNEVYALGAFDGLHTVE
1	. [GRYYLQICTLLKCKTTNLNTCGDSAETASTRFEMFSLSGTFGTQ
	Į		YVFPEVLLSENQLAPGEFQVSTDGRLFSLKPTSGPVLTVTLFGR
5930			LYEKDWASNASSGLTAQARIIMLIVIAPIVCSLSW
5930	113	6082	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK
1	,		KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ
1 1			KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF
1 1			CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM
ł J			LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN
1 1			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV
[}	TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL
į l			KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG
1			FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL
;]	ļ	ļ	CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN
	!	l	SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL
			DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ
		ļ	GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
		Ì	NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT
	İ		KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK
į į			LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP
			- Landing and a second a second and ntaining signal peptide
------	---------------	---------------	--
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j	amino acid	sequence	Codon, /=possible nucleotide deletion,
	· —	sequence	\=possible nucleotide insertion)
	sequence		
]			NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH
			LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR
			NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK
	i		EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM
	ł		RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ
į		ļ	DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF
1		ŀ	IKEKKLMEDRIAECSSQLAEEBEKAKNLAKIRNKQEVMISDLEE
j l		j	RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL
1			AKKEEELQGALARGDDETLHKNNALKVVRELQAQIABLQEDFES
		İ	-
[ļ	EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE
1			QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR
		}	FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV
			QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEAEKKGIK
i '		!	FAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKNSLQ
1	1		EQQEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA
1			KKKLLKDAEALSQRLEEKALAYDKLEKTKNRLQQELDDLTVDLD
1	}	1	HQRQVASNLEKKQ\KKFDQLLAEEKSISARYAEERDRAEAEARE
			KETKALSLARALEEALEAKEEFERONKOLRADMEDLMSSKDDVG
	ļ	<u> </u>	KNVHELEKSKRALEQQV\EEMRTQLEELEDELQATEDAKLRLEV
!			NMOAMKAOFERDLOTRDEONEEKKRLLIKOVRELEAELEDERKO
			RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQLRKLQAQMK
			DYORELEEARASRDEIFAOSKESEKKLKSLEAEILQLQEELASS
i			
1			ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE
1		İ	ELEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR
			QQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQLE
1	ļ		QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA
j			NARMKQLKRQLEEAEEEATRANASRRKLQRELDDATEANEGLSR
1			EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK
		1	TSDVNETQPPQSE
5931	113	6082	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK
i			KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ
ļ			KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF
1	1		CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM
1		1	LODREDOSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN
1			I DODUMDOTHOLOGOVICIEM LIGHT OF THE LIGHT OF THE CONTROL OF THE CO
		1	IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV
			_ ~ ~
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL
	·		IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRMLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRMLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRMLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVBEEEERNQILQNEKKKMQAHIQ
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVBEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALEDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEBKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVBEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFHHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALEDDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVBEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKKLMATLRNTNPNFVVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVBEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVBEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQVLLEBKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVBEEEERNQILQNEKKKMQAHIQ DLEEQLDEEGGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEBKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIABLQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIDELKLQL EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEELHDLESRVBEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEFILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIABLQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQ IAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGPPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVBEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIABLQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEAEKKGIK
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGYLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVBEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKĄSRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEAEKKGIK FAKDAASLESQLQDTGELLQEETRQKLNLSSRIRQLEEEKNSLQ
			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGPPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVBEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIABLQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEAEKKGIK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	_	\=possible nucleotide insertion)
			KKKLLKDAEALSQRLEEKALAYDKLEKTKNRLQQELDDLTVDLD
			HQRQVASNLEKKQ\KKFDQLLAEEKSISARYAEERDRAEAEARE
			KETKALSLARALEBALEAKEEFERQNKQLRADMEDLMSSKDDVG
			KNVHELEKSKRALEQQV\EEMRTQLEELEDELQATBDAKLRLEV
			NMQAMKAQFERDLQTRDEQNBEKKRLLIKQVRELEAELEDERKQ
			RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQLRKLQAQMK
			DYQRELEBARASRDEIFAQSKESEKKLKSLEABILQLQEELASS
			ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE
			ELEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR
			QQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQLE
1			QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA
İ			NARMKQLKRQLEEAEEEATRANASRRKLQRELDDATEANEGLSR
İ			EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK
5932	33	572	TSDVNETQPPQSE
3932	, 33	5/2 .	RHLEEICFLFLQKGRKLKLSGPRWEEGKPRGTGGLWVKAEANMG
1			FGATLAVGLTIFVLSVVTIIICFTCSCCCLYKTCRRPRPV\APP PHPP/PVVHAPYPOPPSVPPSYPGPSYOGYHTMPPOPGMPAAPY
İ			PMOYPPPYPAOPMGPPAYHETLAGGAAAPYPASOPPYNPAYMDA
			PKAAL
5933	1	3190	GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD
****	_	3230	SDMPSRTRPKSPRKHNYRNESARESLCDSPHONLSRPLLENKLK
			AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEG
İ			SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADOKNP
1.			PNQSSNERPPSLLVIBTKKPPLKKGEKEKKKSNLELFKEELKOI
	,		QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL
ŀ			DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP
			LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI
ĺ		÷	MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP
1			RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI
			HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW
i	٠.	• .	KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ
	: •		ETEAFVEEPSKKGALKBEQRDKLBEILRGLTPRKNDIGDAMVFC
	'		LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA
	·		KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM
		1	TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIBEKETEDVPDDLD
	' :		GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV
	;		PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD QHEESEEEENQNQEEESEDEEDTQSSKSEEHHLYSNPIKEEMTE
	:		
			SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGQSF QEQVBHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKEK
		•	DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPSPKSERSERSER
			SHKESSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRRSRSRSP
			KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCDLF
			LCPERSVF
5934	1	3190	GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD
			SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK
			AFSIGKMSTAKRTLSKKEQEELKKKBDEKAAAEIYEEFLAAFEG
			SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP
]			PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI
1			QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL
			DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP
			LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI
			MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP
			RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI
	1		HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW
			KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ
]		ŀ	ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC
	l de la companya de la companya de la companya de la companya de la companya de la companya de la companya de		LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA
] [KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM
j			TCFRAWEDWAIYPBPFLIKLQNIFLGLVNIIEEKBTEDVPDDLD GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV
			GAFIBBBLUGAPUBUVUGIPIDATPIDULUGVPIKSLDDDLDGV

Topo bundished bundished and build commont con	
1	taining signal peptide
ID beginning nucleotide (A=Alanine, C=Cysteine	, D=Aspartic Acid, E=
NO: nucleotide location Glutamic Acid, F=Pheny	lalanine, G=Glycine,
location corresponding H=Histidine, I=Isoleuc	ine, K=Lysine,
corresponding to first L=Leucine, M=Methionin	e, N=Asparagine,
to first amino acid P=Proline, Q=Glutamine	, R=Arginine,
amino acid residue of S=Serine, T=Threonine,	V=Valine,
residue of amino acid W=Tryptophan, Y=Tyrosi	ne, X=Unknown, *=Stop
amino acid sequence Codon, /=possible nucl	eotide deletion,
	insertion)
	VEAVDESELEAQAVTTSKWELFD
	TQSSKSEEHHLYSNPIKEEMTE
	KVMKFQDELESGKRPKKPGQSF
	ERERDKKDKEKLESRSKDKKEK
	RSSSGRRVKSPSPKSERSERSER
	CAKRSPSGSRTPKRSRSRSRSP
KKSGKKSRSQSRSPHRSHKKSK	GKTNTGRKFFKKAVTYWKCDLF
LCPERSVF	
5935 3 4493 SYWLSGWRLSRPPRQFWAGWRG	GIGRFGTMAPVHGDDCEIGASAL
	EALERLKKAKAGERYKYEVEDF
	DWIVDDDGIGYVEDGREIFDDD
	CRNVKKLAVTKPNNIKSMFIACA
	DLNTETPQITPPPVMILKKKRS
	ASPVSRKEPPLTPVPLKRAEFAG
	GDFDEPMEVEEVDLEPMAAKAWD
	YLGSFLPDVSCWDIDQEGDSSFS
	VFHFYWLDAYEDQYNQPGVVFLF
	ERTLYFLPREMKIDLNTGKETGT
	MKFKSKPVEKNYAFEIPDVPEKS
	rfshvfgtntsslelflmnrkik
	VEAMALKPDLVNVIKDVSPPPLV
	MAALVHHSFALDKAAPKPPFQSH
FCVVSKPKDCIFPYAFKEVIE	KKNVKVEVAATERTLLGFFLAKV
HKIDPDIIVGHNIYGFELEVL	LQRINVCKAPHWSKIGRLKRSNM
	DVEISAKELIRCKSYHLSELVQQ
ILKTERVVIPMENIONMYSES	SQLLYLLEHTWKDA\KFILQIMC
	TLMGGRSERNEFLLLHAFYENNY
	IDGDTNKYKKGRKKGAYAGGLVL
	SIIQEFNICFTTVQRVASEAQKV
	LPREIRKLVERRKQVKQLMKQQD
	SMYGCLGFSYSRFYAKPLAALVT
	IYGDTDSIMINTNSTNLEEVFKL
	VFKSLLLLKKKKYAALVVEPTSD
	LAKDTGNFVIGQILSDQSRDTIV
	SOFEINKALTKDPODYPDKKSLP
HVHVALWINSQGGRKVKAGDT	VSYVICODGSNLTASORAYAPEO
LQKQDNLTIDTQYYLAQQIHP	VVARICEPIDGIDAVLIATGWEL
\DPTQFKVHHYHKDEENDALL	GGPAQLTDEEKYRDCERFKCPCP
TCGTENIYDNVFDGSGTDMEP	SLYRCSNIDCKASPLTFTVQLSN
KLIMDIRRFIKKYYDGWLICE	EPTCRNRTRHLPLQFSRTGPLCP
ACMKATLOPEYSDKSLYTOLC	FYRYIFDAECALEKLTTDHEKDK
I.KKOFFTKVI.DVPKI.KNTA	EQFLSRSGYSEVNLSKLFAGCAV
KS	<u> </u>
	LQEFSRLLRAVHRSRAWTCYLAI
5936 1124 139 RGEEQFDAEFRRFACLGFGER	RAPPLRLLVQKREADSSGLAFAS
RMLMATCCPSPTTTACTGPWQ	DDITTEL DODGOMENUSCHERS
NSLQRKKGLLLKPVAPLRTK	PPLLISLPQDFRQVSSVIDVDLL
PETHRRVRLHKHGSDRPLGFY	IRDGMSVRVAPQG\LERVPGIFI
	LEVNGIEVAGKTLNQVTDMMVAN
SHN\LIVTVKPANQRNNVVRG	ASGRLTGPPSAGPGPAEPDSDDD
	PCWDLHPGCRHPGTRSSLPSLDD
OEOASSGWGSRIRGDGSGFSL	•
5937 31 1600 PTSLLKSTVQLMCRLLQDKRY	QCVYSLAEIFKVLASFYVILVIL
YGLTSSYSLWWMLRSSLKQYS	FEALREKSNYSDIPDVKNDFAFI
L.HLADOVDPLVSKRFSIFLSE	VSENKLKQINLNNEWTVEKLKSK
T VVNNODET ET. UT. EMT. MCT. DN	NVFELTEMEVLSLELIPEVKLPS
PARAMETER DI	HPALAFLEENLKILRLKFTEMGK
AVSQLVNDKELKVYHSSLVVD	PEQLSTMQLEGFQDLKNLRTLYL
I PRWYFHLKNLKELYLSGCVL	CIDMEGGRIVALWALAKAMAA AG
KSSLSRIPQVVTDLLPSLQKL	SLDNEGSKLVVLNNLKKMVNLKS
LELISCOLERIPHSIFSLNNL	HELDLRENNLKTVEEIISFQHLQ
I I MILECTLY LIGHTLY TO A TO A	LSNLEQLSLDHNNIENLPLQLFL
CTKLHYLDLSYNHLTFIPEEI	

050	1		
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Doquonoc	\=possible nucleotide insertion)
-	† •		LFQCKKLQCLLLGKNSLMNLSPHVGELSNLTHREPIG\NYLETL
[PPELEGCQSLKRNCLIVEENLLNTLPLPVTERLQTCLDKC
5938	395	1865	YKGEGFFCNQEARGERRKKKKAMSSPNIWSTGSSVYSTPVFSQK
	ļ		MTVWILLLSLYPGFTSQKSDDDYEDYASNKTWVLTPKVPEGDV
į			TVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINME
1			YTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRN
1			SKKADAHWITTPNRMLRIWNDGRVLYSLRLTIDAECQLQLHNFP
l			MDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQFSF
			VGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLI
	Ì		VVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVS
			YVTAMDLFVSVCFIFVFSALVEYG\TLHYFVSNRKPSKDKDKKK
			KNPAPTIDIRPRSATIQMNNATHLQERDEEYGYECLDGKDCASF FCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNT,VYW
			VSYLYL
5939	66	1404	IRPGYLKEVQENSPGHRAGLEPFFDFIVSINGSRLNKDNDTLKD
			LLKANVEKPVKMLIYSSKTLELRETSVTPSNLWGGOGLLGVSIR
1			FCSFDGANENVWHVLEVESNSPAALAGLRPHSDYIIGADTVMNE
			SEDLFSLIETHEAKPLKLYVYNTDTDNCREVIITPNSAWGGEGS
			LGCGIGYGYLHRIPTRPFEEGKKISLPGQMAGTPITPLKDGFTE
		•	VQLSSVNPPSLSPPGTTGIEQSLTGLSISSTP\PAVSSVLSTGV
)			PTVP\LLPPQVNQSLTSVPPMESSYLHLPGLMPFTRQGLPNLPQ
			PSTFNLPR\PTHSWPGVGLYQEFVKPGVLPPLSSMPPRNLPG\I
1			APLPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNAPSDPAT
1			TTAKADAASSLTVDVTPPTAKAPTTVEDRVGDSTPVSEKPVSAA VDANASESP
5940	145	717	RRSASRSASPROSAGTAVTTGTRAGGTCLAAAHHRMRWRADGRS
		,	LEKLPVHMGLVITEVEQEPSFSDIASLVVWCMAVGISYISVYDH
	1		QGIFKRNNSRLMDEILKQQQELLGLDCSKYSPEFANSNDKDDQV
1			LNCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKQKRPTDLDVDT
			LA/AAFAÓWAAFIFI
5941	13	6147	MCLGRMGASSPRSPEPVGPPAPGLPFCCGGSLLAVVVLLALPVA
			WGQCNAPEW\LPFARPTNLTDEFEFPIGTYLNYECRPGYSGRPF
	<u> </u>		SIICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVHVIKGIQFGSQ
	ř l		IKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPP
		•	TITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIY CTSNDDQVGIWSGPAPOCIIPNKCTPPNVENGILVSDNRSLFSL
			NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD
			VLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPOGDW
			SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF
	į į		QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG
Ī			KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNG
}		i	VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE
			CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH
			VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI
			CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV
			FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL
1			VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS
1			CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA
			SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA
			KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI
			RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD
			FPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKT
			PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN
		l	TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR
]		1	CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC
			TPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQA
1			LNKWEPELPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC
			EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRV
	Į		LFPLNLQLGAKVSFVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP
	ĺ		VCEHIFCPNPPAILNGRHTGTPSGDIPYGKEISYTCDPHPDRGM

	S 31 L 3	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide		
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ !	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TFNLIGESTIRCTSDPHGNGVWSSPAPRCELSVRAGHCKTPEQF
			PFASPTIPINDFEFPVGTSLNYECRPGYFGKMFSISCLENLVWS
i '			SVEDNCRRKSCGPPPEPFNGMVHINTDTQFGSTVNYSCNEGFRL
1			IGSPSTTCLVSGNNVTWDKKAPICEIISCEPPPTISNGDFYSNN
1	i		RTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGVW
	ł	İ	SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRFRCQPG
			FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEHTLSHQ
İ	ŀ		DNFSPGOEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPRCTVKS
	İ	•	CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRSASHCV
	<u> </u>		LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDIPYGKE
ļ	1		- ··
		· ·	VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPAPRCEL
ļ	}	1	PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGYLLVGK
		İ	GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMKKVYHY
1	į	1	GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRTHDALI
1	1	1	VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAIHLHSQ
L.			GGSSVHPRTLQTNEENSRVLP
5942	4509	688	YLYVRMRANPLAYGISHKAYQIDPPL\RKHREQ\LVIE\VGRKL
1			DK\AQMIRFEERTGYFSSTDLGRTASHYYIKYNTIETFNELFDA
1		1	HKTEGDIFAIVSKAEEPDQIKVREEEIEELDTLLSNFCELSTPG
		1	GVENSYGKINILLQTYINRGEMDSFSLISDSAYVAQNAARIVRA
1			LFEIALRKRWPTMTYRLLNLSKAIDKRLWGWASPLRQFSILPPH
			MLTRLEEKKLTVDKLKDMRKDEIGHILHHVNIGLKVKQCVHQIP
			SVMMEAFIQPITRTVLRVTLSIYADFTWNDQVHGTVGEPWWIWV
1			EDPTNDHIYHSEYFLALKKQVISKBAQLLVFTIPIFEPLPSQYY
			IRAVSDRWLGAEAVCIINFOHLILPERHPPHTELLDLQPLPITA
ı	1		LGCKAYEALYNFSHFNPVQTQIFHTLYHTDCNVLLGAPTGSGKT
			VAAELAIFRVFNKYPTSKAVYIAPLKALVRERMDDWKVRIEEKL
			GKKVIELTGDVTPDMKSIAKADLIVTTPEKWDGVSRSWQNRNYV
1			OOVTILIIDEIHLLGEERGPVLEVIVSRTNFISSHTEKPVRIVG
	į		LSTALANARDLADWLNIKOMGLFNFRPSVRPVPLEVHIQGFPGQ
	1		
1			HYCPRMASMNKPAFQAIRSHSPAKPVLIFVSSRRQTRLTALELI
			AFLATEEDPKQWLNMDEREMENIIATVRDSNLKLTLAFGIGMHH
1			AGLHERDRKTVEELFVNCKVQVLIATSTLAWGVNFPAHLVIIKG
	•		TEYYDGKTRRYVDFPITDVLQMMGRAGRPQFDDQGKAVILVHDI
]			KKDFYKKFLYEPFPVESSLLGVLSDHLNABIAGGTITSKQDALD
1			YITWTYFFRRLIMNPSYYNLGDVSHDSVNKFLSHLIEKSLIELE
1	ł		LSYCIEIGEDNRSIEPLTYGRIASYYYLKHQTVKMFKDRLKPEC
		Ì	STEELLSILSDAEEYTDLPVRHNEDHMNSELAKCLPIESNPHSF
			DSPHTKAHLLLQAHLSRAMLPCPDYDTDTKTVLDQALRVCQAML
1		1	DVAANQGWLVTVLNITNLIQMVIQGRWLKDSSLLTLPNIENHHL
1			HLFKKWKPIMKGPHARGRTSIECLPELIHACGGKDHVFSSMVES
			ELHAAKTKQAWNFLSHLPEINVGISVKGSWDDLVEGHNELSVST
			LTADKRDDNKWIKLHADQEYVLQVSLQRVHFGFHKGKPESCAVT
1			PRFPKSKDEGWFLILGEVDKRELIALKRVGYIRNHHVASLSFYT
			PEIPGRYIYTLYFMSDCYLGLDQQYD/NLSQRYTSESFCTGQHQ
1			GL
5943	1	2274	DKPTRHKTYLSSSWAKMAAAEGPVGDGELWQTWLPNHVVFLRLR
1,743	1	25/3	EGLKNOSPTEAEKPASSSLPSSPPPOLLTRNVVFGLGGELFLWD
1			GEDSSFLVVRLRGPSGGG\EEPALSQYQRLLCINPPLFEIYQVL
1		1	LSPTOHHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVNCSTTP
Ì			VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSLR
1			EPOTPTNVIILSEAEEESLVLNKGRAYTASLGETAVAFDFGPLA
l	1		AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHSPGN/I
			WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPNILVIATESGML
			YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVFECVELELALKL
]		ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI
			HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPAP
}		-	IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR
]		EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD
1			IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ
	1	1	KKKQLEDLSYCREERKSLREMAERLADKYEEAKEKQEDIMNRMK
1			

Deginning Not leaded Iccation Iccati	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
No: nucleotide corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence se	_			(A=Alanine C=Cysteine D=Aspartic Acid F=
Corresponding to first amino acid amino acid amino acid amino acid sequence Popular (Popular Proposition) Popular (Popular Prop	NO:			Glutamic Acid R-Phenylalanine G-Glycine
La Laurine, Marchine, Nasparagine, befirst amino acid anino acid acid anino acid acid acid anino acid acid acid acid acid acid acid acid		1		H=Histidine T-Isoleucine V-Lucine
to first amino acid residue of amino acid an, Y-Tytosine, X-Unknown, *-stop Codon, /-possible nucleotide deletion, V-possible nucleotide insertion) KLHSPTISELEVISSESSEMENKERGIFPOQUERHONNIKOVIMK KUVQO)GORKKILSERPTIIISAYGKKCQSILKERGHIREMW KQINDINNIWN FRAFTFDEFEVITISPAYGKCQSILKERGHIREMW KQINDINNIWN FRAFTFDEFEVITISPAYGKCQSILKERGHIREMW KQINDINNIWN FRAFTFDEFEVITISPAYGKCQSILKERGHIREMW KQINDINNIWN FRAFTFDEFEVITISPAYGKCQSILKERGHIREMW KQINDINNIWN FRAFTFDEFEVITISPAYGKCQSILKERGHIREMW KQINDINNIWN FRAFTFDEFEVITISPAYGKCQSILKERGHIREMW KQINDINNIWN FRAFTFDEFEVITISPAYGKCQSILKERGHIREMW KQINDINNIWN FRAFTFDEFEVITISPAYGKCQSILKERGHIREMW KQINDINNIWN FRAFTFDEFEVITISPAYGKCQSILKERGHIREMW KQINDINNIWN FRAFTFDEFEVITISPAYGKCQGCILLESTISGSTONISTCTKR KQCQCACCACACACACACACACACACACACACACACACAC		corresponding		LeLeucine M-Methionine N-Agnaragine
### amino acid anino acid sequence ### ami				P=Proline O-Glutamine P-Amainine
maino acid sequence Maino acid sequence Maino acid sequence Maino acid sequence Maino acid sequence Maino acid sequence Maino acid sequence Maino acid sequence Maino acid sequence Maino acid sequence Maino acid Maino			ı	Sasserine Tathreonine Valling
amino acid sequence Codon, /=possible nucleotide deletion,	İ			
Sequence N=Dossible nucleotide insertion		1		Codon /-nossible nucleatide deletion
NLHSPHSELPYLSDSEEDMKRELQLIPFOLDRALIANTIQVTMK			bequence	\-nossible nucleotide insortion\
S944 167 3428		00410000		VILLEGUEST DISCREDENTARIO I TODOS DISCOVA TROVINS
S944 167 3428 SIAFFTDEPEVLTEPPSATTITIGISATWITLAGSHOKENNY ITTISSKRATRKIKITPERVQLIPDDEPISYSQPEKVIGGSKS SISTESGGSINKISTESGSGSSINKSSKSKDNEPAVVTTVS KKQPSVLVTPKEERKSVSGKASIKLSETISGGTSPAVVTTVS KKQPSVLVTPKEERKSVSGKASIKLSETISGGTSPAVVTTVS SRVIGRGGCHIRATREFTGAHIDIDKQKDKTORITTIRGGTES TRQATGLINALIKASPKEQKREEWKEVKRSKKSVPSTVI SRVIGRGGCHIRATREFTGAHIDIDKQKDKTORITTIRGGTES TRQATGLINALIKASPKEQKREEWKEVKSKSKSPSTVI SRVIGRGGCHIRATREFTGAHIDIDKQKDKTORITTIRGGTES TRQATGLINALIKASPTGAHALIAAQTFQALIPPHWI HFGGTFPPAGSTWGPFVVPLASSASTHKTIKGSTES TRAATSIMGIKMTVALSSTSGTATALIVVPAISSASTHKTIKGS TAANTSIMGIKMTVALSSTSGTATALIVVPAISSASTHKTIKGS SEVENDAG VIVVATSSAATTTVTTTASSASTHVAISSASGSPVT TAANTSIMGIKMTVALSTSGTATALIVVPAISSASTHKTIKGS SEVENDAG VIVVATSSAATTTVTTTASSANTAPTOGTSTNOSS PSVROLL VIVVATSSAATTTVTTTASSANTAPTOGTSTNOSS PSVROLL VIVVATSSAATTTVTTTASSANTAPTOGTSTNOSS PSVROLL VIVVATSSAATTTVTTTASSANTAPTOGTSTNOSS PSVROLL VIVVATSSAATTTVTTTASSANTAPTOGTSTNOSSAGSVEROLL VIVVATSSAATTTVTTTASSATSINKVASSEGGEVEPPIQGGS VIVVATSSASTASTAST VIVVATSSAATTATVTTTASSANTAPTASSATSASTAST VIVVATSSAATTATVTTTASSANTATASTASTASTAST VIVVATSSAATTATVTTTASSATSANTASTASTASTASTASTASTASTASTASTASTASTASTAST]	
S944 167 3428 SEIAFFEDEFVLTEPSSATTITIGISATWILLAGSHOKKUN				
TITTSSERNORENKITPERUVOLIEDDE, PISYSPERUWGENES SSTESSGEDSINKE ISSCEDESSINKS SEKNICHED PAVTTTVISS RKROBS VICTOR ISSCEDESSINKS SEKNICHED PAVTTTVISS RKROBS VICTOR ISSCEDESSINKS SEKNICHED PAVTTTVISS RKROBS VICTOR ISSCEDESSINKS SEKNICHED PAVTTTVISS RKROBS VICTOR SERVICE SERVI	5944	167	3429	
SSTSSEGGISNNRISSCSDSSNINSSRISDHISPAVTITIVES KOPSPLISSPNOKLTVASPKERKOVGKREKKUSTISSGTSTINSLISTICK GPSPLISSPNOKLTVASPKERKOVGKREKKVSVPSTITIV SRVIGRGGCINA TREPTGAMILIOKOKOKTORI TITIGGTES TROATOLINALIKOPOKE IDELIPKNRIKSSSANSKIGSSANSKIGSSANT TRANTSIMGIKHTVALSSTSGTATALIVVATISSSANKIGSSANSKIGSSANT TAANTSIMGIKHTVALSSTSGTATALIVVATISSSASTHKITKOP WINNEPGPVSFPLARY PPOPAHALIAAOTPOOLEPPRINTE HEGGTFPPAGSTWERTVALSTSGTATALIVVATISSSASTHKITKOP WINNEPGPVSFPLARY PPOPAHALIAAOTPOOLEPPRINTE HEGGTFPPAGSTWERTVALSTSGAARANTSKCHMINTPHENDONS GSQUNSABSLTSSPTTTSSASTWOTTSTNGSPSSPSVERQLE UTVUKTSSALTTTYTTTSANNITAPTHATYMPTAKHYPVSSP SSPSPPAQPGOVERNSPLDCGSSPRKVASSEGGAGSSPWEVT TYNTEPBASSSGSSAHISNOQOPROSVSGERRPLQGSVVVET TYNTEPBASSSGSSAHISNOQOPROSVSGERRPLQGSVVVET TYNTEPBASSSGSSAHISNOQOPROSVSGERRPLQGSVVVET PATRYPHATISSASTOVASSAVLSVANNIKREPISVPSSV LAPSTLSTOSARONSVIPANKE LAPBYSALPLPGGFTERNST SAHAPHGGSVVSSGSTPESSHLGSKSSVINSDPLHGGDISKANG FREPLQRPASPSSGIVNEDSTVESSTPSSTHLGFRASNISOGOM YGGGAPLIGAGAPAANNINGHFSSLSLITPCSSASNISSAGSVSS GVARAPSASSSVVSGSTPESHLGSKSSVINSDPLHGGDISKANG FREPLQRPASPSSGIVNMBSYCSVIPSSTHLGFRASNISOGOM YGGGAPLIGAGAPAANNINGHFSSLSLITPCSSASNISSAGSVSS GVARAPSADSSVVINDSTVESSKPSNINSORKVVPUTGTERSRATIROYO TSAPSVIGSNILSTSVCHGGINSFEGIGGNORKVPVDIGTERSRATIROYO TSAPSVIGSNILSTSVCHGGINSFEGIGGNORKVPVDIGTERSRATIROYO TSAPSVIGSNILSTSVCHGGINSFEGIGGNORKVPVDIGTERSRATIROYO TSAPSVIGSNILSTSVCHGGINSFEGIGGNORKVPVDIGTERSRATIROYO TSAPSVIGSNILSTSVCHGGINSFEGIGGNORKVPVDIGTERSRATIROYO TSAPSVIGSNILSTSVCHGGINSFEGIGGNORKVPDIGTERSRATIROYO TSAPSVIGSNILSTSVCHGGINSFEGIGGNORKVPDIGTERSRATIROYO TSAPSVIGSNILSTSVCHGGINSFEGIGGNORKVPDIGTERSRATIRO TREATERS (MARMEDIATIVATORA STRINGPEDIAM TORGO OPOPEKPESTLIGAARAPYKALIGOSSAPDSGRSGCTEPABER KRKREN MARMADAVAGAGGANIARDARWTINALDSKOP OPOPEKPESTLIGAARAPYKALIGOSSAPDSGRSGCTEPABER KRKREN MARMADAVAGAGGANIARDARWTINALDSKOP OPOPEKPESTLIGAARAPYKALIGOSSAPDSGRSGCTEPARVEGH KRKREN MARMADAVAGAGGANIARUTARVAGRANTILINAA OEGDLIPELRA HISTORYONALORGANA TORGORA TSAPSVIGGNORMVCORVULINGAGAGAN YCPOLORKKY YSKOGOOGAANSVILGHAANATAL TSAP	3311	107	3420	
KKOPSYLUTPPREBRKSVSGKASIKLSETISBOTSNISLSTCKS GPSPLSSPNKKTLYASPKRGKOREGWEKUVERSKYSVPSTVI SRVIGRGCAINATREPTGAHIDIDKORDETDELTTINGGTES TROATOLINALIKOPEKI DELL PERRIKKSSASSIKIGSAPPT TAANTSIMGIKMTUVALSSTSGTATALIVEATSSASTHRITKOR UN'AWROPPSPSJLAVPPOPGAHALIAAOTPOATSSASTHRITKOR PROME HEGGIFPPAGSTKGPPVBIJSPARATMSSKHHAVPRHENOMSS GSOVMSAGSLISSPTTTTSSASTPUTOSTNOSTSPSVEROLP VTVVIKTSNATTTTVITASNANTAPPNATYPPATKEHPYNSS SSSPPADPGOUSTSPSJLOCSSASTHNASSPELGAGSPVVET TUTTPDPMSSSSGSSAHINAOPPOSVOGENSPPLOCOPPTHIST PATRPPHOTTAPHNASSVQNSVAVISANTICPHOCTOPPTHIST PATRPPHOTTAPHNASSVQNSVAVISANTICPHOSTSSAP FREPLQRPAGSSTSIVANDSSTSILLTPCSSASNASSISSOVS GVARASSALSSTSSANSVASSROSTSILLTPCSSASNASSISSOVS GVARASSALSSVSTESMILGKSSSILTPNSDLIKGDISKAP FREPLQRPAGSSTSIVANDSTVESSTLOMORDSSAGSVS GVARASSALSSVSTOMORDSTGSVTPSSTHIGHFASNISSGM VGGGAPLGGAPAAANNRAKPTVALSTVERGTISKASKOV GVARASSALSSVSTOMORDSTGSVTPSSTHIGHFASNISSGM VGGGAPLGGAPAAANNRAKPTVALSTVERGTISKASTLOMORDSMASILT SPASSVSTANDANNRAKPTVALSTVERGTISKSSCLOROMORDSMASILTPCSSASNASVS GVARASSALSSVSTGSMASSASTLOMORDSTGSAGVSS GVARASSALSSVSTGSMASSASTLOMORDSTGSAGSVSS GVARASSALSSVSTGSAGSTTSSMASGRAVAVOTASSPA VIGNISTATIONASSTENNOQUTWTGTWARAPHNASVIMNOLG 5945 1461 197 GVHLPLFFGRKRENGALSEALGAGDSFTPGHVRAGYMEDFS WILTLILIPPGITSSVLEKAMSPILLTTFTAATDSDLUKKOOG OPOPERESTLICAGAARAPTVEALLGOSSSAPDSGRACTPARRE KRKRETIMKAPAABAVASGAGGHOQGSILEADEMTHTILIRAA GEGLIPPERTRESTENSTQVENOTHOROSHRITSTALLISLSGOP OPNILIFIGVESSAFDSGRACTPARRE KRKRETIMKAPAABAVASGAGGHOQGSILEADEMTHTILIRAA GEGLIPPERTRESTENSTQVENOTHOROSHRITSTALLISLSGOP OPNILIFIGVESSAFDSGRACTPARRE KRKRETIMKAPAABAVASGAGGHOQGSILEADEMTHTILIRAA GEGLIPPERTRESTENSTQVENOTHOROSHRITSTALLISLSGOP OPNILIFIGVESSAFDSGRACTPARRE KRKRETIMKAPAABAVASGAGGHOQGSILEADEMTHTILIRAA GEGLIPPERTRESTENSTQVENOTHOROSHRITSTALLISLSGOP OPNILIFIGVESSAFDSGRACTPARRE KRKRETIMVADAABAVASGAGGHOQGSILEADEMTHTILISLSGOP OPNILIFIGVESSAFDSGRACTPARRE KRKRERIMAPAARAVASGAGGHOQGSILEADEMTHTILISLSGOP OPNILIFIGVESSAFDSGRACTPARRE KRKRETIMVADAABAVATANASPETALLISLSGOP OPNILIFIGVESSAFDSGRACTPARRE KRKRETHVADAABAVATANASPETALLISLSGOP OPNILIFIGVESSAFDSGRACTPAR	1			
GPSPLSSPNCKLTVASPYKROCKREKOKEVRESKYKENSTYTE SRVIGRGGCNINAIREETGAHLDIKKOKKYNENSITITIGGTES TROATOLINALIKDEPKRIDELIPKRELKSSANSKIGSSPTT TRAATSLMGIKMTTVALGSTOATTALTVENSKASTSTHETIKUR WINNYEDFFYSPYLAYPPOFAHALLAAOTPOOLEPPRIJMT HEGGTPPAGATGGPFYKPELEBARATINSPKYRBENDKYS GSOUNSAGSLTSSPTTTTSSSASTYPOTSTNGSPSSPSVROLP VTVVKTSNATTTVTTTASNATTATTMFTRAKHYPYSSP SSPSPPAQPGOVSRNSPLOCGSASPHVATASSROGSPFVAS SSPSPPAQPGOVSRNSPLOCGSASPHVATASSROGSPFVAS SSPSPPAQPGOVSRNSPLOCGSASPHVATASSROGSPFVAS SSPSPPAQPGOVSRNSPLOCGSASPHVATASSROGSPVAPE EVRMITYPLATASSAVAVPSTATTVTFMCTPMCCQPTPFMST THTRE PHOSTAGHAVAVASTATTVTFMCTPMCCQPTPFMST PALTREPHOSTAGHAVAVASTATVTFMCTPMCCQPTPFMST PALTREPHOSTAGHAVAVASTATVTFMCTPMCCQPTPFMST PALTREPHOSTAGHAVAVASTATVTFMCTPMCCQPTPFMST PALTREPHOSTAGHAVAVASTAVAVASTAVAVASTAVAVA LAPSTAGNOGSVVSLOKAVASVAVATAVAVA LAPSTAGNOGSVVSLOKAVASVAVATAVAVA GSGAPLGGAPAANTFRACHTSPLSLLTTCSSASNDSSAGGVSS GVARASPARPSVYLGSKERSVYSOCDKVVPVSICHERASKISGGM YGGGAPLGGAPAANTFRACHTSPLSLTTCSSASNDSSAGGVSS GVARASPARPSVYLGSKERSVYLGSKERSVYDOKAVAVATAVATAVATAVA GGGAPLGGAPAANTFRACHTSPLSLTTCSSASNDSSAGGVSS GVARASPARPSVYLGSKERSVYLGSKERSVYDOKAVAVATAVATAVATAVA HERMSDGVVSSGSTBESGLGWSSVSDAVAVATAVATAVATAVA HERMSDGVVSSGSTBESGLGWSSVSDAVATAVATAVATAVA GGGAPLGGAPAANTFRACHTSPLSLTTCSSASNDSSAGGVSS GVARASPARPSVYLGSKERSVYLGSKERSVAGAMSPELLTTCSSASNDSSAGGVSSVS GVARASPARPSVLGSKERSVAGASTAVATAVATAVATAVATAVATAVATAVATAVATAVATA	Ì			
SRVIGRGCNINAIREFTGAHIDIDKORKDKTOBRITITRGDTS TROATCLINAIR DEPKER LIESSRIGSSAPTT TAANTSIMGIKHTTVALSSTSCTATALTVPAISSASTHET KIND WINVENDEFFEVSPPLLAYPPPOPARHALLAGOTPOLTEPBLPMT TAANTSIMGIKHTTVALSSTSCTATALTVPAISSASTHET KIND WINVENDEFFEVSPPLLAYPPPOPARHALLAGOTPOLTEPBLPMT HEGGTPPAQSTWGPPPVRPLSPARATINSPKPHWVPRHSMONS GSQUNSAGSIJSSPTYTTSSSASTVPGTSTMGSESSPSPKROUP VITVATISMATITVTITTASNATPTARTYPPTAKEHYPVSSP SSPSPPAQPGGVSRNSPLOCSSASPHKVASSSEQRAGSPFVVST TINTPPMSSSSSSSSASHANGOCPOPGUSVOGEPPTACGGPOPTPMST PATRPPHOTTAPHNSASVOROPPOVASSEQRAGSPFVVST TANTPPHOSTSSSSSSSASHANGOCPOPGUSVOGEPPTAGCTPOPTMST PATRPPHOTTAPHNSASVORSVALSVHIKRPHSVPSSVO LPSTLSTOSACONSVHBANKPIANTSPALPPGFSTLFENST SAHAPWGGSVVSSOSTPESMLSGRSSVLINSDPHGSDTSKAPG FRPFLQRRAPSPSGIVMDSPYGSVTPSSTHLGNFASNISGGM VGRAPLSGAPAANFRORIPSFSLILTCTSSANSSAGVSS GVARSPAPSSVLISSEKPSNVSQDRKVPVPIGTERSARIROTG TSAPSVLGSNLSTSVGRSGIVSPEDISLITCTSSANDFORMAN HAPMSDDGVPSQHAMBEDTGIVTPSGTFRCHVPAGYMDPK VGGMPSSVGNAMIPPVALPIPGGGPIFTLUSGAPHACY GVARSPAPSSVLISSLSTSVGLSGURSPEDISLITCTSSANDFORMAN HAPMSDDGVPSQHAMATEPVALPIPGGGGPIFTLUSGAPHACY VGGMPSSVGNAMIPPVALPIPGGGGPIFTLUSGAPVATTGSFRA WLTCLILIPLEGTIFSVLPFAMSRALITGGGSSAPSGRGSTEBARR KRKKRIMANAPARAVACESSGRANGGGNSLBAEDENNSLIK MVSSSTERMOPCTVMTOPHAPHMSVHMOLG QPOPKSPSTLIGGARAFYEALLIGGESSAPSGRGSTSPARR KRKKRIMANAPARAVACESSGRANGGGNSLBAEDENNTHTLIRAA QEGDLPBLURFLEDGTIFSVLPFAMSRALITGGGSAPSGRANGTFORMAR KRKRIMANAPARAVACESSGRANGGGNSLBAEDKATHTLIRAA QEGDLPBLURFLEDHRAGGAGGNINARDAFWYPIMCAARAGG AAVSVLLIGGAAMAVVCCEISGRAGGGSGSABEDKATHTLIRAA QEGDLPBLURFLEDHRAGGAGGNINARDAFWYPIMCAARAGG AAVSVLLIGGAAMAVVCCEISGRAGGGSGSARANIPTV LKRDGEGIGYBSAPGVKINGDPONHATATUAGRENTTIAGA KILADASISGRAFTPSPLIQUENCOTTIFQOSNHATSTAALLISISGGP QPPNLPLSVFI SSEPCKLLIGGGREGMALGFORANIPTIV LKRDGEGIGYBSAPGVKINGDPONHATALUSGAPFTTASQ KILADASISGLAPFTTANGA YSKGGKKVMLTVEGAADAHNYAVGCEICHDVANNAPALUSGAPFTTASQ KILADASISGLAPFTTANGA KYRGKARAGNOCHTERNICHTPWSSCECLEDDDIATATTERA KPQKSAPSPVKISDLATHLEDRCSGVVLIKAGGLEGOFGAPCLKCKEK CESFELHFWKKINFORMAPALGAMBCHUCTURVSKLIEKILLINISA DCIANTATVSSETTYGMVVADLEPKLAUNARSHRAVSININTYRM PPVONALAGGURAFTARAGAMANAC	1			
TRQATQLINALIKDPDKIDELIPKRNIKISSANSKIGSSPTT TAANTSIMGIKMTTVALSSTSCTATALITVPALSTKITKIKNP WNNWRPGFPVSPYLAYPPOPAHALLAAGTPOQLRPPRIPMT HEGGTPPAGSTGGPPVPRISAPARTNSPKUPSHSOMSS GSOWNSAGSLTSSPTTTTSSASTVPGTSTNGSPSSPSVROLP VTVVXTSMATTTVTTTSSASTVPGTSTNGSPSSPSVROLP SSPSPAQPGGVSRNSPLOCGSASPNIVASSSGGSPVVTS SSPSPAQPGGVSRNSPLOCGSASPNIVASSGGSPVVTS TNTRPPNSSSSGSSABLNOQOPPGSVSGERPPLQQSQVPPP EVEMTVPPLATSASPVAVBESTAVTYPMCTPMGCQPTPMET PATRPPHGTTAPHKNSASVONSSVAVLSVHIKRPHSVPSSVO LPSTLSTOSAGONSVHARKEPATVTSMOTPMGCQPTPMET PATRPPHGTTAPHKNSASVONSSVAVLSVHIKRPHSVPSSVO LPSTLSTOSAGONSVHARKEPATVTSMOTPMGCQPTPMET SAHAPMGGSVVSSGSTPESMLSGKSSVLPNSDPLHGSDTSKAPG FRPPLQRAPAPSGGVVSNSGVAVLSVHIKRPHSVPSSVO LPSTLSTOSAGONSVHARKEPATVTSMOTPMGCQPTPMET SAHAPMGGSVVSSGSTPESMLSGKSSVLPNSDPLHGSDTSKAPG FRPPLQRAPAPSGGVVSNSGVAVLSVHIKRPHSVPSSVO LPSTLSTOSAGONSVHARKEPATVTSMOTPMSCOPPSSVO GVGRAPALGGAPAANFRQHFSPLSLLTDCSSASNDSAGOVSG GVARAPAPSSPULGSRENSVGGONVEDVLENSRANISGGON VGGGAPLGGAPAANFRACHSPSLSLTTCSSASNDSAGOVSG GVARAPAPASVLLSKENGTMADLERSAGTENGOMVDMCNDENGMPM LIRPMSDDGVPSQAMARTSCHLTTCSSASNDSAGOVSG GVARAPAPASVLLGSMOTPMSVHANDGLG TSAPSVLGSNLSTSVGGSTGJAGGTFRQHAPADPSWNSLIK MVSSSTENNOPGTVWTOPRAPHMSVHNNOLG GVHILFIFERKLRROTABELERLIGGESSAPDSRGFTPARRF KRKKRIKKRIKAPAARAVAGGASGRIGGGRSLBAEDKHTIRLIRAA QGEDLPHIRRILERHAGGAGDGTINADDAFWHAANAGGA QGEDLPHIRRILERHAGGAGGGATHGGORSLBAEDKHTIRLIRAA QGEDLPHIRRILEPHBAGGAGGNINADDAFWHAANAGRAG QGEDLPHIRRILEPHBAGGAGGNINADDAFWHAANAGRAG QGEDLPHIRRILEPHBAGGAGGNINADDAFWHAANAGRAG QGEDLPHIRRILEPHBAGGAGGNINADDAFWHAANAGRAG QGEDLPHIRRILEPHBAGGAGGNINADDAFWHAANAGRAG QGEDLPHIRRILEPHBAGGAGGNINADDAFWHAANAGRAG QGEDLPHIRRILEPHBAGGAGGANINADDAFWHAANAGRAG QGEDLPHIRRILANGGAAPATVTHPANDTRAVAGGRATITSM RERRRES (NDRAWSRILLINGGGDPADTARARAGRAGAGGARAA)PVDLQCRACHAGAAPATVAGGRATITSM RERRRES (NDRAWSRILLINGGGDPADTARARAGRAGAGGAGGARAA)PVDLQCRAKGA YVSERGORQKKVMLTVEDAQDQHVALVLUNGGAANAYPLLGSIGLSGGAAPATTSAG KIALMAHSSILKSISSISPIYYTCACKGGLEHINGSITYKGCGG CALPTWKKIYYTGAMATALDGRAVATTCACKGGGLEHINGSPOTAPATCACKGGAAPATTCACCACCHACGA PROMATGGGGSTSTAAVGAMBGAGGAAPATTCACCCACCHACGA PROMATGGGGSTSTAAVGAMBGAGAARA	1			
TAANTSIMGIKMITVALSSITSQTATALITVPALSSASTHITIKEN WINNENGFEVES PLLAYPE POPAIALLAAGTOOLTEPELPHIT HEGGIT PPAGSTKGEPEVEPLEPARATNSPKEHHVERHSIONSS GSOWASASILISSPTITTSSSASTVPOTSTINOSSSSPSTROOLTS GSOWASASILISSPTITTSSSASTVPOTSTINOSSSPSPSTROOLF UTVUXTSNATTTTVTTTASNATATYMPTAKEHYPVSSP SSESPRADGGOVERNSPLOCGSASHKVASSSEQGSPPVPUF TNTRPPNSSSSSGSSAHSHOQQPPOSVSGSPRFPILQGSQVPPP EVMITVPPLATSSAPVAVESTAPVTYMPQTPMGCPQFTPMBT PAIRPPHSSTTGSACVANSSTVESTAPVTYMPQTPMGCPQFTPMBT PAIRPPHSSASVOSSVALSVHIKRPHSVPSSVO LPSTLSTQSACQNSVHPSKAPLTAPVTSAPLPFGFFSTLFENSTT SAHAPMGGSVVSSGSTEEMLSGGSSYLHDSDFHGSDTSKAPG FRPFLQRRAPSSPGIVMDSPYGSVTPSSTHLGNFASNISGGM YGGRAPLSGAPAANNTROHEPSFLLITTCSSASSASSS GVARASPAPSSVULSSEKPSNVSQDRKVPVPIGTERSARIRGTG TSAPSVIGSNLETSVGKSGIW PSEGLIGHQNOKNPGMNDHM HAPMSDFGVPSQHQAMERDSTGIVTPSGTFHGHVPAGYMDPFK VGGMPSSVGNAMIP EVPALIPBGAGGF INFORMSVMINGLG TSAPSVIGSNLETSVGKSGIW PSEGLIGHQNOKNPGMNDHM HAPMSDFGVPSQHQAMERDSTGIVTPSGTFHGHVPAGYMDPFK VGGMPSSVGNAMIP EVPALIPBGAGGT INFORMSVMINGLG GVHILFLEGKELRSVGKSGIM ERGLAGAFFFLLUSERAVATSSPRA MICCLILPLEGGII PSVLPIKAMSRPLLITFTPATDPSDLMKDCQQ QPQPEKPESTLIGHARAFYEALIGHDESSAPDSGRSTEPARRR KRKRRIMKAPAARAVAGGASGRIGGGRSLEADENFHIRLIRAA QBGDLPBLARLLEHBRAGGAGGININARDAFWYPILMCARAGGG AAVSVLLIGRGAAWVOCELSGRUGGGSSLEADENFTHRILISASGGP QPPNLPLSVFI SSOPEKLLIRGGAGGFBOHAGEPBARR KRKRRIMKAPAARAVAGCAGGREGGMSLEADENFTHRILISASGGP QPPNLPLSVFI SSOPEKLLIRGGGREGMALGPERARR KRKRRIMKAPAARAVAGCAGGREGMSLEADENFTHRILISASGGP QPPNLPLSVFI SSOPEKLLIRGGREGMGGSREADENFTTILSKGCP QPPNLPLSVFI SSOPEKLLIRGGREGMGGSREADENFTTILSKGCP QPPNLPLSVFI SSOPEKLLIRGGREGMGGSREARNIFTYV LKRDDGSIGVRSAWVOCELSGRUGGREGMALDFERARRO THE TOTAL THE TO		1		
WNINVERGEPUS PP. LAYP PP. CRAITLAGOTFOOL PREINDER HEGGT PP. DOS TRIGH PPUT PL. SPARTATIS PER PROVINCING GSOVMSAGSLTS SPITTISS SASTVECTSTING SPS SPEVROUP VTVUKTSNATTTVTTASNINTAPTMATYPPTAKENTYPEVSS SSPS PPAQPGGVSRNSPLDGSSASNIKVASSEQEAGS PPUVET TUTTE PRISSSS SSSSSAISNOOP PROSVSGEREP PLOGOVPPE EVENTVYP LATTSSAP VAVETSTAVTYPEN POTTOME COPTEMET PAIR PPHOTTAPHKINSAS VONS VALS VINHIKEPHS VESVO LEPSTLSTOSA CONSIVERATIVE I APPER SAL PUT PROPER PSTLFERS PT SARAPIGGS VVSSQSTPES MLSCKSS YLPNSDPLIQGSTEKAPG FRPPLORPAS PSG VINNIB SP VISSTYP STLIER PSTLFERS PT SARAPIGGS VVSSQSTPES MLSCKSS YLPNSDPLIQGSTEKAPG FRPPLORPAS PSG VINNIB SP VISSTYP STLIER PSR THONG YGGAP LIGADRA ANTENDER ST VIST PSD LIQGSTEKAPG FRPPLORPAS PSG VINNIB SP VISSTYP STLIER PSR ST VISST SARAPIGGS VVSSQSTPES MLSCKSS YLPNSDPLIQGSTEKAPG FRPPLORPAS PSG VINNIB SP VISST STR STEEL STR SOG YGGAP LIGADRA SP VISST SE VISST STR STR STR SARAPIGGS FREE PST LICE STR STR SOG YGGAP LIGADRA SP VISST SE VISST STR STR STR STR STR STR STR STR STR				
HEGGTPPAGSTKOPPFURLSPARATHSPKPHMUPHSNOMS GSOVMSAGSLTSSPTTTSSSASTVPGTSSPSSPSVROLP VTVVKTSNATTTVTTTASNINTAPTNATYPMPTAKEHYPVSSP SSPSPBAQPGGVSRNSPLDGGSASPNKVASSSEQBAGSPVVTS TNTRPPNSSSSSGSSANSVASSSQSPVTST TNTRPPNSSSSSGSSANSVQNSSVAVLVSDERPPFLQGSQVPPP EVEMTVYPLATSSASVAVPSTAPVTYPMPGTPMGCPPFMET PATRPPPHGTTAPHNNSASVONSVAVLVSHKENHEYPSSYO LPSTLSTQSACQNSVHPANKPLAPMFSAPLPFGPFSTLTERNST SAHAPMGGSVXSGSTPSENLGSKSXLNPDBLGGSTSKAPG FRPPLQRPASPSGSTVNNDSPVSSVTPSSTHLGNPASNLSGGQM YGRGAPLGGAPAAMFNROHFSSLLLTCHPASNLSGGQM YGRGAPLGGAPAAMFNROHFSSLLLTCHPASNLSGGGV YGRGAPLGGAPAAMFNROHFSSLLLTCHPAGNLGGGTF FREPLQRPASPSSSVDLGSEKPSNVSQDRKVPVPLGTERSARIRQTG TSAPSVLGSNLSTSVLHGS UNSPERIGGONDKVDRCHPSGMTPM INEPMSDPGVPSGHGAMERDSTGLTFSGTFTIGHTPAGYHDFPK VGGMPFGVYGNAMIPPVAP1PDGAGGTFFGHLPVAGYHDFPK VGGMPFGVYGNAMIPPVAP1PDGAGGTFFGHLPVAGYHDFPK VGGMPFGVYGNAMIPPVAP1PDGAGGTFFGHLPVAGYHDFPK VGGMPFGVYGNAMIPPVAP1PDGAGGTFFGHLPVAGYHDFPK VGGMPFGSVYGNAMIPPVAP1PDGAGGTFFGHLPVAGYHDFPK VGGMPFGSVYGNAMIPPVAP1PDGAGAGGTFFGHLDVGAGAGO QPQPREPSTLOGAAARAPCHALIGDESAPDSQSSGTEPARR KRKRIKHAPAABAVARGAGGHQCGREADPHTNILIRAA QEGDLPBLERLLEPHEAGGAGGINARCDAFFWILLAGA GETRSPENRSPFTSLQVCENCDTHPODSINERTSTAHLLSISGGP QPPNLPLGVPISSSPFFSLQVCENCDTHPODSINERTSTAHLLSISGGP QPPNLPLGVPISSSPFFSLQVCENCDTHPODSINERTSTAHLLSISGGP QPPNLPLGVPISSSPFFSLQVCENCDTHPODSINERTSTAHLLSISGGP QPPNLPLGVPISSSPFFSLQVCENCDTHPODSINERTSTAHLLSISGGP QPPNLPLGVPISSSPFFSLQVCENCTHPODSINERTSTAHLLSISGGP QPPNLPLGVPISSSPFFSLQVCENCTHPODSINERTSTAHLLSISGGP QPPNLPLGVPISSSPFFSLQVCENCTHPODSINERTSTAHLLSISGGP QPPNLPLGVPISSSPFFSLQVCENCTHPODSINERTSTAHLLSISGGP QPPNLPLGVPISSSPFFSLQVCENCTHPODSINERTSTAHLLSISGGP QPPNLPLGVPISSDPFKLLLRGGMBPGMGGRGGRANPIPTV LKRDQEGIGGTSAPOPRVTHFPAMTTANAVALRVVDP/TILTEAV YSYRQGKGKWMLTVPQAQDDHVALVLAGGFGAWY-YPQLQKKG YIMPFKYLFVQCNYTLENLELHTTPRSSCECLFDDDITATTKA KRYGSABSFYKISDLATHLEDKTSGVVLIKGGEGGFGAPCLKCKEK CEGFELHFWKLTYPRALMTADGRHDVCTRVESKLLELILLINISA DCLINZVVYSSERTIFGAVUDLFFKLLAGGGEGGFGAPCLKCKEK CEGFELHFWKLTYPRALMTADGRHDVCTRVESKLLEVILDNISG PEVONGALARGVYMLMFEKGVCYCCKCKMRG DPAYJABRAGTVKMHPACFVCSTCCKKRS DPAYJABRAGTVKMHPACFVCSTCCKRMS PEVONGA			1	
GSQUNSAGSLISSPITTISSSASTYPGTSTINGSPSSVIRROLF VTVUKTSNAINTTTYTTEMTAKEHYPVSS SSPSPPAQPGGVSRNPIDGGSASPNKVASSSEQEAGSPPVVET TNTTPPBNSSSSSSSASINNQQPPGSVSGEFRFPLGGGVPFNET TNTTPPBNSSSSSGSSAHISNQQPPGSVSGEFRFPLGGGVPFNET PATRPPPHGTTAPHKNSASVAVSUSVALSVMHIKRPHSVPSSVO LPSTLSTQSACQNSVHPANKIAPNSAVVUSVENHIKRPHSVPSSVO LPSTLSTQSACQNSVHPANKIAPNSAVUSVALSVMHIKRPHSVPSSVO LPSTLSTQSACQNSVHPANKIAPNSAVUSVALSVMHIKRPHSVPSSVO LPSTLSTQSACQNSVHPANKIAPNSAVUSVALSVMHIKRPHSVPSSVO LPSTLSTQSAGSVSSGSTPESMLSGKSSYLPNSDPLIGGSDTSKAPG FRPPLQRPASPSGIVMNBDFPGSTUTPSHGTFHGHVPAGVSDFSKAPG FRPPLQRPASPSGIVMNBDFPGSTUTPSHGTFHGHVPAGVSDFSKAPG FRPPLQRPASPSGIVMNBDFVSSUTPSKLIFPCSSASNDSAQSVSS GVRAPSPAPSSVPLGSEKPSNVSQDRKVFVPIGTERSATIRGTG TSAPSVIGSMLSTSVGHSGTWSFEGIGGNORKVFVPIGTERSATIRGTG TSAPSVIGSMLSTSVGHSGTWSFEGIGGNORKVFVPIGTERSATIRGTG TSAPSVIGSMLSTSVGHSGTWSFEGIGGNORKVFVPIGTERSATIRGTG TSAPSVIGSMLSTSVGHSGTWSFEGIGGNORKVFVPIGTERABRITGTG TSAPSVIGSMLSTSVGHSGTWSFEGIGGNORKVFVPIGTERABRITGTG TSAPSVIGSMLSTSVGHSGTWSFEGIGGNORKVFVPIGTERABRITGTG TSAPSVIGSMLSTSVGHSGTWSFEGIGGNORKVFVPIGTERABRITGTG TSAPSVIGSMLSTSVGHSGTWSFEGIGGNORKVFVPIGTERABRITGTG TSAPSVIGSMLSTSVGHSGTWSFEGIGGNORKVFVPIGTERABRITGTG TSAPSVIGSMLSGTWANTOPHADENSULTS VSGMPSFYGGNAMIPPOLITERADGSGMFTHADADSSANGLSK THE MVSSSTEMNGFOGTVTGWAPHANDAGA MVCLLIDELGGITSPRULFTTAPATDSDLWKNGGQ QPQPEKPESTLDGAARAFYEGIGGONINARDAFWTPILMCARAGOQ AAVSVLLICAGAAVQVCLELGGRDAQALABEAGFPEVARMVRSH GETTSPRNSSPTSLQVCENCDTHFDOSNIRTSTAHLLISLSQGP QPPNLPLLVSPISSPGFKLLIEGENDAAQGARGFGGRANDIPTV LKRDGGIGGYRSAPOPRVTHFPAMDTRAVAGRETPPRVATLSW REFRRESE\KDRAWENDLTTYMNLEF SGSSQRWSISDPVLISSPGFKLLIEGGNAPAGARGGGRANDIPTV LKRDGGIGGYRSAPOPRVTHFPAMDTRAVAGRETPPRVATLSW REFRRESE\KDRAWENDLTYMNLEF TSATATIVALSKGGTAPAGAARAV YSTROKQKKKVMILTVEQAQDYHAVLVINGGAANAYPOLLQRKKG YMSPKYLIFYQCNYTILENLELHTTPWSSCECLFDDDTRATTKAA KFOKASPSFYKKYLIFYQCNYTLENLELHTTPWSSCECLFDDDTRATTKAA KFOKASPSFYKKYLIFYQCNYTLENLELHTTPWSSCECLFDDDTRATTKAA KFOKASPSFYKKYLIFYGGTYNTAMLLSNAPSPCULKKKRFLYCG RETYDSKERFFGFGGRANDARL GGTPRRERGFFGGRANDARL GGTPRRERGFFGGFTGTWNTDLKAKMGIGHEGGFGAPCLKCKEK PPVONGALARGVFKAMBACFCVCSTCHKKRRS PPVONGA	l			
SSPEPAGOGGUSRNSPLOCASASNINVASSEGRAGSPPVYST TNTRPPNSSSSGSSAISNOQOPPGSVOQEPRPPLQQQVPPP EVRMTVPPLATSSAPVAVPSTAPVTYPMCTPMCCPQFTRMET PATRPPHGSTAPHANSAVQNSSVALVSWHEKRPHSVPSSVQ LPSTLSTQSACQNSVHPANKP LAPMYSAPLPGFPSTLFENSFT SAHAPMGSVVSSQSTPSSHLSKSSXLPHSDPLHQGSDTSKAPG FRPPLQRPAPSPSG LVNNDSPVGSVALVSWHEKRPHSVPSSVQ LPSTLSTQSACQNSVHPANKP LAPMYSAPLPGFPSTLFENSFT SAHAPMGSVVSSQSTPSSHLLSKSSXLPHSDPLHQGSDTSKAPG FRPPLQRPAPSPSG LVNNDSPVGSVTPSSTHLLSNPASNISGGGM YGRGAPLIGGAPAAMFNROHFSSLLLTPKSSPTULSNPASNISGGGM YGRGAPLIGGAPAAMFNROHFSSLLLTPKSPSTHLGNPASNISGGGM YGRGAPLIGGAPAAMFNROHFSSLLLTPKSPTHLONPAGNING LHAPMSDPGVVSQHQAMERDSTOLVTPSGTFHQHVPAGVMDFPK VGGMPFSVTQNAMI PVAPI PDGAGGTI FRGPHAADPSNNSLIK MVSSSTERNOPQTVNTGGRAMSPHNOVHNOLVMGNOPGMNM LHAPMSDPGVVSQHQAMERDSTOLVTPSGTFHQHVPAGVMDFPK VGGMPFSVTQNAMI PVAPI PDGAGGTI FRGPHAADRSVNSLIK MVSSSTERNOPQTVNTGGRAMSPLLLTFTADTPSDLMKDGQO QPQPKFFSTLOGAAARAPKVBALLGDESAPDOGRSCHPARGR KKKRIKHAAPABAAVASGSGGHQGGRS LAPMTDSDLMKDGQO QPQPKFFSTLOGAAARAPKVBALLGDESAPDSGRSCHPARGR KKKRIKHAAPABAAVASGSGGHQGGRS LAPMTDSDLMKNGQO QPGPKFFSTLOGAAARAPKVBALLGDESAPDSGRSCHPAGRS KKRRIMKAPABAAVASGSGGHQGGRS LAPMTDSDLMKNGQO QPGPKFFSTLOGAAARAPKVBALLGESAPDSGRSCHPAGRS RKKRRIMKAPABAAVASGSGGHQGGRS LEPMTDFLLRAA QEGDLJBELRSLLEPHBAGGAGGNI HARDAFWHTPLMCAARAGQG AAVSYLLCAGAAVGVCELSGRDAAQLAEBAGFPEVARMYRESH GETRSPENRSPTPSLQVCERCOTHFQDSNRTSTAHLLSLSGGP QPFNLPLGVP ISSBGFKLLLRGGMEPGMGGRGGGGRAPGTKSGR KKRRIMKAPABAAVAGSCHVLTOGAAGAGNAVGEVLTANGABAC GETRSPENRSPTYBLQVCEVVLODLLALVSPFK\HSYLRDLP SGSSPGRNSIDPVLELLEHTTPRNSCECLFDDD IRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKGGELETDERFITKGCF SCLPFTMKKIYTPRAHTTADGRHDVCIRVESKLEITLINISA CKLANAHSSLKSIFSSLPNIVTTGCAKGGELETDERFITKGCF SCLPFTMKKIYTPRAHMTATDGRHDVCIRVESKLEITLINISA DCLNRVIVSSETITGGWVDLFFHLLAVGGGELGGFGAPCLKCKEK CRGFELHFMKICRNC\NVAKKSM\TVLLANBEDKYGKKGLEGDPDAGG PROMNI TGGGDSTPAAAGAMBAL GFGFRFFRRGGGDELIFFBRYTVARGNARL GFFRFRRGGGDELIFFBRYTVARGNARLFFTCSCCCKKKCERPMAGGGFGAPCLKCKER GFFYCDSGCKKCLGGGFGAPCLKCKERSALCGGRCHATDERVCYNCYCYCKKNNEG DAIYABRAGCFLGSCSKKLLGGGKPMVFCSVCKKRNS SP48 39 3370 VRERYFYGGGSVLRSALEVCNDFLSGLTEGSLLUDMIYFFTEN				
SSPSPBAQPGGVSRNSPLDCGSASPNKVASSSEQEAGSPSVVPP TTNTRPDRSSSGSGSSABNNQQDPGSDERPPLQGSQVPPP EVRMTVPPLATSAPVAVPSTAPVTYPMCTPMCCPQFTPKMET PAIRPPHHOTTAPHRNSASVONSSVAVLSVNNIKRPHSVPSSVO LPSTLSTJGSACQNSVLPHANKPLAPMSPTSPTLPFGPFSTLFENSPT SAHAPMGGSVVSSQSTPESMLSGKSSTLPNSDPLHQSDTSKAPG FRPPLQFPASPSGIVNMBPYPGSVTSTHLGSPASNISGQOM YGFQAPLGGAPAAANTNRQHFSPLSLLTPCSSASNDSAGSVSS GVZASPSAPASSVLJGSERSNNSQDRAYDTGTERSARIRQTG TSAPSVIGSNLSTSVGHSGIWSPGIGGNQNKVDWCRPGMGPM IHRPMSDPGVPSQHQAMERDSTGIVTPSGTFPQHVPAGYMDFPK VGGMPESVYGNANIPPVAPIPDGAGGPINGPHAADPSNNSLIK MVSSSTENNGPQTVWTGPAPHNNSVHNNQLG 5945 1461 197 GVTHLFJEFGKKEKRNGLAEDLKGQADFINGADAPSNNSLIK MVSSSTENNGPQTVWTGPAPHNNSVHNNQLG GVTHSPEKRKEKRNGLAEDLKGGADFILDSGADFINGADAPSNNSLIK MVSSSTENNGPQTVWTGPAPHNNSVHNNQLG GVTHLFJEFGKKEKRNGLAEDLKGGADFILDSKAVVATSSPRA WLTCLILPLPGITPSVLPKAMSRPLLITFTPATDPSDLMKDGQQ QPPOPESTLOGAARAPVEALIGDESSAPDSQRSQTEPARER KRKKRRIMKAPAABAVARGASGRHGGGRSLEAEDNWTHRILERA QEGDLFBLRILLEPHBAGGAGGNINARDAFWHTILERAA QEGDLFBLRILLEPHBAGGAGGNINARDAFWHTILERAA QEGDLFBLRILLEPHBAGGAGGNINARDAFWHTILERAA QEGDLFBLRILLEPHBAGGAGGNINARDAFWHTILERAA QEGDLFBLRILLEPHBAGGAGGNINARDAFWHTILLERAA QEGDLFBLRILLEPHBAGGAGGNINARDAFWHTILLERAA QEGDLFBLRILLEPHBAGGAGGNINARDAFWHTILLERAA QEGDLFBLRILLEPHBAGGAGGNINARDAFWHTILLERAA QEGDLFBLRILLEPHBAGGAGGNINARDAFWHTILLERAA QEGDLFBLRILLEPHBAGGAGGNINARDAFWHTILLERAA QEGDLFBLRILLEPHBAGGAGGNINARDAFWHTILLERAA QEGDLFBLRILLEPHBAGGAGGNINARDAFWHTILLERAA QEGDLFBLRILLEPHBAGGAGGNINARDAFWENSH TITLSAKA SESSPQRWNSIDPV\ELLEHLTTPMSSCECLFDDDTRAITKAA VSTRGQKGKKWMUTVEQAGDQCDHYALVHAVLEVUDF/TILITEAV VSTRGQKGKKWMUTVEQAGDQCDHYALVHAVLEVUDF/TILITEAV VSTRGQKGKKWMUTVEQAGDQCDHYALVHAVLEVUDF/TILITEAV VSTRGQKGKKWMUTVEQAGDQCDHYALVHAVLEVUDF/TILITEAV VSTRGQKGKKWMUTVEQAGDQCDHYALVHAVLENGINERTYKAGC SCLPFTMKKIYYPBALMTAIDGRHDVCIRVEKLIEKILLENISA DCLNRVIVPSSETTGMVVADLFBLLAVSABPCVLKIQSLFVL DENSYPLGDFSFVLSDLFYPDIVKHGABARI 5947 3 1317 RGTPPRRRRGPGFRVNMDLERHCKKYMSINSINTYTYPMA PPVQMOALAROYMOLPRKGGPGAPCLKCKEK CEGPELHFMKLICRNC\NVAKKSM/TVLLSNEBERKULCKGLE PPVMSHLASTERPCLGCCGSCKCLLGKCKPMYCNSUCKKMS PPVMGALROYMOLPRVCKPCVYKNIAVVC	1	,		_
TNTRPPNSSSSGSSAHSNQQOPGSVSGERPPLQGSQVPPP EVRMTVPPLATSSAPVAVPSTAPVTYPMPTPMCTPPMCTQPTPKMET PAIRPPBIGITAPHKNSASVONSSVALSVNNIKRPHSVPSSVQ LPSTLSTQSACQNSVIPANKP LAPNTSAPLPPGPPSTLFENSPT SAHAPMGSVVSSGSTPESMLSGKSS VINSPPLHQSDTSKAPG FRPPLQRPAPSPSGIVNMDSPYGSVTPSSTHLGNSPANISGQM YGGRAPLGAPAANATNRGHPSPLSLTPCSSANDSSAGSVSS GVRAPSPAPSSVPLGSEKPSNVSQDRKVPVPIGTERSARIRGTG TSAPSVIGSNLSTSVGHSGINSPEGIGKQDKVVMCPGMGMPPM HIRPMSDFOVPSQHQAMEDSTGIVTPSGTPHQHVPAGYMDPPK VGGMPSVYGNAMIPPVAPIPOGAGGIPTPGGTPHQVPAGYMDPPK VGGMPSVYGNAMIPPVAPIPOGAGGIPTPGGTPAADPSNMSLIK MYSSSTENNGGPVTWTGDAADFLKSGTLSTFSTPHQHVPAGYMDPPK VGGMPSVYGNAMIPPVAPIPOGAGGIPTPGGTPATDPSDLWKDQQ QPOPSKPSTLDGAARAFYEALIGOESSAPSGRSGTBAARER KRKKRRINKAPAARAVASCASGRHGQGRSLEAEDKMTHRILBAA QEGDLPBLRRLLBPHBAGGAGGNINAPHTSTAHLLSLSGGP QPPNLPLGVPISSPGFKLLLGRGAGGAGGNINAPHTSTAHLLSLSGGP QPPNLPLGVPISSPGFKLLLGRGWEPGMGLGPRGERAMPIPTV LKRDGEGLGYRSAPOPRVTHPPAMDTRAVAGREVTPBRVATLSM GETTSPENRESPTSLGJCYCENCDTHGPGAMTYSTAHLLSLSGGP QPPNLPLGVPISSPGFKLLLGHARDAVAGREVTPBRVATLSM GETTSPENRESPTSLGJCYCENCDTHGPGAMTYSTAHLLSLSGGP QPPNLPLGVPISSPGFKLLLGHARDAVAGREVTPBRVATLSM GETTSPENRESPTSLGVLARGWEPGMGLGPRGEGRAMPIPTV LKRDGEGLGYRSAPOPRVTHPPAMDTRAVAGREVTPBRVATLSM GETTSPENRESPTSLGVLARGWEPGMGLGPRGEGRAMPIPTV LKRDGEGLGYRSAPOPRVTHPPAMDTRAVAGREVTPBRVATLSM GETTSPENRESPTSLGVLARGWEPGMGLGPRGEGRAMPIPTV LKRDGEGLGYRSAPOPRVTHPPAMDTRAVAGREVTPBRVATLSM GETTSPENKLYTPAUNTSTAPUTTAVAGREVTPBRVATLSM FERRRESP \NORAMERDETTYMLLTAVAGREVTPBRVATLSM GETTSPENKLYTPAUNTSTAPUTTAVAGREVTPBRVATLSM YSTROGKGKKVMLTVEQAQDCHXALVLMGPGAAM\YPOLQRKKG YIWEPKYLFVQCNYTLENLELHTTPMSSCECLFDDRITYKGCF SCLIPFTMKKITYRPAMTATIOGRHDCTRVESKLIERILINISA DCLNRVIVPSSETTYGMVVADLFHSLLAVSARPCVLKIGSLFPL DENSYLQCOPSLLDFYDIVKHGAMARL SEGSPORVINISDVALLKLSSGETEMPKRVMILITHTVAAKKNVSINTYTYMA PFVONQALARGYMCHPEKGPVKYKYSEGAGVYKKNOSINTYTYMA PFVONQALARGYMCHPEKGPVKKYKSEGAGVYKKNOSINTYTYMA PFVONQALARGYMCHPEKGPVKYKYSEGAGVORKLDAKLPGCDOSI LAGBIYMWNDKPCKPCTYKNINAVCQGCINATDEVORVTYM NSHHASTECFLCSCCSKCKLIGKCHPMHVLKHCCCPOLSI LAGBIYMWNDKPCKPCTYKNINAVCGGCINATDEVORVTYM NSHHASTECFLCSCCSKCKLIGKCHPMTCSVECKKKMS PRETTYDSERFRCFLGC	[
EVENTYPELATISAPVAVBSTAPUTYPMPOTEMGCPQFTEMET PARRPPHOTTAPHENSAPVONSVAVLVNIKERPHSVPSSVQ LPSTLSTQSACQNSVIPANKEIAPNTSAPLFFGFFSTLFENSFT SAHAFMGGSVVSSQSTPESMLSGKSSTLENSDPLHQSDTSKAPG FREPLQFRAPSPSSIVINMDSPVGSVTPSSTHLGNFANISGQGM YGFGAPLGGAPAAANSNRQHFSPLSLLTPCSSASNDSSAQSVSS GVARSPAPASSVILGSKESNSVQGNEVPJEGTERSAFIRGTG TSAPSVIGSNLSTSVCHSGINSPECIGGNQDKVDWCNPCHGMSPM LHEPMSDPOVFSQHQAMERDSTGIVTPSGTPHQHVPAGYMDPPK VGGMPPSVYGNANIPPVAPIPDAGPTIPGNTPHQHVPAGYMDPPK VGGMPPSVYGNANIPPVAPIPDAGPTIPGNTPHQHVPAGYMDPPK VGGMPPSVYGNANIPPVAPIPDAGPTFLLVSBRVVATGSPPA MLTCLILPLGGITFSVLPKANSPPLLITFTPATDPSDLMKDGQQ QPOPEKPESTLDGAARAFYERLIGGSAPSORGGGTPEPABER KRKKRIMKAPAABAVAGCASGRIGQGRSLEAEDHTHRILIRAA QEGDLPELRILEPHEAGGAGGNINARDAFWTPLMCAARAGG AAVSLLGRGAAWVGVCLSGRDAQLAEEAGFFEVARWARSH GETRSFENRSPTSSLQYCENCDTHFQDSHHTSTAHLSLSGGP QPPNLFLGVISSPGFKLLLEGWERGMLGFRGEGRAPIPTV LKRDQEGLGYRSAPQPRVTHPPADUTRAVAGREYTPPRVATLSW REERRRES KORAWRENLILEGWERGMGLGFRGEGRAPIP ITV LKRDQEGLGYRSAPQPRVTHPPADUTRAVAGREYTPPRVATLSW REERRES KORAWRENLITYMNLEF 5946 541 1666 1LGSYSSIQPESYSVVC\SVULQDLLA\VYSPK\SYLRDLF SEGSPQRVNSIDFVLE\LEHLQPDVLVHAVLRVDF/TILTEAV YSYRGQKGKWMLTVEQADDHYALIVANGGAAN\YPOLQRKG YWBFKYLFVQCNYTLENLELHTTPNSSCECLFDDIRAITFKA KRYGSAPSFVKISDLATHLENCSGGVULKAGISELGFFTIASQ KIALMAHSSLKSIFSSLNIVYTGCAKCGLELETDERRIYKGCF SCLPFTMKKIYYPPALMTALDGRHDCVLKKAGISELAFPITASQ KIALMAHSSLKSIFSSLNIVYTGCAKCGLELETDERRIYKGCF SCLPFTMKKIYYPPALMTALDGRHDCVLKKAGNISHNITYFWAA PPVQMQALARGYMOMLPREKGPVAKKYSEALGYDGVKKYGLAKGLFEDT TYTLIAKLKSDGIPMYKRNIMILTHYENSKLINISA DCLNRVIVPSSEITYGMVADLFHLAVSGEGAVYKKGLAKGLPCHDAG PRXMIKISGGGTSTPAAVGAMEDKSAEKKTYTYSKGCF CROFFLHFMKICRNC\NVAKKSN/TVLLSNEBDRKVGKLFEDT KYTTLIAKLKSDGIPMYRRNIMILTHYCGFENDLARGGE DPATYAERAGYDKLHHPACEVCSTCICELLVDNIYFKKNELLYCG RHYCDSEKPRCAGCDELIFFSNETYQARMYNISNINTYTYRM PPVQMQALARGYMOMLPREKCPVKKYKSEALGYDDVKLKFCCDISI LAGEIYWMXDKPVCKPCYVKNIAVVCOGCINAIDEVORVTYN NSWMLSTEETERCHRAGSAARHPSSPCSVKHSPTRETTLTVAQAQRM VRIBHESTEETECTSCSCSCKCLLGKKNPMYCSVECKKKNS				
PAIRPPPHGTTAPHKINSASVQNSSVAVILSVANITREPRISVPSSVQ LPSTLSTQSACQNSVHPANKPI APNFSAPLPPGPPSTLFENSPT SAHAPWGGSVVSQSTPESMLSGKSSYLPNSDPHHQSDTSKAPG FRPPLQRAPSPSGIVMNDSPYGSVTPSSTILIGFASNISGGQM YGGRAPSPAPSSVPLGSEKPSNVSQDRKVPVDITERSARIRGTG TSAPSVJGGNLSTSVGHSGIWSPEGLAPTCSSARINGSTG TSAPSVJGGNLSTSVGHGSIWSPEGLAPTCSSARINGTG TSAPSVJGGNLSTSVGHGSIWSPEGLAPTCHVPAGYMDPPK VGGMPFSVYGGNATPPVAPIPDAGGPITHOPPAGYMDPPK VGGMPFSVYGGMATPPVAPIPDAGGPITHOPPAGYMDPPK VGGMPFSVYGGMATPPVAPIPDAGGPITHOPPAGYMDPPK VGGMPFSVTGAMTPPVAPIPDAGGPITHOPPAGYMDPPK VGGMPFSVTGAMTPPVAPIPDAGGPITHOPPAGYMDPPK VGGMPFSVTGAMTPPVAPIPDAGGPITHOPPAGYMDPSWNSLIK MVSSSTENNGPQTWWTGPMAPHMNSVHNOLG 5945 1461 197 GVYHLFJFGKKRLENGTAEDLKGQADFFFLLVSBAVVATGSPRA WLTCLILPLPGITIFSVLPKMMSSPLTTTFTATDPSDLMKDGQQ OPOPEKPESTLDGAARAPKVLLIGDESSAPDSQRSQTEPARER KRKKRRINKAPAABAVAGSAGGHGQRSLEAEDNHTHILIRAA QEGDLPBLRRLLEPHBAGGAGGNINARDAFWMFILACARAAQG AAVSYLLGRGAAWGVCELSGRDAAQLAEEAGFPEVARWYRESH GETTSPENNSTPTSLQTQCNCTOTHOPMTPTATACARAAQG AAVSYLLGRGAAWGVCELSGRDAAQLAEEAGFPEVARWYRESH GETGSPENNSTPTSLQTQCNCTOTHOPMTPTATACARAAGGA AAVSYLLGRGAAWGVCELSGRDAAQLAEEAGFPEVARWYRESH GETGSPENSTPTSLQTQCNCTOTHAPAWTPTACARAAGAA VSYLLGRGAAWGVCELSGRDAAQLAEEAGFPEVARWYRESH GETGSPENSSTPSLQTCSCNCTONTHTSTAHLLSLSGGP OPPHLLAVPLSSPGKLLLLAGGWEGMGLGPRGGGAPPITTV LKEDQEGLGYRAAPQDFVTHFPAWDTRAVGRECTPPVATLSW REERREB\KDRAWERDLETYMALEF SEGSPQRVNSIDEV\EI\EHLTDWSLGFCFTPPVATLSW YSYRQGKGKKWMLTVEQAQDGHAVLTWLRVURP/TILTEAV YSYRGCKGKKWMLTVEQAQDGHAVLTWLRVURP/TILTEAV YSYRGCKGKKWMLTVEQAQDGHAVLTWLRVURP/TILTEAV YSYRGCKGKKWMLTVEGAQDGHAVLTWLRVURP/TILTEAV YSYRGCKGKKWMLTVEGAQDGHAVLTWLRVURP/TILTEAV YSYRGCKGKKWMLTVEGAQDGHAVLTWLRVURP/TILTEAV YSYRGCKGKKWMLTVEGAQDGHAVLTWLRVURP/TILTEAV YSYRGCKGKKWMLTVUTGACAGGELETDENRTYKCCF SCLPFTWKKLTYPGAWTAMATLOCHAVLTRVLURPCHAALVLLONG KTALLAAHSSLKSIFSSLPNIVYTGCAKGGELETDENRTYKCCF SCLPFTWKKLTYTTAMATLOCHAVCHAVLGARGLGCDHALTVTYTW FPVENGTAMATLOCHAVCHAVLTAGARGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1			
LPSTLSTQSACONSVHBANKP IAPNFSAPLPFGFSTLFENSPT SARAPMGGSVYSSGFSENLSGSKYLPHSDPJHQSDTSKAPG FRPPLQRPAPSPSGIVNMDSPYGSVTPSSTHLGNPASNISGQM YGGGAPLGGAPAAANFRRQHFSPLSLLTTCSSANDSSAGSVSS GVARDSPAPSSVPIGSEKENNVSQDRKVPVPIGTERSARIRGTG TSAPSVIGSNLSTSVGHGGIWSFEGIGONOKVDWCNPGMGMPM IHRPMSDPOVPSGIQOAMERDSTGIVFGFTHQHVPAGYMDFPK VGGMPFSVYGNAMIPPVAPIPDGAGGPIFNOPHAADPSWNSLIK MVSSSTENNGPGTWTGPMPPHANDVHNNQLG S945 1461 197 GVYHLFJFGKKKLENGIGADLKGQADFFFLL GVYHLFJFGKKKLENGIGADFFFLLWSEAVVATGSPRA WLICLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDQQQ QPQPEKPSTLDGAARAFYEALIGDESSAPDSGRSOTEPARER KKKKRINKAPAARAVAEGASGRHQGGKSLEAEDKYTHFILRAA QEGDLPELRELLEPHERGGAGGNINARDAFWHTPLMCAARAGQG AAVSVLLGGRAAWVGCELSGRDAAQLAEEAGFPEVARAVKESH GETRSPENRSFTPSLQYCCRVCHOFHQDSNRRTSTARLLSLSGGP QPPNLPLGGGAGVCELSGRDAAQLAEEAGFPEVARAVKESH GETRSPENRSFTPSLQYCCRVCHQDLAYVSFK\HSYLRDLP SEGSPQRVNSIDPVSELLLEGWBEPGMGGPRGEGRANPIFTV LKRDGEGIGYRSAPQPRVTHFPAMDTRAVAGRE\TPPRVATLSW REERRERS\KORAWERDLETYMNLEF 11GSVSSTQPEEVS\SVVC\EVVLQUDLLA\YVSFK\HSYLRDLP SEGSPQRVNSIDPV\SL\FHLQPDVLVHAVLRVUDP\TILTEAV YSYRGQKQKVMLTVEQAQDQHYALVLWARGRAAV\YPQLQRKKG YWBEYKYLFYQCAYTLENLEHTTTWSSCECLEPDDIRAITTKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KKLIANAHSSLKSIFSSLFMIVYTGGKGLELETDERRIYKQCF SCLPFTMKLIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSABPCVLKKIQSLFVL SCLPFTMKLIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSABPCVLKKIQSLFVL SCLPFTMKLIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSABPCVLKKIQSLFVL KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTEWA FPVQNGALARQYMCMLPEKGPVLKYKSMCLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTEWA FPVQNGALARQYMCMLPEKGPVLKYKSMCLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTEWA FPVQNGALARQYMCMLPEKGPVLKYKSMCLYGFDMDQG PKQMIPGGBRSTPAAVGAMBUKSABHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLMIPACFVCSTCHELLVDMIYFMKNEKLYCG RYCDSEKPRAGGCESKLIGGNFROACHHECCFDCDSI LAGETYWAVNDKPVCKPCYVKNHAVVCQGCHNAIDEPCQRVTYN NSHMASTECFLCSCCSCKLIGGNFROACHHECCFDCDSI LAGETYWAVNDKPVCKPCYVKNHAVVCQGCHNAIDPECQRVTYN NSHMASTECFLCSCCSCKLIGGNFROACHHECCFDCDSI LAGETYMVANDKPVCKPCYVKNHAV	1	1.		
SAHAF#GGSVVSQSTEEMLGKSSYLPNSDLHQSDTSKAPG FRPPLQRAPSPSGLUMMDS PYGSVSTHLGMFASNIGGGM YGPGAPLGGAPAAANFNRQHFSPLSLLTPCSSASNIGSAGGVSS GVRAPSPAPSSVPLGSEKPSNVSQDRKVPUPIGTERSARIRGTG TSAPSVVIGNISTSVVGIGUMSPEGLGKONQKVDWCMPGMGMPM IHRPMSDPGVPSQHQAMERDSTGIVTPSGTFHOHVPAGYMDPFK VGMMPSSYGRMAN PVADIP IPOGAGATYPHONYBADPSWNSLIK MVSSSTENNGPQTVWTQPWAPHMNSVHNNQLG 5945 1461 197 GVTHLFLFGTRKRENGTAEDLKGQADFFFLLVSRAVVATGSPRA WLTCLILPLEGIISVLPKAMSSPLTTFPSATTPSDLWKDQQQ QPQPERPSTLUGAAARAFYEALIGDESSAPDSGRSGTSPARER KRKKRIMKAPAARAVAGAGGGHGGSLEADENWHILIRAA QEGDLPBLRILLEHBAGGAGGNINARDAFWFPIMCAARAGQ AAVSTLLGRGAAWGYCCELSGRDAAQLAEBAGFBVARHTILRAA QEGDLPBLRILLEHBAGGAGGNINARDAFWFPIMCAARAGQ AAVSTLLGRGAAWGYCCELSGRDAAQLAEBAGFBVARHTILBASGP QPPNLPLGVPISSFGFKLLLEGGBRPAGGGFRGGRANFIFTV LKRDQGGGGYRSAPGRVTHFFAWTAVGARE\TPPRVATLSW REERRBE\KNAWARABARDLETYMNLEF 15946 541 1666 ILGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP SKSSPQRVNSIDPV\EL\BHLQFDVLHAVLRVUPF/TLLTAV YSYRQQKGKKWMLTVEQAQDGHYALVLMGGAAM\YPQLQRKKG YHBFRXYLFYQQYSTLEBNLEHLTTBASGCELFDDDIRITTKA KFOKSABSFFVKISDLATHLEDKCSGVVLIKAGISELAFFITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSETTYGMVADLFHSLLAVSAEPCVLKIQSLFVL DRNSYPLQOPSSLIDPTPDIVKHANDARL 5947 3 1317 RGIPDRRRGGIVGNVMDLPBKGVQAGSEGAQYRKKQLAKGED DRNSYLDQOPSSLGHENGPVKKYKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKM/TVLLSNBCRKVGKLEDT KYTTLIAKLKSDGIPMYKNWNLINIVPVAAKKNVSINTVTYEWA FPVQNQALARQYMMMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSSCHELSPREVKREGCTVKKYKSMGTGHEGGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNBCRKVCKCEMSG DRAIYAERAGYDKLMHPACFVCSTCHELLUDMIYFWKSEKLIVGG RKQMMIDGGDRSTPAAVGAMBDKSAEHKRTQYGCYCCKLISMKEG DPAIYAERAGYDKLMHPACFVCSTCHELLUDMIYFWKSEKLIVGG RKYGMSTEGCFCCSCKLIGGKREGCYVAKYDARDANDHHLKHCCCPDCDSI LAGEIYWAWNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NSWMASTETEFCLGSCSCKLIGGAPGARQMOWHHLKHFCCPDCDSI LAGEIYWAWNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NSWMASTETEFCPLGSCSCKLIGGAPGARGANGHDEVGCKKMS 5948 39 3370 YRERYPVSGGSVURSALEVONDFLSGITEGSLIPEGFFFGDPIDO GNYQMRRKGRCHRGSAARHPSSPSCVKKHNSERP				
FRPPLQRPAPSISGIVNNDSPYGSVTPSSTHLGNPASNISGQOM YGPGAPLGGAPPAAMFNRQHFSLITPCGSASNDSAQSVSS GVRAPSPAPSSVPLGSEKPSNVSQDRKVPVPIGTERSARIRQTG TSAPSVIGSNLSTSVGHAGIGINESTSGIGNOKVDMCNPGMGNPM IHRPMSDPGVPSQHQAMERDSTGIVTSGOTHQHVPAGYMDPPK VGGMPFSVYGNAMIPPVAPIPDGAGGPIFMGPHAADPSWNSLIK MVSSSTENNGPQTVWTGPWAPHMSVHNQLG 5945 1461 197 GVTHHFLFGKRKLRNGIAEDLKGGADFFFILUVSRAVVATGSPRA WLTCLILPLPGIIFSVLPKAMSRPLLITTPATDPSDLWKDGQQ QPOPERPSTLDGAARARFVEALIGDES SAPDSGRSGTEPARER KRKKRIMKAPAARAVARGAGGRIGQGRSLEAEDLWHTHILRAA QEGDLPPLBRLLEPHEAGGAGGNINARDAFWYPILMCAARAGQG AAVSYLLGRGAAWVGVCELGGRDAAQLAEEAGFPVARMVRSH GETTSPENNSPTPSLQYCENCDTHFQDSNHRTSTAHLLSLSGGP OPPNLPLGVPTISSPGYKLLLRGGKPERMGLGPRGGRANPIPTV LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW REERRRBE\KDRAWERDLRTYMMLEF 5946 541 1666 11GSVSSJQPENSSJOVC\GDLLA\YVSPK\HSYLRDLP SEGSPQRVNSIDFV\EL\EHLQPDVLMHAVLRVVDP/TILTEAV YSVRGGKKKWHLTVEQAQDQHYALLWGFGAAW\YPQLQRKKG YIWEPKYLFVQCNYTLENLELHTPWSSCECLFDDDIRAITFKA KRQKSAPSFVKISDLATHLEDKCSGVVLIKAGISELAFPITASQ KIALMAHSSLKSIFSSLPNIVTYGCKKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLMISA DCLNRVIVPSSEITYGMVVADLPHSLLAVSAEPCVLKIQSIFVL DENSYPLQOPSLLDFYPDIVKGAMARL 5947 3 1317 RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEGGFGAPCLKCKEK KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKERQPVAGSEGGAPKKQLAKQIPAHD OPPSKCHLSPREVKENGPVKKYKSEALGVODVKULPCEMDAQG PKQMMIPGGDRSTPAAVGAMEDKSAHKRTYSCCCCLISKEG OPAIVAREAGVGKLMHPACFVCSTCHELLVDMLYFWKNELYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYWWNDKPVCKPCYVKNHAVVCOGCHNAIDPSVORVTYN NSWHASTEFCIECCSCKLILGKKEPGVRAVTSRUKLDGGRTYN NSWHASTEFCIECCSCKLILGKYMPVEGWPCSVECKKKMS YERYPVSGGSVLRSALEVCNHPSISGLEPEGFSGFDDO GNHYQMRRKGRCHRGSAARHPSSPCCKHSPTRTLTTYAQARQRM VEIETEGRLHHISTFPDLEILEDDLTAQEMSECNSKNENSERF	ļ			
YGRGALGGAPAANFINGHPSPLSLLTPCSSASNDSSAGSVSS GVRAPSPAPSSVPLGSEKPSNVSQRKVPVPIGTERSARIRQTG TSAPSVIGSNLSTSVGHGJUSFSGIGNQDKVDVCNCHOMGNPM IHRPMSDPGVPSQHQAMERDSTGIVTPSGGTFHQHVVPAGYMDFPK VGMMPFSVYGNMIP PVAP IP DGAGGE I PMGPHAADPSWNSLIK MVSSSTENNGPQTVWTGPWAPHMNSVHMNQLG 5945 1461 197 GVTHHFLFFGKRLENGGADFFFHLUSEAVVATGSPRA WLTCLILPLPGII FSVLPKAMSRPLLTFTPATDPSDLWKCGQQ OPOPEKPESTLOGAARAFVEALIGGESSAPDSGRSQTEPARER KRKKRRIMKAPAABAVAEGASGRHUGGSLLAEDLKWTHRILRAA QEGDLPBLRRLLEPHEAGGAGGNINARDAFWWPLMCAARAQQG AAVSYLLGRGAAWVGVCGLGGRDDAQLAEBAGFPEVARAWVESSH GETRSPENRSPPTSLQVCENCOUTHFODSHRTSTARLLSLSGGP OPPNLPLGVPISSPGFKLLLRGGWEPGMGLGPRGEGRANPIPTV LKRDQEGIGATSAPOPRVTHFPAWDTRAVAGRE\TPPEVATLSW REERRRES\KDRAMERDLRTYMLLEF 5946 541 1666 ILGSYSSIOPEYSISVVC\BVVLQDLLA\VSPR\HSYLRDLP SEGSPQRVNSIDFV\EL\LPLQPDVLVHAVLRVUFYTILTEAV YSYRGQKQKKWLTVEQAQDQHYALVHAVLRVUFYTILTEAV YSYRGQKQKKWLTVEQAQDHYALVHAVLRVUFYTILTEAV YSYRGQKGKKWLTVEQAQDHYALVHAVLRVUFYTILTEAV YSYRGGKGKKWLTVEQAQDHYALVHAVLRVUFYTILTEAV YSYRGYKGKKWLTYEQAQDHYALVHAVLRVUFYTILTEAV YSYRGYKGKKWLTYEQAQDHYALVLHAVLRUFSLEAPFITASQ KIALNAHSSLKSIPSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYRPALMTAIDGRHDVCIRVEKKLEKILLMISA DCINXVIVPSSEITYGMVVADLPHSLLAVSABFOLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRGPIGRVNMDLENKKKMGLGHEQGFGAPCLKCKEK CEGFFLHFWRRICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILITMPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPRZVKENGFVKKYKSEALGVUGVKLPCEMDAQG PKQMMIPGGDRSTFPANGAMEDKSABHKRTQSCCYCCKLSMKEG UPAKTABRAGDKLMHPACFVCTELLVDMIYTWKNBKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCPDCDSI LAGBIYVMVNDKPVCKFCVYKHHAVVCOGCINAIDPSVQRVTYN NSWHASTECFLCSCCSKCLIGGKMPVPEGMYFCSVECKKKMS NSWHASTECFLCSCCSKCLIGGKTMPVEGMYTCSVECKKKMS SHAPCDSEKPRCAGCORLIFSSLIPEGFFSGPIDQ GNHYQMRKGRCHRCSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIETEGRLHISISTPDLEILEDDLTAQEMSECNSNKENSERE]			
GVRAPSPAPSSVPLGSERPSNVSQDRKVPVPIGTERSARIRQTG TSAPSVIGSNLSTSVGHSGIWSPEGIGNQDKVDWCNPGMGNPM IHRPMSDPGVFSQHQAMERDSTGIVTPSGTFHGHVPAGYMDPPK VGGMPFSVYGNAMIPPVAPIPDGAGGF PRGPHAADPSWNSLIK MVSSSTENNBPQTVTWTGWAPHMNSVEMMOLG 5945 1461 197 GVTHLFLFGKRKLRNGIAEDLKGQADFFFILVSRAVVATGSPRA WLTCLILPLPGITESVLPKAMSRPLLITFPATDESDLWKDGQ QPOPERPESTLOGAARAFYEALIGDESSAPDSGRGTEPARER KRKKRRIMKAPAABAVAEGAGGNINARDAFWYPIMCAARAGQG AAVSYLLGRGAAWAVGVCELGGGDDAQLAEBAGFEVARWTESH GETRSPERNSPPELQVCENCDTHFQDSNHRTSTAHLLSLSQGP QPPNLPLGVPISSPGFKLLLRGGWERDDAQLAEBAGFEVARWTESH GETRSPERNSPPELQVCENCDTHFQDSNHRTSTAHLLSLSQGP QPPNLPLGVPISSPGFKLLLRGGWERDHAGGRGGRANPIFTV LKRDQEGIGYRSAPQPRVTHFPAMDTRAVAGRE\TTPPRVATLSW REERRRES\KDRAWERDLRTYMALEF 5946 541 1666 1LGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP SESSPQRVNSIDPV\EL\EHLQPDVLVHAVLRVVDP/TILTEAV YSYRGQKQKWMLTVEQAQDQHVALVLWGGAAW\YPQLQRKKG YWBEFYLFVQCTVTLENLELHTTPMSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFFITASQ KIALMAHSSLKSIFSSLPNIVYTGCAKCGLEETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLMISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDPSLLDFYPDIVHGAMARIL 5947 3 1317 RGFDPRRRGFIGRNUNDLENKVKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKMM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIFMYKRNVMLITNPVAAKKNVSINTYTEWA PFVQNQALARQYMMMLPKEKQPVAKSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRYQSYCCKLINKEG DPAIYAERAGYDKLMHPACFVCSTCHELLVDMIYFWKNBELLYCC RHYCDSEKPRCAGCDELIFSNETYQBEGQVFRVNBEVLYCC RHYCDSEKPRCAGCDELIFSNETYQBCORCHNAIDPEVQRVYIN NSWBASTECFLCSCCSKCLIGQKFMPVEGWYFCSVECKKMKS DPAIYAERAGYDKLMHPACFVCSTCHELLVDMIYFWKNBELLYCC RHYCDSEKPRCAGCDELIFSNETYQBCMNAIDPEVQRVYIN NSWBASTECFLCSCCSKCLIGQKFMPVEGWYFCSVECKKMKS GNHYQMRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIETEGRLHFISTFPDLEITLEDDLTAQEMSECNSNKENSERF	İ			
TSAPSVIGSILSTSVCHSGIWSPEGIGMODKVDWCNPGMOMPPK IHRPMSDPGVFSQHQAMERDSTGIVTPSGFTPHQHVPAGYMDFPK VGGMPFSVYGNAMIPPVAPIPDBAGGPIFNGHAADPSWNSLIK MVSSSTEINGPQTVMTGPMAPHMNSVHNNQLG GVPHLPLFGKRKRINGIABELGAGADFFFLLVSERAVVATGSFRA WLTCLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDGQQ QPOPEKPKIKINGIABELGAGADFFFLLVSERAVVATGSFRA WLTCLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDGQQ QPOPEKPESTLDGAARAFYEALIGDESSAPDSGRSGTEPARER KRKKRIMKAPABAVABGASGGHGGGRSLEBEDMMTRRILIRAA QEGDLPBLERLLEPHERAGAGGNINARDAFWHTPLMCARRAGQG AAVSYLLGRAAWVGVCELSGRDAAQLAEEAGFPEVARMVRESH GETRSPENSSPTPSLQYCENCOTHPQDSNHRTSTAHLLSLSGGP QPPNLPLGVPISSPGFKLLLRGGWEPGMGLGFREGGRANPIPTV LKRDDGGLGVRSAPQPRVTHPADMTRAVAGRE\TPPRVATLSW REERREB\KDRAWERDLRTYMNLEF 5946 5946 541 1666 ILGSYSSIQPESYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP SESSPQNVMSIDPV\EL\BHIDPULVALVURDP\/TLITEAV YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG YIWBFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKLSDLATHLEDFUVCISVESVLIEKGLLINISA DCLNRVIVPSSEITYGMVADLFHSLLAVSAEPCULKIQSLFVL DENSYPLQQDFSLLDFYDIVKHGANARL 5947 3 1317 RGIPDRRRGPIGRVNMDLENKYKKMGLGHEQGFGAPCLKCKEK CEGFFLHWRKICRNC\NVAKKSM/TVLLSEEDRKVGKLFEDI KYTTLIAKLKSDGIFMYRRNVMILTNPVAAKKNYSINTVTYEWA PFVQNALARGYMONLPKEKGPASSEGAVKKOLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG FRQMMIPGDRSTPAAVGAMBDKSAEHRRTQYSCYCCKLSMKEG DPAIYAERAGTWOMALPKEYGCSTCHELLDWINTYFWKNBKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNHHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYNKHAPVCCGCHNAIDPEVQRVTVN NFSWHASTECFLCSCCSKCLIGGKFMPVEGMYFCSVECKKRMS 5948 39 3370 YRERYPYSGGSVLRSALEVCHOFLSGLTEGSLLDEGFFSGFIDD GNHYMRKGRCHRGSAARHPSSPCVKHSPTRETLTYAQAQRM VEIELEGRLHHISTFDLEILLEDDLTAQEMSECNSNKENSERP				CUDADEDA DESUDI CERUDCADUCODDIVIDUE CORDO A DEDOCA
IHRPMSDPGYFSQHQAMERDSTGIVTPSGTFHQHVPAGYMDFPK VGGMPFSVYGNAMIPPVAPIPDGAGGPIFNGHVAGYMDFPK VGGMPFSVYGNAMIPPVAPIPDGAGGPIFNGHAADPSWNSLIK MVSSSTENNGPQTVVTGFWAPPHMSVHNNQLG 5945 1461 197 GVTHLFIFGKRKLRNGIAEDLKGQADFFFLLVSRAVVATGSFRA WLTCLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDGQQ QPQPEKPESTLOGAAARAFYEALIGDESSAPDSGRSCTEPARER KRKKRIMKAPAABAVBGASGRHGQGRSLEAEDKMTHRILRAA QEGDLBELRRLEPHBAGGAGGNINARDAFWHTPIMCAARAGQG AAVSYLLGRGAAWVOVCELSGRDAAQLAEEAGFFEVARMVRESH GETTSPENRSPTPSLQYCENCDTHPQDDSNHRTSTAHLLSLSGGP QPPNLPLGYPISSPOFKLLLGGWBPEGMGLGRPPTPV LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW REERRBEK KDRAWBEDLRTYMNLEF 5946 541 1666 1LGSYSSIQPESYS,VVVC_EVUODLLA\YVSPK\HSYLRDLP SEGSPQRVNSIDFV\EL\EHLQPDVLVHAVLRVVDF/TILTEAV YSYRGQKGKWMLTVEQAQDCHYALVUMGGAAM\YYDQLQRKKG YLWEFKYLFVQCOYYTIENLEHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALMAHSSLKSIFSSLPNIYYTGGAKGGLELETDERRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGAMARL 5947 3 1317 RGIFDRRRRGPIGRVNMDLEHKVKMGGGHERGGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEBRKVGKLFEDT KYTTLIAKLKSDGIFMYKRNVMILTNPVAAKKNVSINTVTYEMA PFVQNQALARQYMQMLPKEKGPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMRGFVKKYKSEBLGYGDVKLDCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKASAHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLMHPACFVCSTCHELLVDMIYFMKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAEROMNHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCINAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGGKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERYPYSGGSVLRSALEVCHDFLSGLTEGSLLDEGFFSGFIDD GNHYMGRKKGRCHRGSAARHPSSPSVVKHSPTRETLTYAQAQRM VEIELEGRLHRISTFDDLEIILEDDLTAQENSCNSKENSERP	ļ			
VGGMPPEVYGNAMIPPVAPIPDGAGGPIFNGPHAADPSWNSLIK MVSSSTENNGPQTVWTGPWAPHHNSVHMNQLG 5945 1461 197 GVTHLFLFGKRKLRNGTAEDLKGGADFFFLLVSKAVVATGSPRA WLTCLILPLPGITFSVLPKAMSRPLLITFTPATDPSDLWKDGQQ QPQPEKPESTLOGAARAFYEALIGEDSSAPDSGRSGTEPARER KRKKRIMKAPAABAVAEGASGRHGQGRSLEABEKMTHILRAA QEGDLPBLRRLLEPHEAGGAGGNINARDAFWWTPLMCAARAGQG AAVSYLIGKGAAWWGVCELSGRDAAGLAEBAGFFEVARMVRESH GETTSJENKSPTTSLQYCGNCDTHFQDSNIRHTSTAHLISLSGGP QPPNLPLGVPISSPGFKLLLRGGWEPGMGLGPRGEGRANPIPTV LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW REERRREBK\DRAWRRDLETYMMLEF 5946 541 1666 1LGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP SBGSPQRWSIDFV\BL\EHLQPUVLHAVLRVVDF/TILTEAV YSYRGGKQKKVMLTVERQADQDHVALVLWGRGAMV\PSQLQRKKG YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA KRQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDERIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPINKLAWGAMAFKNYSINTVYTEWA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPINKLIAVSAEPCVLKIQSLFVL DENSYPLQDPSLLDFYPINKLITNPEVARKNYSINTVYTEWA PFVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLFEDT KYTTLIAKLKSDGIPMYKRMULTHRPVARKNYSINTVYTYEWA PFVVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QPSKCHELSPREVKEMEGFVKKYKEBALGVGDVKLPCEMDAQG PKQMMI PGGBRSTPAAVGAMEDKSABHKRYQSCYCCKLBMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKFRCAGCDELIFSNEYTGAENQNWHLKHFCCFPCDSI LAGGETYWMUNDRVCKPCYVXYKHAVVQOGCHNAIDEPSVRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVPCSVECKKMS 5948 39 3370 YERRYPVSGGSVLRSALEVCONDFLSGLTEGSLLPEGSLPGFFSGPIDQ CMHYYQMRRKGRCHRGSAAPHPSSPCSVKHSPTRETLTYAQAQRM VEIETEGLHRISTDPLEILLEDDLTAGEMSECNSNKENSERP	J			
MYSSTENNGPQTVWTGPWAPHNNSVHMNQLG 5945				
S94S 1461 197 GVTHLFLFGKRKLRNGIAEDLKGQADFFFLLVSEAVVATGSPRA WITCILIPIPGIIFSVLPKAMSRPLITFTPATDPSDLWKDGQQ OPOPERPESTLDGAAARAFYEALIGDESSAPDGGRGCPEPARER KRKKRRIMKAPAABAVAEGASGRHGQGRSLEAEDKMTHRILRAA QEGDLPELRRLEPHEAGGAGGNINARDAFWITHCAARAGQQ AAVSYLLGRGAAWGVCLEGGDDAQLAEEGGPPEVARMVESH GETRSPENRSPTPSLQYCENCDTHFQDSNHRTSTAHLLSLSQGP QPPNLPLGVPISSPGFKLLIRGWEPGMGLGPRGEGRANPIPTV LKRDOBGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW REERREE\KDRAWERDLRTYMNLEF SEGSPQRVNSIDPV\EL\EHLQPDVLVHAVLRVVDP/TILTEAV YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG YIWEFKYLFVQCNYTLENLELHTTPMSCECLFDDDIRAITFKA KFQKSAPSPVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALMAHSSLKSIFSSLPNIVYTGCAKCGLELETDERRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGAMARL SGTPDRRRGPIGRVMMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTMPVAAKKNVSINTYTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEGFVKKYKSEALGVGDVKLPCEMDAQG PRQMNI PGGDRSTPAAVGAMEDKSAEHKRTYSSYCYCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQSKYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQSKYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQSKYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQSKYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQSKYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQSKYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQSKYCCKLSMKEG DPAIYAERAGYDKLWNDRVCKPCYVYXNHAVVCQGCHNAIDPEVORPYTN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKMS YERFYPUSGGSVLRSALEVCWDFLSSLIFEGSLIPEGSLIPEGFFSGPIDO CHMYQMRRKGRCHASAAAPPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEILLEDDLTAGEMSECNSNKENSERP				
WLTCLILPLEGITFSVLPKAMSRPLLITFTPATDPSDLWKDGQQ QPQPERPESTLDGAARARFYEALIGESSAPDSQRSGTEPARER KRKKRRIMKAPAABAVAEGASGRHGQGRSLEAEDKMTHRILRAA QEGDLPELRRLLEPHEAGGAGGNINARDAFWWTPIMCAARAGQG AAVSYLLGRGAAWUGVCELSGRDAAQLAEEAGFPEVARMVESH GETRSPENRSPTPSLQYCENCDTHFQDSNHRTSTAHLLSLSQGP QPPNLPLGVPISSPGFKLLLRGWEPGMGLGPRGEGRAPPIPTV LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW REERREB\KDRAWERDLRTYMNLEF 5946 541 1666 ILGSYSSIOPEEYS\SVV_EVVLQDLLA\YVSPK\HSYLRDLP SEGSPQRVNSIDFV\EL\EHLQPDVLVHAVLRVVDF/TILTEAV YSYRGGKQKKVMLTVEQADDCHYALVLMGPGAAM\YPQLQRKKG YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA KROKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAPPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRGPIGRVMMDLENKKMGLGHEGGFGAPCLKCKEK CGFBLHFFRKICRNC\NVAKKSM/TVLLSNEEDRRVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEMA PPVONQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEGFVKKYKSEALGVGDVKLPCEMDAQG FKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAITVAERAGYDKLMHPACFVCSTCHELLUDMIYFMKNRKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYWMVNDKFVCKRYCYVKNHAVVCGGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERTPVSGGSVLRSALEVCWBFIGTTEGSLLPEEFFFSGPIDQ GNHYGMRRKGRCHRGSAARHPSSPCSVKHSPFRETLITYAQAQRM VEIBIEGRLHRISIFDPLEIILEDDLTAQEMSECNSKKENSERP	5945	1461	197	
QPOPEKPESTLIGAAARAFYEALIGDESSAPDSQRSQTEPARER KRKKRRIMKAPAABAVAEGASGRHGQGRSLEAEDKMTHRILRAA QEGOLDEBLRRILEPHEAGGAGGRINARDAFWHTPILMCAARAGQG AAVSYLLGRGAAWVGVCELSGRDAAQLAEEAGFPEVARMVRESH GETRSPENRSSTPSLQYCENCOTHFQDSINHRISTAHLLSLSQGP QPPNLPIGVPISSPGFYKLLIRGGWEPGMGLGFRGGRANPIPTV LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW REERREE\KDRAWERDLRTYMMLEF 5946 541 1666 1LGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP SBGSPQRVNSIDFV\EL\EHLQPDVLVHAVLRVVDF\TILTEAV YSYRGQKQKKWMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG YIWEPKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILINISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRRGPIGRVNMDLERNVKKMGLGEEQGFGAPCLKCKEK CEGFELHFMRKICRNC\NVAKKSM\TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIFMYKRNVMILTMPVAAKKNVSINTVTYEMA PPVQNQALARQYMMDLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEGFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLMHPACFVCSTCHELLUDMIYFMKNEKLYCG RHYCDSEKPRCACCDELIFSHTYQAENQNWHLKHFCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCOGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERTPVSGGSVURSALEVCMBFLSGLTEGSLIPEGFFSGPIDQ GNHYYMRKRGKCRKRSGAARHPSSPCSVKHSPTRETLTVAQAQRM VEIBIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	3343	1401	137	
KRKRRIMKAPAABAVAEGASGRIGGGRSLEAEDKMTHRILRAA QEEDLEBLRILLEPHEAGGAGGNINARDAFWITPIMCAARAGGG AAVSYLLGGGAAWVOYELSGRDAAQDAEBEAGFPEVARWYESH GETRSPENRSPTPSLQYCENCDTHFQDSNHRTSTAHLLSLSGGP QPPNLPLGVPISSPGFKLLLRGGWEPGMGLGFRGGRAMPIPTV LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW REERRREE\NDRAWERDLRTYMNLEF 5946 541 1666 1LGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP SBGSPQRVNSIDFV\EL\BHLQPDVLVHAVLRVVDF\TTLITEAV YSYRGQKKWMLTVEQAQDQHYALWGPGGAW\YPQLQRKKG YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVHGANARL 5947 3 1317 RGIPDRRRGFIGRVMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICKNC\NVAKKSM\TVLLSNEEDRKVGKLFEDI KYTTLIAKLKSDGIPMYRRNVMILTMPVAAKKNVSINTVTYEMA PPVQNQALARGYMOMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD OPPSKCHELSPREVKEMEQFVKKYKSEALGYGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLUDMIYFWKMEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGBIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGNVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVURSALEVCWDFLSGLIFESSLIPEGFFSGPIDQ GNYYQMRRKGRCRRGSAARHPSSPCSVKHSPTRETLTVAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	•			
QEGDLPELRRLLEPHEAGGAGGNINARDAFWWTPLMCAARAGQG AAVSYLLGRGAAWGVCELGGRDAAQLAEEAGFPEVARMVREEH GETRSEPRINSPTPSLQYCENCDTHFQDSNHRTSTAHLLSLSQGP QPPNLPLGVPISSPGFKLLLRGGWEPGMGLGPRGEGRANPIPTV LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW REERREE\KDRAWERDLRTYMNLEF 5946 541 1666 1IGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP SEGSPQRVNSIDFV\EL\EHLQPDVLVHAVLRVVDF/TILTEAV YSYRGQKQKKWLTVEQAQDDHYALVLWGFGAAM\YPQLQRKKG YIWEFKYLFVQCNYTLENLEHHTTPWSSCECLFDDIRAITFKA KFQKSAPSFVKISDLATHLEBKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDERRIYKQCF SCLPFTMKKIYRPALMTATDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQOPFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIFMYKNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMONLPKEKQPVAGSEGAQYRKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAEMONWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGOKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNYYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIBIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP				
AAVSYLLGRGAAWVGVCELSGRDAAQLAEEAGFPEVARMVRESH GETRSPENRSPTPSLQYCENCDTHFQDSNHRTSTAHLISLSQGP QPPNLPLGVPISSPGFKLLLRGGWEPGMGGPRGEGRAPPIPTV LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW REERRREE\KDRAWREDLRTYMNLEF 5946 541 1666 1LGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP SEGSPQRVNSIDPV\BL\EHLQPDVLVHAVLRVVDP/TILTEAV YSYRGQKQKKWMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG YIWEFKYLFVQCNYTIENLELHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITTGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRRGPIGRVMMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIFMYKRNVMILTNPVAAKKRVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEGFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLMHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIBIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	1			
GETRSPENRSPTPSLQYCENCDTHFQDSNHRTSTAHLLSLSQGP QPPNLPLGVPISSPGFKLLLRGGWEPGMGGPRGGRANPIPTV LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW REERREE\KDRAWBRDLRTYMNLEF 5946 541 1666 1LGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP SEGSPQRVNSIDFV\EL\CHLQPDVLVHAVLRVUDF\TILTEAV YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG YWEFKXLFVQCONYTLENLELHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDERRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRGFIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM\TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFMKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNNHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGRVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSAELEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSSTRETLITYAQAQRM VEIBIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	İ	.		AAVSVI.GDGAAWVGVCELGGDDAAOLABEACEDEVADMIDESU
QPPNLPLGYPISSPGFKLLLRGGWEPGMGLGPRGEGRANPIPTV LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW REERRBE\KDRAWERDLRTYMNLEF 5946 541 1666 1LGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP SEGSPQRVNSIDFV\EL\EHLQPDVLVHAVLRVVDF/TILTEAV YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALINAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLINRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL CEGFELHFWRKICRNC\NVAKKGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKGM\TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA FPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIVVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRYTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP		·		
LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW REERRRES\KDRAWERDLRTYMNLEF 11666 11GSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP SEGSPQRVMSIDFV\EL\&HLQPDVLVHAVLRVVDP/TILTEAV YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYRRNVMILTINPVAAKKNVSINTVITYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGGKFMPVBGMVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP		1 '		
REERRBE\KDRAWERDLRTYMNLEF 5946 541 1666 1LGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP SEGSPQRVNSIDF\LE\LEHLQPDVLVHAVLRVVDF\TILTEAV YSYRGQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG YIWEFKYLFVQCNYTLENLEHLHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM\TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA FPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGWVFCSVECKKMS 5948 39 3370 YRERYPPVSGGVLRSALEVCNDFLSGLITEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	ŀ	· l		
1666 1IGSYSSIQPEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP SEGSPQRVNSIDFV\EL\EHLQPDVLVHAVLRVVDF/TILTEAV YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRGPIGRVMMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA FPVQNQALARQYMQMLPKEKQPVAGSEGAQVRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYWMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTVAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP		ļ:		
SEGSPQRVNSIDFV\EL\EHLQPDVLVHAVLRVVDP/TILTEAV YSYRGQKQKKVMLTVEQAQDQHYALVLWGFGAAW\YPQLQRKKG YIWEFKYLFVQCNYTLERLEHTTPWSSCECLFDDDTRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCTRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	5946	541	1666	
YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	3540	247	1000	CECCOODING TOEW ET LEUT ODDUT THAN DIEDE (MIT MOAN
YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRRGPIGRVNMDLENKVKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	·			
KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	}			
KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRGPIGRVMMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP				
SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYRRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP				
DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL DENSYPLQQDFSLLDFYPDIVKHGANARL 1317 RGIPDRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	i I	į		· · · · · · · · · · · · · · · · · · ·
DENSYPLQQDFSLLDFYPDIVKHGANARL 5947 3 1317 RGIPDRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP				
1317 RGIPDRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 199 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	1			i
CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 1948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	5947		1310	
KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 199 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	354,		1317	,
PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 19 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP				
QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP				
PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP				
DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	į (UDPSACHEDSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG
RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	f 1			
LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP		1		
NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS 5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP				
5948 39 3370 YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	[
GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	<u></u>			
VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	5948	39	3370	· ·
PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVEY				· ·
				PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVEY

			, , , , , , , , , , , , , , , , , , ,
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
]	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			SPPSAPRRPPVYYKFIEKSABELDNEVEYDMDEEDYAWLEIVNE
1		İ	KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQQSLIDEDA
			VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/
ļ			RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
ļ		}	E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
1		•	QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR
Į.		1	
1			KKAKKAKKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ
			FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM KAAKEKLKYWORLRHDLERARLLIELLRKREKLKREQVKVEQVA
1			
			MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV
		Ī	FYRAAVRLRDOGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
			RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG
			SRSKRAKLIKKEIALLRNKLSQOHSQPLPTGPGLEGFEEDGAAL
		[GPEAGEEVLPRLETLLOPRKRSRSTCGDSEVEEESPGKRLDAGL
			TNGFGGARSEOEPGGGLGRKATPRRRCASESSISSSNSPLCDSS
			FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAARIAAEV
]	GOSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV
ĺ	Í		PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWQ
1			WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
1	!		SRVHGEPTSDLSDID
5949	39	3370	YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ
3949	33	3370	GNHYOMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM
.			VEIEIEGRLHRISIFDPLEIILEDDLTAOEMSECNSNKENSERP
			PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVEY
1			SPPSAPRRPPVYYKFIEKSAEELDNEVEYDMDEEDYAWLEIVNE
			KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQQSLIDEDA
			VCCICMDGECONSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/
			RAHCLOSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
1	ļ		E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
			QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA
	}	4	YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR
			KKAKKAKKALAEPCAVLPTVCAPYIPPORLNRIANOVAIORKKO
	1		FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM
1	}	,	KAAKEKLKYWORLRHDLERARLLIELLRKREKLKREQVKVEQVA
		ĺ	MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI
			KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV
1	1		FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
1			RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG
1			SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL
			GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEESPGKRLDAGL
			TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSSNSPLCDSS
	1		FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAARIAAEV
		1	GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV
1			PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWQ
			WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
		1	SRVHGEPTSDLSDID
5950	1166	373	ESRSLTMSTSQPGACPCQGAASRPAILYALLSSSLKAVPRPRSR
			CLCRQHRPVQLCAPHRTCREALDVLAKTVAFLRNLPSFWQLPPQ
1			DQRRLLQGCWGPLFLLGLAQDAVTFEVAEAPVPSILKKILLEEP
			SSSGGSGQLPDRPQPSLAAVQWLQCCLESFWSLELSPKE\YACL
1		Ì	KGPILFNPDVPGLQAASHIGHLQQEAHWVLCEVLEPWCPAAQGR
			LTRVLLTASTLKSIPTSLLGDLFFRPIIGDVDIAGLLGDMLLLR
5951	143	5449	WNVKPSLLVVQLFKFSDKEEHEQNDSISGKTGETGVEEMIATRK
			VEQDSKETVKLSHEDDHILEDAGSSDISSDAACTNPNKTENSLV
			GLPSCVDEVTECNLELKDTMGIADKTENTLERNKIEPLGYCEDA
	1		ESNRQLESTEFNKSNLEVVDTSTFGPESNILENAICDVPDQNSK
			QLNAIESTKIESHETANLQDDRNSQSSSVSYLESKSVKSKHTKP
		Į.	VIHSKONMTTDAPKKIVAAKYEVIHSKTKVNVKSVKRNTDVPES
			QQNFHRPVKVRKKQIDKEPKIQSCNSGVKSVKNQAHSVLKKTLQ

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
			DQTLVQIFKPLTHSLSDKSHAHPGCLKEPHHPAQTGHVSHSSQK
	1		QCHKPQQQAPAMKTNSHVKBELEHPGVEHFKEEDKLKLKKPEKN
İ			LQPRQRRSSKSFSLDEPPLFIPDNIATIRREGSDHSSSFSKYM
1	!		WTPSKQCGFCKKPHGNRFMVGCGRCDDWFHGDCVGLSLSQAQQM
l	1		GEEDKEYVCVKCCAEEDKKTEILDPDTLENQATVEFHSGDKTME
1			CEKLGLSKHTTNDRTKYIDDTVKHKVKILKRESGEGRNSSDCRD
ı			NEIKKWQLAPLRKMGQPVLPRRSSEEKSEKIPKESTTVTCTGEK
1			ASKPGTHEKQEMKKKKV\EKGVLNVHPAASASKPSADQIRQSVR
ļ	J .		HSLKDILMKRLTDSNLKVPEEKAAKVATKIEKELFSFFRDTDAK
ŀ			YKNKYRSLMFNLKDPKNNILPKKVLKGEVTPDHLIRMSPEELAS
1			KELAAWRRRENRHTIEMIEKEQREVERRPITKITHKGEIEIESD
			APMKEQEAAMEIQEPAANKSLEKPEGSEK\RKEEVDSMSKDTTS
1			QHRQHLFDLNCKICIGRMAPPVDDLSPKKVKVVVGVARKHSDNE
i			AESIADALSSTSNILASEFFEEEKQESPKSTFSPAPRPEMPGTV
1			EVESTFLARLNFIWKGFINMPSVAKFVTKAYPVSGSPEYLTEDL
			PDSIQVGGRISPQTVWDYVEKIKASGTKEICVVRFTPVTEEDOI
1	1		SYTLLFAYFSSRKRYGVAANNMKQVKDMYLIPLGATDKIPHPLV
1)
			PFDGPGLELHRPNLLLGLIIRQKLKRQHSACASTSHIAETPESA
	1		PPIALPPDKKSKIEVSTEEAPEEENDFFNSFTTVLHKQRNKPQQ
1	{		NLQEDLPTAVEPLMEVTKQEPPKPLRFLPGVLIGWENQPTTLEL
1	1		ANKPLPVDDILQSLLGTTGQVYDQ\AQSVMEQNTVKEIPFLNEQ
	ł i		TNSKIEKTDNVEVTDGENKEIKVKVDNISESTDKSAEIETSVVG
1	1		SSSISAGSLTSLSLRGKPPDVSTEAFLTNLSIQSKQEETVESKE
1	:]	•	KTLKRQLQEDQENNLQDNQTSNSSPCRSNVGKGNIDGNVSCSEN
			LVANTARSPQFINLKRDPRQAAGRSQPVTTSESKDGDSCRNGEK
1			HMLPGLSHNKEHLTEQINVEEKLCSAEKNSCVQQSDNLKVAQNS
1	ŀ		PSVENIQTSQAEQAKPLQEDILMQNIETVHPFRRGSAVATSHFE
1			VGNTCPSEFPSKSITFTSRSTSPRTSTNFSPMRPOOPNLOHLKS
1	1		SPPGFPFPGPPNFPPQSMFGFPPHLPPPPLLPPPGFG\FA\ONPM
1			VPWPPVV\HLP\GQPQRMMGPLSQASRYIGPQNFYQVKDIRRPE
			RRHSDPWGRQDQQQLDRPFNRGKGDRQRFYSDSHHLKRERHEKE
1 .			WEQESERHRRRDRSODKDRDRKSREEGHKDKERARLSHGDRGTD
1	<i>:</i>		GKASRDSRNVDKKPDKPKSEDYEKDKEREKSKHREGEKDRDRYH
5952	3336	C20	KDRDHTDRTKSKR
3334	3226	639	PPARRSARDLPRALSMEAARPSGSWNGALCRLL\LVTL\AFLIF
	1	İ	ASDACKNVTLHVPSKLDAEKLVGRVNLKECFTAANLIHSSDPDF
	.		QILEDGSVYTTNTILLSSEKRSFTILLSNTENQEKKKIFVFLEH
	<u> </u> :		QTKVLKKRHTKEKVLRRAKRRWAPIPCSMLENSLGPFPLFLQQV
	† 1		QSDTAQNYTIYYSIRGPGVDQEPRNLFYVERDTGNLYCTRPVDR
J.	1		EQYESFEIIAFATTPDGYTPELPLPLIIKIEDENDNYPIFTEET
1	1		YTFTIFENCRVGTTVGQVCATDKDEPDTMHTRLKYSIIGQVPPS
1	. 1		PTLFSMHPTTGVITTTSSQLDRELIDKYQLKIKVQDMDGQYFGL
1	[1		QTTSTCIINIDDVNDHLPTFTRTSYVTSVEENTVDVEILRVTVE
1	.		DKDLVNTANWRANYTILKGNENGNFKIVTDAKTNEGVLCVVKPL
1			NYEEKQQMILQIGVVNEAPFSREASPRSAMSTATVTVNVEDQDE
1			GPECNPPIQTVRMKENAEVGTTSNGYKAYDPETRSSSGIRYKKL
i			TDPTGWVTIDENTGSIKVFRSLDREAETIKNGIYNITVLASDOG
1			GRTCTGTLGIILQDVNDNSPFIPKKTVIICKPTMSSAEIVAVDP
	[,	· · · · · · · · · · · · · · · · · · ·
1			DEPIHGPPFDFSLESSTSEVQRMWRLKAINDTAARLSYQNDPPF
	ŀ		GSYVVPITVRDRLGMSSVTSLDVTLCDCITENDCTHRVDPRIGG
	ŀ		GGVQLGKWAILAILLGIALFFCILFTLVCGASGTSKQPKVIPDD
			LAQQNLIVSNTEAPGDDKVYSANGFTTQTVGASAQGVCGTVGSG
1			IKNGGQETIEMVKGGHQTSESCRGAGHHHTLDSCRGGHTEVDNC
			RYTYSEWHSFTQPRLGEESIRGHTLIKN
5953	330	811	PLLCNPDPGWYWWVKQESEISKESQEMDARPKLDLGFKEGQTIK
			LCIGNITNKKGGASKPRTARGGGLSLLPPPPGGKVTIPPPSS/V
			KLPSTNHVTPPSIPKSNHGGSDADILLDLDSPAPVTTPAPTPVS
			VSNDLWGDFSTASSSVPNQAPQPSNWVQF
5954	32	2130	PPPPPPKLANMADLEAVLADVSYLMAMEKSKATPAARASKRIVL
			PEPSIRSVMQKYLAERNEITFDKIFNOKIGFLLFKDFCLNEINE
į l			AVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSCSH
Ll			**** **** * PRIVE LEVERNICE DESCRIPTION TANKED POCON

Predicted Predicted on uncleotide Ination acid segment containing signal peptide Ination uncleotide Ination acid I				
Degimning location	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence Profile, Q.G.Clutamine, R.Arginine, acid amino acid sequence Profile, Q.G.Clutamine, R.Arginine, acid amino acid sequence Profile, Q.G.Clutamine, R.Arginine, acid amino acid sequence Profile, Q.G.Clutamine, R.Arginine, acid sequence Profile, Q.G.Clutamine, R.Arginine, acid sequence Profile, Q.G.Clutamine, R.Arginine, acid sequence Profile, Q.G.Clutamine, R.Arginine, acid sequence Profile, Q.G.Clutamine, R.Arginine, acid sequence Profile, Q.G.Clutamine, R.Arginine, acid sequence Profile, Q.G.Clutamine, R.A.C.Clutamine, R.A.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.		beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence p-proline, Q-Glutamine, R-Arginine, S-Serine, T-Threenine, V-Vallan, Codon, Y-Syrosine, R-Morknown, *-Stop Codon, Y-possible nucleotide deletion, Y-possible nucleotide delet	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence solvente percente pe		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first amino acid residue of amino acid residue of amino acid anino acid sequence ##Typtophan, Y=Tyrosine, X=Unknown, *=Stop codon, Y=possible nucleotide deletion, Y=possible nucleotide deletion, Y=possible nucleotide deletion, Y=possible nucleotide deletion, Y=possible nucleotide insertion) ### PFKGAMPHOSHLEKENDYSTERPFYTEETCESURGDI7QKFM ESDKFTRFCQWINVELMILLEMBETSURGITAMESTER MISJENTEDEPT VCMTYA=HTPEKUCPILDIMMOGDIAHILSQRUFSERUMPTYA ### PFKGAMPHOSHLEKENDYSTERPFYTEETCESURGDI7QKFM ESDKFTRFCQWINVELMILLEMBETSURGITAMESTERMAPTA ### TEILIGLEMBMRFVYURGATADESADDFERGALEGIL RRGISFFRANKCHERE INSERTEDIAHILSGRUFSERUMPTA ### TEILIGLEMBMRFVYURGATADESADDFERGALEGIL RRGISFFRANKCHERE INSERTEDIAHILSGRUFSERUMPTA ### TEILIGLEMBMRFVYURGATADESADDFERGALEGIL RRGISFFRANKCHERE INSERTEDIAHILSGRUFSERUMPTA ### TEILIGLEMBMRFVYURGATADESADDFERGALEGIL RRGISFFRANKCHEREPSATVELERRENGESESKOMILTMEN HAVENDALGAMPTADMORDEEDTKOILLILOOQELYMPPUTISER ### TEILIGLEMBMRFVYURGATADESADDFERGALEGIL RRGISFFRANKCHEREPSATVELERRENGESESKOMILTMEN HAVENDALGAMPTADMORDEEDTKOILLILOOQELYMPPUTISER ### TIPEAQHILIRANDHORDEEDTKOILLILOOQELYMPPUTISER ### TIPEAQHILIRANDHORDEEDTKOILLILOOQELYMPPUTISER ### TIPEAQHILIRANDHORDEEDTKOILLILOOQELYMPUTISER HAVENDALGAMPTADMORDEEDTKOILLILOOQELYMPUTISER HAVENDALGAMPTADMORDEEDTKOILLILOOQELYMPUTISER HAVENDALGAMPTADMORDEEDTKOILLILOOQELYMPUTISER HAVENDALGAMPTADMORDEEDTKOILLILOOQELYMPUTISER HAVENDALGAMPTADMORDEEDTKOILLILOOQELYMPUTISER HAVENDALGAMPTADMORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKOILLINGENDALGAMPTADHORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKOILLINGENDALGAMPTADGATADHORDEEDTKANALGAMPTADGATADHORDEEDTKANALGAMPTADGATADHORDEEDTKANALGAMPTADGATADHORDEEDTKAN				L=Leucine, M=Methionine, N=Asparagine,
amino acid residue of amino acid sequence solvente properties of amino acid sequence solvente sequence code, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide insertion) PFSKQAMENUGSHISKQUISTLEPPYIESICSSIRGDIFQKFM ESSKREDBLE NUCLEUTE SERVENDE SERVENTE SERVENDE SERVENTE SERVENDE SERVENDE SERVENTE SERVENDE SERVENTE SERVENDE SERVENTE SERVENDE SERVENTE SERVENDE SERVENTE SERVENDE SERVENTE SERVENDE SERVENDE SERVENTE SERVENDE SE				P=Proline, O=Glutamine, R=Arginine,
maino acid sequence mino				S=Serine T=Threonine, V=Valine,
amino acid sequence Codon, /=possible nucleotide deletion,				W-Trumbonhan V-Turosine X-Unknown, *=Stop
### Appearable mucleotide insertion ### PFKONDEWINGHINEKKYPTSTLOPPY LBEICESLANDIFOKEN ### BSNKTRFCQMKNVELNIHLTMEPSVHRIIGRGFGEVYGCKK ### BSNKTRFCQMKNVELNIHLTMEPSVHRIIGRGFGEVYGCKK ### ADTGGMANKCLINKKK IMMAGETLALMER IMLSUVSTGOPPY VCMTYAFETPDYLCFILDLENGGLHYHLSGRGVGVYGCKK ### TEILIGLEHHNERSVYDLKAPAILLEHGHARIS JULGACO ### FSKKKPHASVOTHOYMADEVLIKGHTAVDSADMFSLGCHLFKLI RGHSPFRGKKTKOMERIBIRHTLTVNUHELDFISFELLSLEGLL GRUSSKLIGCHGGSGEVKEHSFKGVUNGHVYLDKYDPPLIPP RGEVMAADAPTOISFBEDTKGIKLLDCOPLIKYRPLVISER QGEVTETVVEANADTDILTBARKANKKCLGHEEDYALGKDCIH HGYMLKIKNPFLTGMORRYFYLPPSHTUSKRGGESSGRADGHT TPKEAQORVTETVVEANADTDILTBARKANKKCLGHEEDYALGKDCIH HGYMLKIKNPFLTGMORRYFYLPPSHTUSKRGGESSGRADGHT TPKEAQORULKERN PLENTUH PRESIDTENSKELLSKALL WARGULIKRAP PLENTUH PRESIDTENSKELTHRISBGIL #### PANRODVLSGWINLPPGCHUNGTENSCCLEVERAMENT WARGULIKRAP PLENTUH PRESIDTENSKELTHRIBBG VMKRCININGBURGHVINGHTUNGKELTHRIBBGURGHTUNGKELTHRIBBG VMKRCININGBURGHVINGHTUNGKELTHRIBBGURGHTUNGKELTHRIBBG VMKRCININGBURGHVINGHTUNGKELTHRIBBGURGHTUNGKELTHRIBBG VMKRCININGBURGHVINGHTUNGKELTHRIBBGURGHTUNGKELTHRIBBG VMKRCININGBURGHVINGHTUNGKELTHRIBBGURGHTUNGKETHRIBBGURGHTUNGKETHRIBBGURGHTUNGKETHRIBBGURGHTUNGKETHRIBBGURGHTUNGKETHRIBBGURGHTUNGKETHRIBBGURGHTUNGKETHRIBBGURGHTUNGKETHRIBBGURGHTUNGKETHRIBBGURGHTUNGKETHRIBBGURGHTUNGKETHRIBBGURGHTUNGKETHRIBBGURGHTUNGKETHR				Goden /
PFSKQAVENVQSHLSKKQVISTLFOFVIEEICESLRGDLTQKKW BISKSTRPCQMKWNEINILHTMINEPSWITI IGRGGFGGVYCCKK ADTGRMYANKCLNKKRIINKTQGRTIALMERIMLSJUSTGDCPI VCMTYAPHTDKLCFILDLMNGGLIHJHLSGUSYERSEMMFYA TEILIGLEHHENREVVYTDLKRANILLDEHGHARIS DIJGLACD FSKKUPHASVUTHGHVARPEULQKSTANDSADMFSLGCHLYKLI RGISFFRQHKTKDKHBIDRHTLTWVELDDTTSPELKSLLISGLL RGISFFRQHKTKDKHBIDRHTLTWVELDDTTSPELKSLLISGLL RGISFFRQHKTKDKHBIDRHTLTWVELDDTTSPELKSLLISGLL RGISFFRQHKTKDKHBIDRHTLTWVELDDTTSPELKSLLISGLL RGISFFRQHKTKDKHBIDRHTLTWVELDDTTSPELKSLLISGLL RGYBVARADARPIGSPDEDTKGIKLLDCOGLIKAFPELVISERN GREVNAADARPIGSPDEDTKGIKLLDCOGLIKAFPELVISERN GREVNAADARPIGSPDEDTKGIKLLDCOGLIKAFPELVISERN HOYMLKLGNPFLTQWGREYFYLPPRILERRGGGESGROPLOKE HOYMLKLGNPFLTQWGREYFYLPPRILERRGGGESGROPLOKE HOYMLKLGNPFLTQWGREYFYLPPRILERRGGLGSGGPADCRE PANRODVLSGWINLPVLQLIKTOGLBDEPTQWKELBLA TFKEAQRILLRRAPFITINTPRSGTVELKFSCICLGSGGPADCRE PANRODVLSGWINLPVLQLIKTOGLBDEPTQWKELBLA WESCHLINBEDGLIABFAQVTHNISSSCCLRYFAMHHT NEAVALLDDSVRYIVARSSTVEDSLKRIKQDWNSLAKRILAGE VLAVAGOSCILLWILDDYSLSTRPBSGCAQVLSHPGHTPVTELA WASSLINGSLEPHLISBEDLLBEFAQVTHNISSCCLRYFAMHHT NEAVALLDDSVRYIVARSSTVEDSLKRIKQDWNSLAKRVLLAS VLAVAGOSCILLWILDDYSLSTRPBSGCAQVLSHPGHTPVTELA WASSGRILASPFDAARIRWSTYDETCVPLPFFRGGGVTVILLW SPDGSKILATFSAVFRWERGAMWTCERRPTLGGRCGTGCWSPD GSRLLGTVJGEBLIYJSFPRGCGRGWALEVGGACWMGTCL RGOYRHOWWERGLGERLTPMSGTPGWWALCL SCHOOL TOWN TOWN TOWN TOWN TOWN TOWN TOWN TOWN		• **	sequence	Codon, /=possible indirection defection,
ESNKTTPFCOMKAVELINIKHER INLIGETIGLEGFGEVYGCHK ADTGGWAMKCLINKEN INMGGETLAMER INLIGETIGLEF VCMTYAPHTPDKLOFILDIANGGLHYHLSGHGVPSEKEMEFYA TEI LIGLEHMENREYVPDLKAPAILLBEHGHARIS JÜLGLACD FSKKKPHASVOTHOWARDEVLIKKTAYDSADMFSLGGUPKLI BGISPFRCHKTKOKEILDINNIGGLHYHLSGHGVPSEKEMEFYA TEI LIGLEHMENREYVPDLKAPAILLBEHGHARIS JÜLGLACD FSKKKPHASVOTHOWARDEVLIKKTAYDSADMFSLGGUPKLI. BGISPFRCHKTKOKEILDINNIGLUSDTSPELKISLLIGGLI CRDVSKRIACHGGSGDEVIKHSFRGUUNGHVYLIKYPPPLIPP BGEVMAADAPDIGSPEDYNGKIKLLDCOSIKNSPHJUSER CQRVTETVYKAVNADTDLIBAKRAKNKOLGHEBEDYALGKOCHM HCYMUKLGNPHJTGWORRYPYLPPRILEKRGGEGERGNLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG GGRAMANTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG LILVERTOLKOKKILPFIKGGORGPROMLITMEG		sequence		\=possible nucleotide insertion/
ADTIGMYAMICLINKER I MINGGETLALBER IMISJUSTEDOPPT V CHTYAFTPPIKLE FILLDIAMGGILIPHISJUSTEMSKERMEYAY TESTIGGERMINREVVYPOLIKEANI LIDEHGHARIS DIGGACO PSIKUPHASVOTHONA PEULAKOTA MOSSANDESJACHURILL BRISSPFRICHKTROHISTRATUTAVNELDOTES PELKSLLEGILL GRUSKELGCHEGGSGEVERISFEYRUNGWIVTLIKAVPOPLIP BRISSPROHETVERANDATURI ELARREMINGUNGWIVTLIKAVPOPLIP BRISSPROHETVERANDATURI ELARREMINGUNGWIVTLIKAVPOPLIP BRISSPROHETVERANDATURI ELARREMINGUNGWIVTLIKAVPOPLISERI HENORILLER PERUTVERANDATURI ELARREMINGUNGWIVTLIKAVPOPLISERI HENORILLER PERUTVERANDATURI ELARREMINGUNGWIVTLIKAVPOPLISERI HENORILLER PERUTVERANGUNGWIVTLIKAVPOPLISERI HENORILLER PERUTVERANGUNGMINTURI ELARREMINGUNGWIVTLIKER SICKURSINGUNG LILUVERETURI HENORILLER PERUTVERANGUNGMINTURI HENORILLER PERUTVERANGUNGMINTURI HENORILLER PERUTVERANGUNGMINTURI HENORILLER PERUTVERANGUNGMINTURI HENORILLER PERUTVERANGUNGMINTURI HENORILLER VILVAVALLED SVILVAVALLER PERUTVERANGUNGMINTURI HENORILLER VILVAVALLER VILVAVALLED SVILVAVALLER PERUTVERANGUNGMINTURI HENORILLER VILVAVALLER PERUTVERANGUNGMINTURI HENORILLER VILVAVALLER PERUTVERANGUNGMINTURI HENORILLER VILVAVALLER PERUTVERANGUNGMINTURI HENORILLER VILVAVALLER PERUTVERANGUNGMINTURI HENORILLER VILVAVALLER PERUTVERANGUNGMINTURI HENORILLER VILVAVALLER PERUTVERANGUNGMINTURI HENORILLER VILVAVALLER PERUTVERANGUNGMINTURI HENORILLER VILVAVALLER PERUTVERANGUNGMINTURI HENORILLER VILVAVALLER PERUTVERANGUNGMINTURI HENORILLER VILVAVALLER PERUTVERANGUNGMINTURI HENORILLER VILVAVALLER PERUTVERANGUNG PERUTVERANGUNGMINTURI HENORILLER VILVAVALLER VILVAVALLER PERUTVERANGUNGMINTURI HENORILLER VILVAVALLER VILVAVALLER PERUTVERANGUNG PERUTVERANGU				PFSKQAVEHVQSHLSKKQVTSTLFQPYIKEICESLRGDIFQKFM
TEITIGLEHHINFEVYYERLEPADILDERIGIALS OLIGIACO FSEKKPHASVOTHOYAPAPULQKOTAYOSADWFSIACKULFKUL RGISPPROHETEMPYVERLEPATILDERIGIALS OLIGIACO FSEKKPHASVOTHOYAPAPULQKOTAYOSADWFSIACKULFKUL RGISPPROHETEMPYVERLEPATSPEKKSLEGILL ORDVSKRIGCHEGGSGEVEKSEFFKOUNGHYLQKYPPPLIJE BEVANADAPDIGSPEEDTETGIKLLDCODELYKRIPPLIJEER OQEVTETVYVEAVNADTOKIERRKRANNKQLGHEEDYALGKULFKUL HCYMLKLENPFLYGORGRYFLLPRILDEROBLITHEO TEKERORILERAPAKUNKOLGHEEDYALGKULTUR LUSVEETGIKDKKCILFRIKGGKOPTAJCESDPEVQNKKSLAN TYKEAQRILLERAPKUNKSRGSTVELERGICKSGOBFADULTUR TEKERORILERAPKUNKSRGSTVELERGICKSGOBFADULTUR TEKERORILERAPKUNKSRGSTVELERGICKSGOBFADULTUR TEKERORILERAPKUNKSRGSTVELERGICKSGOBFADULTUR TEKERORILERAPKUNKSRGSTVELERGICKSGOBFADULT TYMEROUNISMULTURUULTURUULTURIDERPETGERKTAPHHIREO VIKRCININEDVOLIKUMILDVOLITUDELTOELROLGKSGOBFADULT NASHIGSLIPPHISLSSEDILABFADVINNSSCALVAMIDHT NERAVALLIDDSVEVYNASSTIVPELKHELQRAVASLAKKPLSAB VLANACOSCILLIPPIDTEILSTPSGGCADVISHEVYTSLA HABBGGRILLABPVDAJIRVBOVSTRICVPLPPFREGGVIVLIL SDOGSKILAPTVILDFILLSTPSGGCADVISHEVYTSLA HABBGGRILLABPVDAJIRVBOVSTRICVPLPPFREGGVIVLIL SDOGSKILAPTVILDFILLSTPSGCADVISHEVYTSLA HABBGGRILLABPVDAJIRVBOVSTRICVPLPPFREGGVIVLIL SDOGSKILAPTVILDFILLSTPSGCADVISHEVYTSLA HABBGGRILABPVDAJIRVBOVSTRICVPLOKKKSDIT FEDSSCSILKRYTII ONDOGLOKENKILVSTRAVADAJKSSDIT FEDSSCSILKRYTII ONDOGLOKENKILVSTRAVADAJKSSDIT SASLEDLIMBILSISHENADEVVOLOKADIRVSDITANNASNYDDRGILK AYSDSGEDEMISAAIDCSSCLIPPONTVINNASNYDDRGILK AYSDSGEDEMISAAIDCSSCLIPPONTVINNASNYDDRGILK AYSDSGEDEMISAAIDCSSCLIPPONTVINNASNYDDRGILK SILKULLDFONREPRINDSTVINGTIAKLUNKEILALDAN ELLEPANSTVINNASNYDDRGILKSCRIPPONTSTRAVADA SILKULLLOFONREPRINDSTVINGTIAKLUNKEILALDAN TESKALVUNKULSKGRATDAHISTORMANIK SILKULLLOFONREPRINDSTVINGTIAKLUNKEILALDAN TESKALVUNKULSKGRATDAHISTORMANIK SILKULLLOFONREPRINDSTVINGTIAKLUNKEILALDAN TESKALVUNKULSKGRATDAHISTORMANIK SILKULLABPONREPRINDSTVINGTIAKSTVINGTIAKUNKEILALDAN TESKALVUNKULSKGRATDAHISTORMANIK SILKULLABPONREPRINDSTVINGTIAKSTVINGTIAKUNKUL GGRANATVTKIKLORDSTRAKKRYNILDERISTKSCRATPRIE LEEMGSSLOVARASTORDIVKSCRATTARVANSTRAVATOR TERMORITARVANSTRAVATOR TARVATOR TARVATOR TERMO	i	1	[ESDKFTRFCQWKNVELNIHLTMNEFSVHRIIGRGGFGEVYGCRK
TEILIGLERHHNREVYTRÜLEPANTLLDERIGHARIS ÖLGILEVÄLL RGISPPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES LIEVERTOTTONKEKULTERISLISCHENDIGGESERONLITUTEG LIEVERTOTTONKEKULTERISLISCHENDIGGESERONLITUTEG LIEVERTOTTONKEKULTERISLISCHENDIGGESERONLITUTEG REFELIEVE PERVESSORIALITEN SERVERVERVERSEGEFADORE PARRODVILSGUILDEN LIEVERDIGGESTATSPERTERISCHENDIGGESTATSPERTERISLISCHENDIGGESTATSPERTERISLISCHENDIGGESTATSPERTERISCHENDIGGESTATS				ADTGKMYAMKCLNKKRIKMKQGETLALNERIMLSLVSTGDCPFI
TEILIGLERHHNREVYTRÜLEPANTLLDERIGHARIS ÖLGILEVÄLL RGISPPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES RGISPROHETKONHEIDENTLITUVILEPOTTSPELISLISLES LIEVERTOTTONKEKULTERISLISCHENDIGGESERONLITUTEG LIEVERTOTTONKEKULTERISLISCHENDIGGESERONLITUTEG LIEVERTOTTONKEKULTERISLISCHENDIGGESERONLITUTEG REFELIEVE PERVESSORIALITEN SERVERVERVERSEGEFADORE PARRODVILSGUILDEN LIEVERDIGGESTATSPERTERISCHENDIGGESTATSPERTERISLISCHENDIGGESTATSPERTERISLISCHENDIGGESTATSPERTERISCHENDIGGESTATS				VCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSEKEMRFYA
FSKKPHASVGHROWADEVIQKGNAYDSSADWFSLGKLLEGILL RGISPPRORHETIONELDEDTISPELKSLEGILL RGISPPRORHETIONELDEDTISPELKSLEGILL QRIVSKRIGCHGGGSGEVERISPFKGUUMQHYLQKYPPPLISERR QGEVTETVYEAVAADTOLEARKAANKQLGHEBDYALGKUL HGYMLKLINPPLINGKREYPLIPPBLISHRESBERINLITME LLSVERTQLTIDKKCTLEFT.KGGKQFVLQCSSDPEFVQWKKELAR TYKEAQRLLRRADKKTLINFRGKGFVLGSSDPEFVQWKKELAR TYKEAQRLLRRADKKTLINFRGKGFVLGSSDPEFVQWKKELAR TYKEAQRLLRRADKKTLINFRGKGFVLGSSDPEFVQWKKELAR TYKEAQRLLRRADKKTLINFRGKGFVLGCSSDPEFVQWKKELAR TYKEAQRLLRRADKKTLINFRGKGFVLGCSSDPEFVQWKKELAR TYKEAQRLLRADKKTLINFRGKGFVLGCSSDPEFVQWKKELAR TYKEAQRLLRADKTLINFRGKGFVLGCSSDPEFVQWKKELAR TYKEAQRLLADKGWKATANTOLTKOLKTFGRLDHGTTATAFIHHERG WARSCHGSSJPFHISLRSEDLLAEFAQVTNNSSCCLRVFAWHERT NKFAVALLDDSVYGVANSSTUTVELBEFTGGGVTALLAG WASSLHGSLFFHLISLGRUEGVLGTGCTGCSSDP GSRLLSTTJGAPTAVRSQCGVLGTHGHTEVTSLA WAPSGGRLLGASPDAARLWYMNSSTUTTCVLFBYFGGGVTALLAG SPDGSKLLATTPSAVFKVWRQMWTCERWFTLSGRCQTGCKSDP GSRLLSTTJGAPTVANSDAARLWYNGGGAKGALANGGGGTGCTGCSSDP GSRLLSTTJGAPTVANSTTUTSLSFPFRGGGKVALLEVGGGTGCTGCSSDP GSRLLSTTJGAPTVANSTTUTSLSSSPFRGGGKGALALVGGGTGCTGCSSDP GSRLLSTTJGAPTVANSTTUTSLSSSPFRGGGKGALAGUNGGGTGLTG RQCYRRGWWRRGLGGRLTFWSGTFVGNWWLCSSSPFGGATAGTGCTGCTGCSSDP GSRLLSTTJGAPTVANGTATTGVSTFVGNWATCHARTTGGGTTNLLAGUNGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC			ļ	TEILGLEHMHNRFVVYRDLKPANILLDEHGHARIS\DLGLACD
RGISSPERGHETIONHELDERMILITVANVELEDITSPELKSLLEGGL QROVERVELGHEGGGSOVEKEISFEREVUNMONYLIQKYPPLIPE RGEWNAADADTGSFEREDITKGIKLLICCOGELYKNFPELIPE RGEWNAADADTGSFEREDITKGIKLLICCOGELYKNFPELIPE RGEWNAADADTGSFEREDITKGIKLLICCOGELYKNFPELIPE RGEWNAADADTGSFEREDITKGIKLLICCOGELYKNFPELIPE RGEWNAADADTGSFEREDITKGIKLLICCOGELYKNFPELIPE RGEWNAADADTGSFEREDITKGIKLLICCOGELYKNFELICKE HGYMLKLLENPFLOMOREYPILPENELSENGGESERONLITMED TEVEROGULERAPKTINERRIGGTVELPRESIGEGESGGEFADCER TEVEROGULERAPKTINERRIGGTVELPRESIGEGESGGEFADCER FARRODVILSGWINDFULGUTUDELKTPGELGKRINGGIACH WASSIGSLEPHINDFULGUTUDELKTPGERLIGHTKTAFHHERD WIKKCINIWRDVGLIGVILBELANSEERVFERWKTASGNALLACK WASSIGSLEPHINDFULGUTUDELKTPGERDIGHTKTAFHHERD WIKKCINIWRDVGLIGVILBELANSEERVFEWKYTASGNALLACK WASSIGSLEPHINDFULGUTUDELKTPGERGUTVILBH ROVERDOWNERGENTENSGGAOUSHEGTTPVENGTHCH WASSIGSLEPHINDFULGUTUDELKTPGERGUTVILBH ROVERDOWNERGENTENSGGAOUSHEGTTPVENGTHCH ROVERDOWNERGENTIPWSGTPVENGWLCL ROVERDOWNERGENTENSGCAOUSHEGTTPVENGTHCH ROVERDOWNERGENTENSGCAOUSHEGTTPVENGTHCH ROVERDOWNERGENTENSGCAOUSHEGTTPVENGTHCH ROVERDOWNERGENTENSGCAOUSHEGTTPVENGTHCH ROVERDOWNERGENTENSGCAOUSHEGTTPVENGTHCH ROVERDOWNERGENTENSGCAOUSHEGTTPVENGTHCH ROVERDOWNERGENTENSGCAOUSHEGTTPVENGTHCH ROVERDOWNERGENTENSGCAOUSHEGTTPVENGTHCH ROVERDOWNERGENTENSGCAOUSHEGTTPVENGTHCH ROVERDOWNERGENTENSGCAOUSHEGTTPVENGTHCH ROVERDOWNERGENTENSGCAOUSHEGTTPVENGTHCH ROVERDOWNERGENTENSCUNCTORNUMBER RO			}	FSKKKPHASVGTHGYMAPEVLOKGTAYDSSADWFSLGCMLFKLL
QRPVSKRIGCHEGGSGEVERISFFKSUDWOHYTLGXYPPPLIJEERY RGWANADAPDTOSPEDETTISKILLDCODELYKRIPPLIJEERY QOEVTETVYEAVAADTOK I PARKAANNGLIGHEEDYALGKOUT HGWALKLIN PITLONGER YTLEPRILENGEGGERANLITUME LISVEETOJIKOKSCILERI KIGKGOPULOCESDPEPVOMKKELME TYEKEAORILLERA PKIKINKPRGRUTULER PETELGRINGTATAPHHEED FARRODVISGWILLIFULGULTKOLKT PERCILIORISKIN TYEKEAORILLERA PKIKINKPRGRUTUKOLKTOPIKTYPHHEED PARRODVISGWILLIFULGULTKOLKT PERCILIORISKINT PHHEED WARKCININKBUUGULTKOLKT PERCILIORISKAT PHHEED VIKRCININKBUUGULTKOLKT PERCILIORISKAT PHHEED WARSCRILGASPONALIKUM PROBLINGTATAPHHEED WARSCRILGASPONALIKUM PROBLINGTATAPHHEED WARSCRILGASPONALIKUM PROGRUTUKOH PHEED GRILLETVILGEPLUSISJPPREGEGKGA LAEVOSOGRIMOIT CL RQOYRHOWRRGLGERITYMSOTTVCHWINTEGGVITILLM SPOOSILLATTPSAVFKVWEAQMWITCERWITISGRCQTGCOSP) GRILLETVILGEPLUSISJPPREGEGKGA LAEVOSOGRIMOIT CL RQOYRHOWRRGLGERITYMSOTTVCHWINTCL SPOOSILLATTPSAVFKVWEAQMWITCERWITISGRCQTGCOSP) GRILLETVILGEPLUSISJPPREGEGKGA LAEVOSOGRIMOIT CL RQOYRHOWRRGLGERITYMSOTTVCHWINTCL SPOOSILLATTPSAVFKVWEAQMWITCERWITISGRCQTGCOSP) GRILLETVILGEPLUSISJSPREGEGKGA LAEVOSOGRIMOIT CL RQOYRHOWRRGLGERITYMSOTTVCHWINTCL SPOOSILLATTPSAVFKVWEAQMWITCERWITISGRCQTGCOSP) GRILLETVILGEPLUSISJSPREGEGKGA LAEVOSOGRIMOIT CL RQOYRHOWRRGLGERITYMSOTTVCHWINTCL SPOOSILLATOSSE SAUDUTSSISSPREGEKGA LAEVOSOGRIMOIT CL RQOYRHOWRRGLGERITYMSOTTVCHWINTCH CHAVORET LAEVO SPOOSILLATOSSE SAUDUTSSISSPREGEKGA LAEVOSOGRIMOIT CL RQOYRHOWRRGLGERITYMSOTTVCHWORT STANDALFKSSIST CL SPOOSILLATOSSE SAUDUTSSISSPREGEKGA LAEVOSOGRIMOIT CL RQOYRHOWRRGLGERITYMSOTTVCHWORT STANDALFKSSIT CHAV AYSOSOEMULASALOS SUUDUVAVILKSVA PROPORTULVK ELIFDAIGRYYSERSPILLAHLIDUHMOIT LAELUNGKTETALEAT QLLIKLLINGTONGEN SAUDUKSSISTANDALFKSKATATAPOUT UNKERDEN NITAVA RISKALUNGAS SAUDUKSSISTANDALTICAR CL RUMANTYKULUKANAAN SAUDUKSSISTANDALT			1	PGUSDEPOUKTKDKHEIDPMTI.TVNVEI.PDTFSPELKSLLEGLL
RGEVNAADAPDIGSEDEEDTKGIKLICOQELYKNIPPLVISEKN QGEVTETVYEAVABOTIKELEAKRANKKQLEREDVALJGNCIM HGYMLKIGNPFITQNQRYFYLPORILERGEGESQNILMMG LEVERTQIKKKKCLIPRIKGEGESQNILMMG TYKEAQRILRRAPKITAHKPESGTVELEKGELGESGGEFADORR TYKEAQRILRRAPKITAHKPESGTVELEKGELGESGGEFADORR TYKEAQRILRRAPKITAHKPESGTVELEKGELGESGGEFADORR PANRODVLSGMINLFVLQUIKUPLKTPGRLDHGTRTAPIHHREQ WKRCINIWROVLISGMINLFVLQUIKUPLKTPGRLDHGTRTAPIHHREQ WKRCINIWROVLISGMINLFVLQUIKUPLKTPGRLDHGTRTAPIHHREQ WKRCINIWROVLISGMINLFVLQUIKUPLKTPGRLDHGTRTAPIHHREQ WKRCINIWROVLISGMINLFVLQUIKUPLKTPGRLDHGTRTAPIHHREQ WKRCINIWROVLISGMINLFVLQUIKUPLAPQRUDHGTRTAPIHHREQ WKRCINIWROVLISGMINLFVLQUIKUPLAPQLOHGTRTAPIHHREQ WKRCINIWROVLISGMINLFVLQUIKUPLAPQLOHGTRTAPIHHREQ WKRCINIWROVLISGMINLFVLQUIKUPLAPQLOHGTRAPIHHREQ WKRCINIWROVLISGMINLFVLQUIKUPLAPQLOHGTRAPIHHREQ WKRCINIWROVLISGMINLFVLQUIKUPLAPQLOHGTRAPIHHREQ WKRCINIWROVLISGMINLFVLQUIKUPLAPQLOHGTAPIHHREQ WKRCINIWROVLISGMINLFVLQUIKUPLAPQLOHGTAPHHREQ WKRCINIWROVLISGMINLFVLQUIKUPLAPQLOHGTAPIHHREQ WKRCINIWROVLISGMINLFVLQUIKUPLAPQLOHGTAPHHREQ GGUNALPTURGUIKUPLAPQLOHGTAPIHHREQ 5955 1705 139 GUGUGGARAMATVOGELGAAINILSAHSPARRPOFSVAGKEPA GUGUGGARAMATVOGELGAAINILSAHSPARRPOFSVAGKEPA GUGUGGARAMATVOGUBGARVEKTEPARRAPIKVOGESAVOUTSHIL LQINUDPLIDSILKQGAVEKTEQERKQSTWINSSNILDARIS SASIEDLEMBINSKAPANSPINNISTISPOVINSSNILDARIS SASIEDLEMBINSKAPANSPINNISTISPOVINSSNILDARIS BARIEDLEMBINSKAPANSPINNISTISPOVINSSNILDARIS GULLKLLIDGARSPINNISSNINNISTISPOVINSSNINTENTTORI GULLKLLIDGARSPINNISSNINNISTISPOVINSENTITABEAT GULLKLLITADEDSKLSAKKKINLLOFINNISTISPOVINSENTITABEAT GULLKLLITADEDSKLSAKKKINLLOFINNISTISPOVINSENTITABIT SKKSDCSLEMGSSHINKGFRINNINGERMINERTITAPINISTISPOVINSENTITABIT SKKSDCSLEMGSSHINKGFRINNINGERMINISTISPOVINSENTITABIT SKKSDCSLEMGSSHINKGFRINNINGERMINISTISPOTITISPOM SKKSDCSLEMGSSHINGENNINGERMINISTISPOMINERTITATISPOM SKKSDCSLEMGSSHINGENNINGERMINISTISPOMINERTITATISPOM SKKSDCSLEMGSSHINGENINGERMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINISTISPOMINIST		· I	1	OPPICE TO CONCOCCO OF VEHICLE AND MOHAMI OKABBBI TED
GORVETTUVEAVNADTIDKIEARKRAINKKOLGREEDVALDCEN HGYMLKIANPI-PORQORPTY-PIPPRIEBREGGESRONLITMES LISVERTOIKOKKCILERI KGGKOPVLOCESDPEFVOMKKELEN TYKKAORLIRARA KYLIAKPESTVEDENSELGENENSINGI KREREFRLAVCPLRYSAYESSEGTELREGGLCRSGGERADCRR PANRODVLSGMINLEVULGUTKOPLKTPGRÜCHSTRATBIHHER WARSCHLESSLIPHISLRSEDLILAEFAQVTINISSCCLEVFAMIEHT NKERVALLEDDSVLYVANSSTIVESLKHRUCHNSALAMKPLSAS VLAVACOSCILINTLEDTSLSTRESSGCAQVLSHPGHTYVTSLA WAPSGRILGASPVDAARTWUDSVITMOSTETOVELWERGGGVTALLM WAPSGRILGASPVDAARTWUDSVITMOSTETOVELWERGGGVTALLM WAPSGRILGASPVDAARTWUDSVITMOSTETOVELWERGGGVTALLM WAPSGRILGASPVDAARTWUDSVITMOSTETOVELWERGGGVTALLM WAPSGRILGASPVDAARTWUDSVITMOSTETOVELWERGGGVTALLM WAPSGRILGASPVDAARTWUDSVITMOSTETOVELWERGGGVTALLM WAPSGRILGASPVDAARTWUDSVITMOSTETOVELWERGGSVITMOST GORVENOWURGGGERLIPHSGTPGGWWALCL ROOYNOWREGGGERLIPHSGTPGGWWALCL ROOYNOWREGGGERLIPHSGTPGGWWALCL ROOYNOWREGGGERLIPHSGTPGGWWALCL ROOYNOWREGGREENTINOSCORGENENTSTANADALFKSDIR SASLEDLWENISLKANADSPIVMISATLSPQVINGSWREYDER LQUINDPLIBLISHLOVENGERENTSPORTAVADALFKSDIR SASLEDLWENISLKANADSPIVMISATLSPQVINGSWRETHER LQUINDPLIBLISHKOPANYETGPRKOGENVINSSNYLDRGILK AYSDSGDEBWISAAIDCSBVINGPRKINGPRAVADALFKSDIR SASLEDLWENISLKORADSVRIPGPRKOGENVINSSNYLDRGILK AYSDSGDEBWISAAIDCSBVINGPRAVADALFKSDIR SASLEDLWENISLKORADSVRIPGPRKOGENVINSSNYLDRGILK VS\VK\LMALONGRDPREDAGVIYCHDRUDSWNTEKTTEDE LLIALLATIODSSKIARKKK\LLDGPVKCHTDGTLJWKITTEDE SVS\VK\LMALONGRDPREDAGVIYCHDDIPSKNINTEKTTEDE LLIALLATIODSSKIARKKK\LLDGPVKCHTDGTTLJWKITTEDE SKAIVNINGKCEGGTRAMITTERDER SKASCSLEMFGSINKKERPINLIGENTYMUMINISLIGIENFF SKKASCSLEMFGSINKKERPINLIGENTYMUMINISLIGIENFF SKKASCSLEMFGSINKKERPINLIGENTYMUMINISLIGIENFF SKKASCSLEMFGSINKKERPINLIGENTYMUMINISLIGIENFF SKKASCSLEMFGSINKKERPINLIGENTYMUMINISLIGIENFF SKKASCSLEMFGSINKKERNINGUTERTYMUMINISLIGIENFF SKKASCSLEMFGSINKKERNINGUTERTYMUMINISLIGIENFF SKKASCSLEMFGSINKKERNINGUTERTYMUMINISLIGIENFF SKKASCSLEMFGSINKKERNINGUTERTYMUMINISLIGIENFF SKKASCSLEMFGSINKKERNINGUTERTYMUMINISLIGIENFF SKKASCSLEMFGSINKKERNINGUTERTYMUMINISLIGIENFF SKRATURDGRANGGVTANASCHAR LEEMFSSLOWENSTANGUTERTYMUMINISLIGHTENFF SKRATURDGRANGGVTAN	ļ			OKDVSKIGCRGGSQEVKERSTYKGVDWQRVIEQXXXXX
HGYMLKLONPFILTONORRYFYLFPRILEBRGGGGSROLLTMGO ILSVERTGILKOKCLIPRI KGGKOPVIQCESSDEPFVQMKKSLME TPKEAGRILRRAPKITAKTPRSGTVELPRSLCHRNENGI TPKEAGRILRRAPKITAKTPRSGTVELPRSLCHSGGGFADCRE PARRODVISGMINLEVIQUIKDPLKTPGRLDHGTRTAPIHHRQ WKRCINIWROVLISGMINLEVIQUIKDPLKTPGRLDHGTRTAPIHHRQ WKRCINIWROVLISGMINLEVIQUIKDPLKTPGRLDHGTRTAPIHHRQ WKRCINIWROVLISGMINLEVIQUIKDPLKTPGRLDHGTRTAPIHHRQ WKRCINIWROVLISGMINLEVIQUIKDPLKTPGRLDHGTRTAPIHHRQ WKRCINIWROVLISGMINLEVIQUIKDPLKTPGRLDHGTRTAPIHHRQ WKRCINIWROVLISGMINLEVIQUIKDPLKTPGRLDHGTRTAPIHHRQ WKRCINIWROVLISGMINLEVIQUIKDPLKTPGRLDHGTRTAPIHHRQ WKRCINIWROVLISGMINLEVIGUIKDPLKTPGRLDHGTRTAPIHHRQ WKRCINIWROVLISGMINLEVIGUIKDPLKTPGRLDHGTRTAPIHHRQ WKRCINIWROVLISGMINLEVIGUIKDPLKTPGRLDHGTRTAPIHHRQ WKRCINIWROVLISGMINLEVIGUIKDPLKTPGRLDHGTVSTLAW WKRAVALLDDSVLYNASSTIVSLKAWASSTIVSLKAWASSTIVSGRCTGCKSPD GSRLLFTVIGEPLIYSLSFPERCGEGGKIALBYGGCTGCKSPD GSRLLFTVIGEPLIYSLSFPERCGEGGKIALBYGGCTGCKSPD GSRLLFTVIGEPLIYSLSFPERCGEGGAVALBYGGCTGCKSPD GSRLLFTVIGEPLIYSLSFPERCGEGGAVALBYGGCTGCKSPD GSRLLFTVIGEPLIYSLSFPERCHSTRAPICHTSGRCTGCTGCKSPD GSRLLFTVIGGPLIYSLSFPTOWNENGLIKSPORTYCKPGGEAVOYLTSH SPOSSELLFTVIGGSLKKRKKKLKSHRAPICHTGGEAVAYDTKYGGDKKPT FEDSSCSLYRFTTIPNGDSGLGKENKLYSPAYADALFTKSDIR LQLIVATGOPLEVIKARTATION TORMANSTYLLDATI LQLIVATDPLLDSLLKXQGCAVPKIPQFRQGSTWINSSNLYDGGILK AYSDSQBEWLSAAIDCSFYLPQAWASSNLORGILKA KAYSDSQBEWLSAAIDCSFYLPQAWASSNLORGILKA KAYSDSQBEWLSAAIDCSFYLPQAWASSNLORGILKAWAVK RIFSKAIVUNNINSKCKPORTULFI,MONDKYWKIPGFPLOPTBLKTTRDB LLLLLKTLDEDSKISAKKKKK,LLGQFYCHPOFTSHRWOK KIPSKAIVUNNINSKCKPORTULFI,MONDKYWKIPFFTTRDB LLLLKTLDEDSKLSAKKKKK,LLGQFYCHPOFTSHRMLIK GGRANATYTKVLKOVALKKYRVAVLYKKKITPFFEDDTSLEFF SKKSDCSLFFFGSSHNKKRPNILVIGRFBCYNAUSKKNILIGHTFY SKKSDCSLFFFGSSHNKKRPNILVIGRFBCYNAUSKKNILIGHTFY SKKSDCSLFFFGSSHNKKRPNILVIGRFBCYNAUSKRNILIGHTFY SKKSDCSLFFFGSSHNKKRPNILVIGRFBCYGGAVAGASFFGTSLGQ PTVNNIRLGLGSVALFFFGSSHNKAFFFSNIRFSKLILDFFFGG ARTAFTVARTHAPFFGSCAVATAFFFSTENCONADD EGGGYCGAFFSLDFYNGDLIVGGAAYYCDWPAGGSACCOPP TYTTON RKIRGRGTGTAAAFFSTENCAAAFFSCGAVAAFFTSTVV VSDNASBGLDDUTUNGAAFFTSSCGGAAFFTGSGG GLUYDGGAFFACKO GRATIAFTCAATA		1	1	RGEVNAADAFDIGSFDEEDIRGIRDDCDQEBIRGFFBVISEON
TLEVERTQIKOKKCLIERIKGGKPIJGCESDPEFFOWKREALER TPERAGRILIARA KEIAKRPSATVELKPESLICHINSINGI KREEFFILAVCIPARYESYESSEGTELREGGCSGGERACORR PANRQDVLGWINLEVLQLIKDGLIKDGLIKGGERACOR PANRQDVLGWINLEVLQLIKDGLIKDGLIKTGGLINGTAPIHIREG VWRCINIXMEDVGLIGVIRIA IANSEEVPEWVKTASGARLALCR WASSLHESSLFFHISIRESGLILERAQVTWNSSCLRVPAWHHHI NKRAVALLIDDSVAVINASSTIVPSIGHTIQTAVSIAMURPILSAS VLAVACOSCILIWILDFTSISTRESGCAQVLSHPGHTYVTIA WASSCHESSPVDARIRVWDSTETCVPLEWRGGGVTALLM SPOGSKILASPPOARIRVWDSTETCVPLEWRGGGVTALLM SPOGSKILATTJSAVFRWBRAMWTCERWFTISGRCTICKSPD GSRLLFTVLGEPLIVISLSFFERGEGGKGVALUSTGCH ROQYRAMPATGEGARINIALMISABLEPDGFSVAQKPGA TYWSSINTLQTQVEVKKRRHLKRHNDCFVGSEADQUIPSHL IQNKYRGOVDIPRAKVVRCQALMDYKVPEAVPTVVGKDKKPT FEDSSCSLYRTTIONQDSGLGKERKLYSFAYADALFKSDDIR SASLEDLWENISIKRANDSFYNNISATISPQVINEVMGESTIGRL LQLVDLPLLDSLIKQQEAVPKTGPRGGTWNSNNILDRGILK AYSDSQEDEWISAAIDCSBYLPDQWVEISRSFPEQDPTLUK ELLEDAIGRYYSSREPLINISISVENGIARLUNGKVETALEAT OLLLKLIDDGNREFFRILYFMAVAANDSSFYLQKESDNRWVK RIFSKAITUNNINSKKTDLAVFLOYBYKGRKKLYSESTRITUNGKVETALEAT COLLIKILDEGONREFFRILYFMAVAANDSSFYLQKESDNRWVK RIFSKAITUNNINSKKTDLAVFLOYBYKGRKKTERETTLDE TEFKAITUNNINSKKTDLAVFLOYBOKKKKISTDTISHED SKKOKSKCPGTYRMLIFAGDDFOVTEDYRRIKSLILDFFRG PTVSNIRLAGGEVYLFFTANKGIYFRYKLIKKRSCEDTAPI SKKOCSLERWGSHNKKYFNILVIGKNYDVHILMISLIGIBNFY SKKSCSLERWGSHNKKYFNILVIGKNYDVHILMISLIGIBNFY SKKSCSLERWGSHYNKEFNILVIGKNYDVHILMISLIGIBNFY SKKSCSLERWGSHYNKEFNILVIGKNYDVHILMISLIGIBNFY SKKSCSCSLERWGSHYNKEFNIKKYFNILVIKKRSCETPFLE LEEMGPSLDLVLRRTHLASDDLVKLSKMMKALKPKKKKNISHD TETTYGRITHMOKOLDIKTGNYDVHILMISLICIBPG PTVSNIRLAGGSTYADGARASFYDGSTAVALHKSSCGVAD PTTNIRKIRVNGTKEPIERGSMAAHGDLINKGYFRABRITEDBEKKS KRIKKKIMSLOOPLLFHCULKRITIKHGSIOGSFI GGGGCCAGFSLDFYNKOLLVGRAYNGKYRARBRITODBGCAGSTYCTAVTOV VSDNABGGLDDVILVARPLIKREFESNNEGSFYGAVDFHIPD TRINKRIRVNGTKEPIERGSAMAHGDLINKGSFTFREGGVANALDIA NYSFOLLKKLAGGKTGVARASFYDSVAAGGFTODSQ ELVAGIPROGADGAVYSIINSTDMTTIQNFGGOASTYTTVV VSDNABGGLDDVILVARPLEMREFESNNEGSFOFFTLAGG SLIKAGIIKGTHFFREGONGATHARGENTENTINGTORGOTASTYTTVV VSDNABGGLDDVILVARATHERFFESNNEGSFOFFTLAGG GGGCKILTYRGKKKARATSQBSTYKKGGGTATHTVILMSVLD AAALGMLLT	ļ	ŀ	ļ	QQEVTETVYEAVNADTDKIEARKRAKNKQLGHEEDYALGKDCIM
TEKEAGRILERAPKTINKPRGGTVELPKPS-LICHENSOLS 1726 444 KREEFFILAVCPLRYPSASTSOFTILEKEGLICRSGOBFACER PANRQDVLSGWINLPVLQLITXDPLKTPGRLDHGTRTAPHHREO VWKRCINIWRDVGLFGVLINTLDPTLANSEBEVFEWVTAASGWALALCR WASSLHGSLFPHJSIRSEDLIAFFAQVTNWSSCCLRVPAWHPHT NKRAVALLDDSVRVYRASSTIVESLEHRLQRNVASLAKFLSAS VLAVACQSCILIWTLDPTSLSTPRSSGCAQVLSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRVHDVSTETCVFLPPWFRGGGVTLLIW SPDGSKILATTYGAPTHVSGTPVGNWERPTLSGRCQTGCMSPD GSRLLFTVLGPBLIYSLSFPERCGEKGVALEVQSQQRLWQICL RQQYENGWVRRCLGERLTPWSGTPVGNWERPTLSGRCQTGCMSPD GSRLJFTVLGBPLIYSLSFPERCGEKGVALEVQSQQRLWQICL RQQYENGWVRRCLGERLTPWSGTPVGNWERPTLSGRCQTGCMSPD GSRLJFTVLGBPLIYSLSFPERCGEKGVALEVQSQRLWQICL RQQYENGWVRRCLGERLTPWSGTPVGNWINDVFNGLGL IQNKYGDDVBTPAKVVRVCQALMVKVPCVEAVFXVPGKQDKFP FDDSSCSLVRFTTIPNQDSQLGKERKLYSPARVADALFKSBDIR SASLEDLWRINSLSKPANSPFVNIFATLSSFPEQDFWTCHKY FDDSSCSLVRFTTIPNQDSQLGKERKLYSPARVADALFKSBDIR SASLEDLWRINSLSKPANSPFPUNIFATLSSFPEQDFWTCHLVK AYSDSQDBEMJSAIPLOSRFPDMVNSTATLDRVVNGWETTGRL LQLVDLPLIBLISLLKQQEAVPKIFQFRRQSTWVNSSNYLDRGILK AYSDSGDBEMJSAIPLOSRFPLDMVNSTATLDRVNGVWGETTGRL LQLVDLPLBLISLLKQQEAVPKIFQFRRQSTWOMSPRTLAKEND CLLKLLKTLDEDSKLSAREKKYLLGGGFYKGFEQKTBPLIKKT RIFKATVONKNLSKGKTDLLVJELVMBQKDVFKFRTETALBAT QLLKLKLLDFQURBFFRRLLYFMAVAANPSEPKLEKSEDLIDHAV RLHLLKLLDFQURBFFRRLLYFMAVAANPSEPKLEKSLEIDDFRG SKSGCSLPFMGSSHNKKRPNNIVJGRNYDYHVLIMITRFEDFOTSLEFF SKSGCSLPFMGSSHNKKRPNNIVJGRNYDYHVLIMITRFEDFOTSLEFF SKSGCSLPFMGSSHNKKRFNNIVJGRNYDYHVLIMITRFEDFOTSLEFF SKSGCSLPFMGSSHNKKRFNNIVJGRNYDYHVLIMITRFEDFOTSLEFF SKSGCSLPFMGSSHNKKRFNNIVJGRNYDYHVLIMITRFEDFOTSLEFF SKSGCSLPFMGSSHNKKRFNNIVJGRNYDYHVLIMITRFEDFOTSLEFF SKSGCSLPFMGSSHNKKRFNNIVJGRNYDYHVLIMITRFEDFOTSLEFF SKSGCSLPFMGSSHNKKRFNNIVJGRNYDYHVLIMITRFEDFOTSLEFF SKSGCSLLFFMGSSHNKKRFNNIVJGRNYDYHVLIMITRFEDFOTSLEFF SKSGDSLDVARRTHLASGDLYTGRNYKALKSLGJURFFRF SKSGCSLCAGARASLFVMIRPFRCAGAFYTOSPQV SKLGKLITHMORDGLIKKKFYGLVKKKRKARFKKRKNISHD LENKRLMBLSGPLIFFTGLIKRGGLTGFGSFTWQQVYTTAVADITLA NTSFEDILERHMSGTAFSLFTANSAGPTTTVV VSDVNSGGLAGLTAFVAGALFAVADASDOSTLITAVADATLA NGGGGAVEAUFFREFFESFRAGFFILKGRAFAVADOSTLITAVRANTENTYBE GEGGYCQAGFSLIDPTNGGLIVGGRGFTWQQQVTL	Į.		1	HGYMLKLGNPFLTQWQRRYFYLFPNRLEWRGEGESRQNLLTMEQ
S955 1726	1			ILSVEETQIKDKKCILFRIKGGKQFVLQCESDPEFVQWKKELNE
PANRODVLSGHINLPULGITTOPELHTTGRELDHGTTRATHERS VWRCITIN MEROVALGOURIANS CLEAVERMIPHT NKRAVALLDSVRVYNASSTIVPSLKHRLQRIVASLAKELSAS VLAVACQSCILIWTLDPTSLSTRPSSGCAQULSHPGHTPVTSLA WASSIGRILGS.SPVDAIRWIDDTSLTTDPLPWFRGGYTNLIW SPOSKILATTPSAVSTWEAQAWITCERKPTLISGRCYTGCWSPD GSRILLFTVLGEPLIYSLSFPSRCGECKG\ALEVQSQQRLWQICL RQQYRHQWRMCGLGERLIPWSGTPVGNWLCL SOUGYGRARMATVQGEKAAALNISALUSPAHPDFFSSVAQKFGA TYVWSSINTLQTQVEVKKRRHLKHNDVGSAVDYLFSHL IQNKYRGDVDIPRAKVVRUCQAMDYKVPEAVPTKVPGKDKKPT FEDSSCSLYRFTTIPRQDSQLGKENKLYSPARYADALKSDIR SASLEDLWRHISLSKPANSPHVISATLSSQVINEVVQEEAVDVISHL LQLVDLPLLDSLLKQOEAVPKIPQPKRQSTWNSSYNJURGILK AYSDSQBEBUSAAAIOSSKIPDQMVVETSRSFFEQPDRTDLVK BLLEDAIGRYYSSREPLANHLSDVHNIATLSSGPTONLYKSDIR GLUKLLDFQNEEFFRELLYFMAVAANDEKKSENTRAVK RIFSKALVUNKNISKSKTDLLVLFL\MDHQKOVFKTPATLAKKTVD LANLKTLDEDSKLSAKEKKK\LLGQPYKCHPDIFIEHEGD 5957 1479 451 ELQVAVMDTLDRVVKKKTKRAKRFLEKREPKLNENIKTAKTLDE LELMLKTLDEDSKLSAKEKKK\LLGQPYKCHPDIFIEHEGD 5958 1 3138 ANGKLENFRUKKRYBOLVYKKKYFYGLVKKKLKKRKKTKSTEDDSLEFF SKKSDCSLEPMGSSHNKKRPNNIVTGRNYDYHVLDMIELGIRNFV SLKDIKNSKCPPGTYRMLIFADDDFVTSRKKKSLLDFFKG PTVSNIRLAGLEVVLHFTALNCKTYFSVKLLLKRSGCTPRE LEEMGPSLDLVLRRTHLASDDLYKLSKKLDFFKKKSLLDFFKG PTVSNIRLAGLEVVLHFTALNCKTYFSVKLLLKKSGCTPRE LEEMGPSLDLVLRRTHLASDDLYKLSKKRPSRITTEDHEKKS KRIKKLMBLSQPLIFFCULLKRIIKFGBLSGLDFFK RIKKKLMBLSQPLIFFCULLKRIIKFGBLSGCFTPTED DTTNNRKRIKMPFACQAFFLOWEKLTYTSFSKGSYFGYAVDFHIPD ARTASVLVGAFKANTSOPDIVEGGAVYCPWBERGSAGCQIPF DTTNNRKRIKMMELSQPLIFFCULLKRIIKFGSLGSTFRISD ELVAGIPRGAQNFGVYSIINSTDMTFIQHFTSVAADLIA NYSFEDLIRAHMSCADSFLYPREFESSPREVGGYTILLOVSSLL FRDPQILTGTETTGFFGSMAHLGBLNQOGYNDIAGPPGAKG QRGKVLITNONKDGLINTKPPFKCGGYMAAHAVGSGCGPUAP ELVAGIPRGAQNFGVYSIINSTDMTFIQHFTSVAADLIA NISSEDLIRAHGSRACHEVPBFFKCGGWAAHAVPGGFGFFLIRGD SDIDKNDYPDLIVGAFGTGVAAVRAAPROGGFPTLICD SDIDKNDYPDLIVGAFGTGVAAVRAAPROGGFFTLRGD SDIDKNDYPDLIVGAFGTGVAAVRAAPROGGFPTLICD SLKGGGATKALFWHPEREFESSPREVGQTYTLTLOVSSLL FRDPQILTGTGTFTGRFGSMAHLGBLNQOGYNDIALHPMTENTSD GEGGATEARLFWHIPEERDYGGIFRNKKFRINGTHRINGTRENTSCHLOLL ETEPROKLSPINGSDNINGTGRAAFAVDIGERNMANGFPT				TFKEAQRLLRRAPKFLNKPRSGTVELPKPSLCHRNSNGL
PANRODVLSGHINLPULGITTOPELHTTGRELDHGTTRATHERS VWRCITIN MEROVALGOURIANS CLEAVERMIPHT NKRAVALLDSVRVYNASSTIVPSLKHRLQRIVASLAKELSAS VLAVACQSCILIWTLDPTSLSTRPSSGCAQULSHPGHTPVTSLA WASSIGRILGS.SPVDAIRWIDDTSLTTDPLPWFRGGYTNLIW SPOSKILATTPSAVSTWEAQAWITCERKPTLISGRCYTGCWSPD GSRILLFTVLGEPLIYSLSFPSRCGECKG\ALEVQSQQRLWQICL RQQYRHQWRMCGLGERLIPWSGTPVGNWLCL SOUGYGRARMATVQGEKAAALNISALUSPAHPDFFSSVAQKFGA TYVWSSINTLQTQVEVKKRRHLKHNDVGSAVDYLFSHL IQNKYRGDVDIPRAKVVRUCQAMDYKVPEAVPTKVPGKDKKPT FEDSSCSLYRFTTIPRQDSQLGKENKLYSPARYADALKSDIR SASLEDLWRHISLSKPANSPHVISATLSSQVINEVVQEEAVDVISHL LQLVDLPLLDSLLKQOEAVPKIPQPKRQSTWNSSYNJURGILK AYSDSQBEBUSAAAIOSSKIPDQMVVETSRSFFEQPDRTDLVK BLLEDAIGRYYSSREPLANHLSDVHNIATLSSGPTONLYKSDIR GLUKLLDFQNEEFFRELLYFMAVAANDEKKSENTRAVK RIFSKALVUNKNISKSKTDLLVLFL\MDHQKOVFKTPATLAKKTVD LANLKTLDEDSKLSAKEKKK\LLGQPYKCHPDIFIEHEGD 5957 1479 451 ELQVAVMDTLDRVVKKKTKRAKRFLEKREPKLNENIKTAKTLDE LELMLKTLDEDSKLSAKEKKK\LLGQPYKCHPDIFIEHEGD 5958 1 3138 ANGKLENFRUKKRYBOLVYKKKYFYGLVKKKLKKRKKTKSTEDDSLEFF SKKSDCSLEPMGSSHNKKRPNNIVTGRNYDYHVLDMIELGIRNFV SLKDIKNSKCPPGTYRMLIFADDDFVTSRKKKSLLDFFKG PTVSNIRLAGLEVVLHFTALNCKTYFSVKLLLKRSGCTPRE LEEMGPSLDLVLRRTHLASDDLYKLSKKLDFFKKKSLLDFFKG PTVSNIRLAGLEVVLHFTALNCKTYFSVKLLLKKSGCTPRE LEEMGPSLDLVLRRTHLASDDLYKLSKKRPSRITTEDHEKKS KRIKKLMBLSQPLIFFCULLKRIIKFGBLSGLDFFK RIKKKLMBLSQPLIFFCULLKRIIKFGBLSGCFTPTED DTTNNRKRIKMPFACQAFFLOWEKLTYTSFSKGSYFGYAVDFHIPD ARTASVLVGAFKANTSOPDIVEGGAVYCPWBERGSAGCQIPF DTTNNRKRIKMMELSQPLIFFCULLKRIIKFGSLGSTFRISD ELVAGIPRGAQNFGVYSIINSTDMTFIQHFTSVAADLIA NYSFEDLIRAHMSCADSFLYPREFESSPREVGGYTILLOVSSLL FRDPQILTGTETTGFFGSMAHLGBLNQOGYNDIAGPPGAKG QRGKVLITNONKDGLINTKPPFKCGGYMAAHAVGSGCGPUAP ELVAGIPRGAQNFGVYSIINSTDMTFIQHFTSVAADLIA NISSEDLIRAHGSRACHEVPBFFKCGGWAAHAVPGGFGFFLIRGD SDIDKNDYPDLIVGAFGTGVAAVRAAPROGGFPTLICD SDIDKNDYPDLIVGAFGTGVAAVRAAPROGGFFTLRGD SDIDKNDYPDLIVGAFGTGVAAVRAAPROGGFPTLICD SLKGGGATKALFWHPEREFESSPREVGQTYTLTLOVSSLL FRDPQILTGTGTFTGRFGSMAHLGBLNQOGYNDIALHPMTENTSD GEGGATEARLFWHIPEERDYGGIFRNKKFRINGTHRINGTRENTSCHLOLL ETEPROKLSPINGSDNINGTGRAAFAVDIGERNMANGFPT	5955	1726	444	KREREFRLAVCPLRYPSAYESSPGTELRECGLCRSGQEFADCRR
WERCINTARDUGLIGULEIANSEEVFEWURTSGRALALCER WASSLIGSI-PPHLSIRSEEDLLAERAOVTNNSSCILVVRASGRALALCER WASSLIGSI-PPHLSIRSEEDLLAERAOVTNNSSCILVVRAMPHT NKFAVALLDDSVRVYNNSSTIVESLKHRLQRNVASLAKKPLSAS VLAVACQSCILUMILDFISLSTRPSGGCAQVLSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRVNDVSTETVVFLEWFR8GGVTNLLW SPDOSKILATTPSAVFRVWEAQMWTCERWFILSGRCQTGCMSPD GSRLLFTVLGBFLIVSISFPERCEGEKS(ALEVGSQGNAGICL RQQYRHQMVRRGLGERLTPWSGTPYGWWLCL RQQYRHQMVRRGLGERLTPWSGTPYGWWLCL RQQYRHQMVRRGLGERLTPWSGTPYGWWLCL RQQYRHQMVRRGLGERLTPWSGTPYGWWLCL RQQYRHQMVRRGLGERLTPWSGTPYGWWLCL LQUADLPHOSGLGKERKLYSPARVADALFKSSDIR SASLEDLWENLSLKFANSPHVNISATLSPQVINEWQEETIGRL LQUADLPLLISLIKQRGAVKTPGVENWSSNYLDRGILK AYSDSQEDEMLSAAIDCSEVLPDQWVWEISRSPEPGPDRTDLVK ELLDAIGRYYSREPLLINHLSDVHNGIARLLUNGKTETALEAT QLLKKLLDFQNREEFRRLLYFMAVAAMPSEFKLQKESDNRWVK RIFSKATVDNKHLSKGKTDLLUFF, WHORQWFKIPGTLYHRI VS\VK\LMAIQWGRDPROBAYYYCGTDGRDSNNTERTTKDB LLNLKTLDEDSKLSAKEKK, LLCQFYKCHPDIFIEHEGD SKKSDCSLFWFGSHKKRFFNLVIGRMYDYRLDGHIELGIENFV SKKSDCSLFWFGSHKKRFFNLVIGRMYDYRLDGHIELGIENFV SKKSDCSLFWFGSHKKRFFNLVIGRMYDYRLDGLIELGIENFV SKKSDCSLFWFGSHKKRFFNLVIGRMYDYRLDMIELGIENFV SKKSDCSLFWFGSHKKRFFNLVIGRMYDYRLDMIELGIENFV SLKDIKKNSCPBGTTPWLIFAGDDLYKLSKAGCCTPRIE LEEMOPSDLUVLRFTHLASDDLYKLSKMPKALKPKKKKISHD TFGTTYGRIHMKRQDLSKLGTRMKJRKLKFRGCCTPRIE LEEMOPSDLUVLRFTHLASDDLYKLSKMPKALKPKKKNISHD TFGTTYGRIHMKRQDLSKLGTRMKJRKLKFRGCCTPRIE LEEMOPSDLUVLRFTHLASDDLYKLSKMPKALKPKKKKISHD TFGTTYGRIHMKRQDLSKLGTRMKJRKLKFRGGCTPRIE DTTNNRKIRVINGTKB IEFKSNOWGA'ATVVAHKKKSGCFVAP LLFTMRFILKPTBEKSPYGTCTVAIQNFSAVAGEFTGDSQ ELVAGIFFRGRANATHGRUNGTREDGRASYFGTVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQ ELVAGIFFRGRANAHHGDLNOHGASYFGTLKGD SDLDKNDYPDLIVGARFTRSAKTRUDLIVGRGAYTCDUPMASSTPGTLAGD SDLDKNDYPDLIVGARGTSKVAVYRRPVVTVOQLILLHMIIN LENKTCQVPDSMTSACTSLEVCASVTQGSIANTIVLMARVQLL GRGKVLIVNGNKGGINTYSLINSTUTTGRSTTAGQIANTIVLMARVQLL SLKOKGAIKRTLFLUNGABROVATGGSATANTIVLMARVQLD SLKOKGAIKRTLFLUNGABROVATGGSATANTIVLMARVQLD SLKOKGAIKRTLFLUNGBROPULKSARRPOKTYDGLLLHMIIN LENKTCQVPDSMTSAGTSLEVCASVTGGSIANTIVLMARVQLD SLKOKGAIKRTLFLUNGBROPULKSARRPOKTYDGLLHEMIIN SGCAVEALGHUNGBROUNGSLGROW	",,,,,	1] == 1	PANRODVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHHREQ
WASSLIGSLFPHISLRSEDLIABERQVTNNSSCCRAVFAMHPHT NKFAVALLDDSVRYVNASSTIVESLKHRLQRNVASLANKELSAS VLAVACQSCILIWILDPTSLSTRPSSGCAQVLSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRVWDVSTETCVFLWFRSGGVTNLIM SPODSKILATTPSAVFVWEAQMYTCGRWPTISGRCQTGCNSPD GSRLLFTVLGSPLIVSLSTPERCEGKS\ALBUSGQCRLWGICL RQQYRHQMVRRGLGERLTPNSGTPVGMVMCLCL 5956 1705 139 GVGVRGARAMATVQEKARALNLSALHSPAHRPGFSVAQKBFGA TYVWSSIINTLGTQVEVKKRRHLKRNDCFVGSBAUVUTPSHL IQNNYFQDVDIPRAKVVRVQALMWYKYFEAVPTKVPGKDKKFT FEDSSCSLVRFTIFNODSGLKENKLYSPARYADALFKSSDIR SASLEDLEMINLSLKPANSPHWINSATLSPQVINEVWGESTIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVMSSMYLDRGILK AYSDSGDEWLSAAIDCSBYLPDQMVVEISRSPPEQPDRTDLVK ELLEDAIGRYYSSREPLLNHISDUNINGIABLUNGKTEIALBAT QLLLKLLDFQNBEBFRELLYFMAVAANDSBEKLQKESDNRMVVK RIFSKALVDNKHLSKGNTDLIVLFI, VMQVAMDSBEKLQKESDNRMVVK RIFSKALVDNKHLSKGNTDLIVLFI, VMEQVFVKFTIRLBERT GGNANATVTKVLKDVYALKKPVGVLYKKNTITRPEDQTSLEFTG SKKSDCSLEFMSSHKKKKLLLGGFYKCHSPDIFTEHFGD 5957 1479 451 ELQVAVMDTLDRVVKERTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPVGVLYKKKNTITRPEDGTSLEFT SKKSDCSLEFMSSHKKKKNLLLGGFTKGMTDYHVLDMTELGIENFV SLKDIKNSKCPBGTXPMLIPAGDGPDVTEDYRRIKSLLIDFFRG PTVSNIRLAGLEYVIHFTALMGKIVFRSYKLLKKSGCGFTRIE LEEMGPSLDLVLRRTHLASDLYKLSMKMPKALKPKKKKNISHD TFGTTYGRIHMGKQDLSKLGTREM\KGLKKRPARTTEDHBRKS KRIKKMELSGPLLFHCVLLKRI LHGSIGSFL KRIKKMELSGPLLFHCVLLKRI LHGSIGSFL KRIKKMELSGPLLFHCVLLKRI LHGSIGSFL KRIKKMELSGPLLFHCVLLKRI LHGSIGSFL VSDVNSDGLDVLVRAPASYDDSYLGYGVAAGEFTOSGQ ELVAGIPRGAONFGVYSLINSTNMTGYGPNGOVITASVADIIA NYSFKDILRILAGEKQTEVAPASYDDSYLGYGVAAGEFTOSGQ ELVAGIPRGAONFGVYSLINSTNMTGYGFGYTAVGALIH NYSFKDILRILAGEKQTEVAPASYDDSYLGYGVAAGEFTOSGQ ELVAGIPRGAONFGVYSLINSTNMTGYFGYTOVY VSDVNSDGLDDVLVGAPFGFGSAVAHLGDLANDGTUDLIAGVFFGKGV SDIDKNDYPDLIVGARGTGKVAVYRARPVVTVOALLHLHMTIN LENKTCOVPDSMTSAACFSIRVCASYTGGSIANTIVLMARVQLD SLKQKGAIKRTLFLDNHQAHRVPPLVTRRQKSHGCODPTVYLKD ETEFEDKLSPINISLNYSLDBSTFKEGLEVKPILNYTERIVSE QAHLUVDGGBDNLCVPDLKLSARPDKHQVIIGDENNKHMLIINAR NGGGAVBALLFWMIPERADYGTLERNNKGRFPLSCGYKMENVT BMVCDLORDHWSGTNYSLGJERAVERNMSINTDLQIRS	j		1	VWKRCINIWRDVGLFGVLNEIANSEEEVFEWVKTASGWALALCR
NKFAVALLDDSVRYNNASSTIVPSKRRLQRWVASLAKRYCIASA VLAVACQSCILIWTDFTSLSTRPSKGCAQVLSHPCHTPVTSLA WAPSGGRLLSASPVDARIZWMDVSTETCVPLPWFRGGGVTVLLW SPDOSKILATTPSAVFRVWEAQMWTCERWFITISGCGTGCWSSP GSRLLFTVLGSPLIVSESPFERCEGEKS\ALBVGSQGRLWGICL RQQYRHQMVRRGLGERLTPKSGTPVGNVWLCL RQQYRHQMVRRGLGERLTPKSGTPVGNVWLCL RQQYRHQMVRRGLGERLTPKSGTPVGNVWLCL RQQYRHQMVRRGLGERLTPKSGTPVGNVWLCL RQQYRHQMVRRGLGERLTPKSGTPVGNVWLCL RQQYRHQMVRRGLGERLTPKSGTPVGNVWLCL RQQYRHQMVRRGLGERLTPKSGTPVGNVWLCQ FEDSSCSLVFPTTIPNOSCLKERKHKNDCFVGSEAVDVIPSHL IQNKYGDUDIPRAKVVRVCQALMDYKVFEAVFVFKKKKFSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQUVDLPLLDSLLKQEAVPKIFPPRRGSTMVNSSNYLDRGILK AYSISOGDEWLSAALDCSEVLEPQWVWSISRSPPEQPRRTDLKK AYSISOGDEWLSAALDCSEVLEPQWVWSISRSPPEQPRRTDLKK RLEPDATGRYYSSREPLLINHLSDVRNGTABLLNORGTELALEAT CLLIKLLKDPONEEPERFLLYFMVANAMPSGFKLQKESDNRMVVK RIFSKAIVDNKALSKGKTDLLJUFL\MDHOKDVFKIFPGTLHKI CLLIKLLKDPONEEPERFLLYFMVANAMPSGFKLQKESDNRMVK RIFSKAIVDNKALSKGKTDLLJUFL\MDHOKDVFKIFPGTLHKI VS\VK\LMAIQRGPDNRDAGYIYCQRIDQDYSNNTEKTTKDE LLINLLKTLDEDSKLSAKEKKK\LLCOPYKCHEDIFIEHFGD SKKSDCSLFMFGSHNKKRFNNLVIGRMYDYNJUMGKTELALEAN SLKDIKNSKCPBGTKPMLIFAGDFDVTEGDYKLGELINNIKTRAMLIK VS\VK\LMAIQRAMTTALORDVYNKTKTRPFEDOTSLEFF SKKSDCSLFMFGSHNKKRFNNLVIGRMYDYNJUMTELGIRNFV SLKDIKNSKCPBGTKPMLIFAGNDFVYNYLKKNITHPFEDOTSLEFF SKKSDCSLFMFGSHNKKRFNNLVIGRMYDKALKLKKKKLLLIDFFRG PTVSNITLAGLEVYLHFALNGKLYFRSYKLLLKKSGCRFTRIE LEEMSPSLDLVLRRTHLAGDEDVKLSTYRSFYKLLLKKSGCRFTRIE LEEMSPSLDLVLRRTHLAGDEDVKKSTYRFSYKLLLKKSGCRFTRIE LEEMSPSLDLVLRRTHLAGDEDVKKSTYFRSYKLLLKKSGCRFTRIE LEEMSPSLDLVLRRTHLAGDEDVKKSTYFRYTVLYNGFRSYFGYTAVDFHIPD ARATASVLVGAFRANTSGDFLOTSCSYKCKNISHP TTTTYTGTTMGTHTGKFGTSKANGKPKKKKNISHD DTTNNRKIRNGKPBFTKNOMFG\ATVYLFARPEBEKSK KRKKKMBLSQFLLFTCNLLKRTHLGDLNQGCYNTDLAIGVSALLIANTLVMASVLDLIANTLVMASVLDBSTFKEGGSVAGGFTLRDD SLOVAGIFRGANGTSTRUANTLYNGAGEFTGGSSCACCONTYNDIAGNASVAGEFTGGSCACCONTYNGANTANTLYNGAGEFTGGSCACCONTYNGANTANTLYNGAGEFTGGSCACCONTYNGANTANTLYNGAGGGGGTVANTLYNGAGGGGGTTANTLYNGAGGGGGATANTL				WASSLHGSLFPHLSLRSEDLIAEFAQVTNWSSCCLRVFAWHPHT
VLAVACQSCILIWTLDFISISTRPSSGCAQVISHPGHTPVTSLA WAPSGGRILSAPVDNAIRWWWSTCUPPFRRSGGYTNLLW SPDGSKILATTPSAVFRVWEAQMWTCERWFTLSGRCQTGCWSPD GSRLIFTVIGBELIYSLSFPERCEGGKS\ALBVYGQCRLWQICL RQQYRIQMYRGLGERLITPSGTPYGBYAWLCL 5956 1705 139 GVGWGRARMATVOEKRAAINISALHSPAHRPGGFSVAQKPGA TYVWSSIINTLQTQVEVKRRHRLKANDAUFVSGCNLWQICL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRFTIINDGSQLGKENKLYSPARTADALFKSSDIR SASLEDLWENLSLKRANSPHWISATTSPQVINEVWQEETIGRI LQLVDLPLLDSLLKQGRAVPKHTQPKRQSITWMSSNYLDRGILK AYSDSQDEMISAAIDGE SELPDQWYGISRSPPEQDPRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIABLLVNGKTEIALEAT QLLLKLLKTVDNKLISKGTDLIVLFI,WHOKQDUFKLPGTL\HKI VS\VK\LMAIQWGRPPNRDAGYIYVQRIDQRDYSNTEKTTKDE LLINLLKTLDEDKLSAKKKK\LLQCKHPDIFIEHFGD LLINLLKTLDEDKLSAKKKK\LLQCKHPDIFIEHFGD 5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEREEPKLNEHTKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLEFFGSHKKKKKLLGKHRDYNVLMHELGIENFV SLKDIKNSKCPBGTKPMLIFAGDDFUVTEDVRELKSLLDEFRG PTVSNIRLAGLEVVLHFFALNGKITYRSYKLLKKSGCGFVAP SLKBIKNSKCPBGTKPMLIFAGDDFUVTEDVRELKSLLDEFRG PTVSNIRLAGLEVVLHFFALNGKITYRSYKLLKKSGCFVAP LEFMGPSLDLVLRTHLASDDLVKLSMMPKALKPKKKNISHD TFGTTYGRIHMGKQLSKLQTRRM\KGLKKRPABRITEDHEKKS KRIKKMELSQPLIFHCVLLKRILKHGSIGSFL ARALGMLINFPACQAFNDLVBKLTVVSGFKGSYFGTAUFHIPD TTNNRKIRLNGTKEPSFKCQGVAPAGEFTGSDQ ELVAGIPRGANNGTVSLINSTUMTYCPPBAGSGQCRCIPF DTTNNRKIRVNGTKEPIFFSSNOMFG\ATVXA\HKGKSCGPVAP LLFTWRFFLKPTERGPUGTVAIQNFSAVAGEFFGDSSV VSDVNSDGLDDVLVGAPLFRESFSNOMFG\ATVXA\HKGKSCGPVAP ERQQFCQGGSSLDFYKNODLIVGGRSYFWGGOVITASVADIIA NYSFKDILRIKAGEKGTEVAPASYDDSYLGYSVAGEFFGTSGV SDIDKNDYPDLIVGARGTSKVAVYRARPVVTVADALLLHPMIIN LENKTCOVPDSMTSACFSIRVCASYTGGSIANTIVLMARVQLL FRDPOILDTGTETTGRFGSAMAHLGDLNQGCOPTYVIRG SDIDKNDYPDLIVGARGTGSKVAVYRARPVVTVADALLLHPMIIN LENKTCOVPDSMTSAACFSIRVCASYTGGSIANTIVLMARVQLD SLKQGAIKRTLFLDNHQARRVPPLVIRRGKSHCCOPTYVIRG ETEFROKUSPINISINYSLDESTFKEGLEVKPILNYTERIVSE QAHILVOGGDNLCVPDSMTSAACFSIRVCASYTGGSIANTIVLMARVQLD SLKQGAIKRTLFLONHQARRVPPLVIRRGKPRLSCSYKMENVT PRWYCDLONDMISSTYSLGGFRAVPGKOYIGDENNEHMLIINGR				NKFAVALLDDSVRVYNASSTIVPSLKHRLORNVASLAWKPLSAS
### ### ### ### ### ### ### ### ### ##				VI AVACOGCII INTI DDTSI STRPSSGCAOVI SHPGHTPVTSLA
SPDOSKILATTPSAVFRVERAÇMYTCERRPTISGRCOTGCMSPD GSRLLFTVIGEPLIYSLSFPERCEGEKG ALEVQSQQRLWQICL RQQYRHQMVRRCIGERLTPMSGTPVONVALCL SQUGVERGRANATOGEKALANISALHSPAHRPGFSVAQKPFGA TYWKSSIINTLQTQVEVAKRHRLKRENDCFVGSSAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT FEDSSCSLYRPTTIPNGDSLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSIKPANSPHVITSPQVINEWORDETIGRI. LQLVDLPLLDSLLKQQEAVPKIPQPKVGSTMYNSSNYLDRGILK AYSDSQEDEWLSAAIDCSBYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHRGIARLLVNKKTEIALEAT QLLLKLLDFORREFFRILIYFMAVAANPSFFLQVESDNRNVVK RIFSKALVONKNISKKTDLLVIELINDHKOEVFKIPGTLYKKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLKTLDEDSKLSAKEKKK\LLGGPYKCHDIFIERFGD VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLKTLDEDSKLSAKEKKK\LLGGPYKCHDIFIERFGD SKKSDCSLFFFFSSHNKKFPENNLVIGRYDYDVLDMIELGIENFV SKKSDCSLFFFFSSHNKKFPENNLVIGRYDYDYVLDMIELGIENFY SKKSDCSLFFFFSSHNKKFPENNLVIGRYDYDYVLDMIELGIENFY SKKKSDCSLFFFFSSHNKKFPNNLVIGRYDYDYVLDMIELGIENFY SKKSDCSLFFFFSSHNKKFPNNLVIGRYDYDYVLDMIELGIENFY LEMGPSDLDVLURFTLANDCLYYSGFKSSFGSAVDFHIPD FFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKLMBLSQFLLFHCVLLKRIIRHGSIGSFL LEMGPSDLDVLURFTLANDCLYYSGFKSSFGSAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTRMFLKFTEEKGPVATCTVAIQNFSAYABFSFCONSNADP EQQGYCQAGFSLDPYKNGDLIVGGFGSFYWQGVTTASVADIIA NYSFKDLIRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQ ELVAGIPRGAQNRGGVTSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVMSDGLDDVLVGAPLTMEREFSSNEREVGJYLYLQVSSLL FRDPQILTGTTSTFGRFSSAMAHLGBLNQDGYNDIAGVPFAKKD GRGKVLIYNGNKDGLNTKPPPKFCQSVARSHAVPSGFFTLKD SDLDKNDYPDLIVGARGTKKAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVASVTQSGIANTIVLMREVGLO SLKQKAX KRTLFLDNHQARRYPLVTURQKTGRJCCOPTLVVLRD ETEFRDKLSPINISLNYSLDESTFEEGLEVKPILNYRENIVSE OAHLLVDCGEDNLCVPDLKLSRPDKHQVIGENHIMLIINAR NBGEGAYEAELFYWIEBEADYGISRNKNORPLSCEYKMRNVT PMVCCHONPWYGGAYFASLEFTYNSLGLEREFRLSCETKRENVT	1		ļ	WARROOT I CACDUDA A TRUMDUSTETCUDI. PWFRGGGVTNI. LW
GSRLLFTVLGEPLIYSLSFPERCEGKQALEVGSQQRLWGICL RQQYRHQMYRRGLERLTPWSGTPVWNLCL SV956 1705 139 CVGYRGARAMATVQEKAAALMLSALHSPAHRPFGFSVAQKPFGA TYWSSIINTLOTQVEVKKRHRLKRHNDCFYGSEAUDVIFSHL IQNYYGDUDIPRAKVVEVQALMUKVEVGALMUKVFGKPKFTV FEDSSCSLYRPTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWRFJDDVIDROLGKENKLYSPARYADALFKSSDIR LQLVDLPLLDSLLKQQEAVPKIPQFKRQSTMVNSSNYLDRGILK AYSDSQEDENLSAAIDCSSYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSRSPLINHLSDVHNGIARLLVNGKTIALBAT QLLKKLDDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFI\MDIGKDVFKIPGTL\HKI VS\VK\MAATQNGDPNDNAGYIVCQRIDQRDYSNNTEKTTKDB LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD 5957 451 ELQVAVANDTLDEVKKFKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDYYALKKFYGVYKKKNITRFFEDGTSLEFF SKKSDCSLFWFGSHNKKPRNILVIGRNYDYHVLDMIELGIENFV SKKSDCSLFWFGSHNKKPRNILVIGRNYDYHVLDMIELGIENFV SKKSDCSLFWFGSHNKKPRNILVIGRNYDYHVLDMIELGIENFV SLKIIKNSKCPEGTFWLIFAGDDLYKLGKNERPARERITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKGSIQGFL TFGTTYGRIHMQKDLSKLQTRKM\KALKKRNEKALIDFFRG PTVSNIRLAGLEYVLHFTALNGKTYFSYKLLKKSGCRTPRIE LEEMGPSLDUVRRTHLSDDLYKLGWSFKGSVGYAVDFHIPD ARTASVLVGAFKANTSQDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIERKSNQMFG\ATVXA\HKKSCGCVAP LLFTRMFNLKFTERGFOSMAMILGDLNQGGYTAGAMDIIA NYSFKDIIRKLAGEKGTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNRGYYSINSTYMPTIQNFTGEQMASYFGTTVV VSDVMSDGLIDVUGAPLFMREFFSNIPRSYGJTVLYLQVSSLL FRDPQILTGTETFGFRGSMAMILGLNQDGYNDLTAGVFFAKG QRKVLIVNGNKDGLNTKPFRFSCQSVANSHAVPSGFGFTLKGD SDIDKNDYPDLIVGAFSTGKVAVYRARPVVTVAQLLLHPMIN LENKTCQVPDSMTSAACFSLRVALSVTQSTANTVANAEVLD SLKQKGATKRTLFLDMHQARRYPFLVTROKSHGCQDFTVVTRD ETEFFEDKKLSPINISLNYSLDESTFKEGLEVEPTLNYTRENIVSE GAHLUNDGGENNLCVPDLKLSRFRKIGVTIGENHIMLIINAR NBGEGAYEAELFYMIPERADYYGISRKRTPLSCEYKMENVT	!		i	WAPSGGKLESASPVDAAIKVWDVSIBICVFBIWIRGGGVIKEDD
RQQYRHQMVRRGIGERLIPWSTTPUGNVLCL 5956 1705 139 GVGVRGARAMATVQEKAAALNISALHSPAHRPPGFSVAQKPFGA TYWRSSIINTLQTQVEVKKRRRILKRHHDCFVGSEAVDVIFSHL IQNRYFGDVDIPRAKVVRVQALMDYKVFBAVPTKVFGKDKKFT FEDSSCSLYRFTTIPMOGSQLGKEKKLYSPARYADALFKSSDIR SASLEDLWERLSKPANSPHVNISATLSPQVINEVWQBETIGRL LQLVDLPLLDSLLKQQBAVPKIPQFKRGSTWNSSNYLDRGILK AYSDSQBDEWLSAAIDCSSTLPQMVWSISRSFPEQPDRTULVK ELLFDAIGRYYSSREPLAHHLSDVINGIARLLVNGKTEIALEAT QLLLKLLDFONREFFRRLLYFMAVAANPSEPKLQKESDNRMVVK RIFSKATVDNKNINSKGKTDLLVLFLVMDHQKVDFKIPGTLVHK VS\VK\LMAIQNGRDPNRDAGYIYCGRIDQRYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGGFYKCHEDTFIEHFGD 5957 1479 451 ELQVAVAMDTLDRVVRFKTRAKRFLEKREPKLNENIKNAMLIK GGNANATYTKVLKDVYALKKPYGVLYKKKNITRPFEDGTSLEFF SKKSDCSLFMGSINIKKRPNLIGMTYPHYLDMIELGIBNFV SLKDIKNSKCPEGTKPMLIFAGDDPDVTEDYRRLKSLLIDFFRG PTVSNIKLAGLEYVLHHFALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRTHIASDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTTRM\KGASKKRFARRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL AAALGMLLWFPACQAFNLDVEGGAVYCPWPABGSAQCRQIPF DTTNNKKIRVNGTKEPIEFKSNQWFG\ATVKA\HGKSCGPVAP LLFTMRNFLKFPEKGPVGTCYVAIQNFSAYABFSPCGNSNADP EQGGYCQAGFSLDFYKNGDLIVGGRGSYFYQGVUTTAGVADIIA NYSFKDIIRKLAGEKQTEVAPASYDDSYLGYSVAAGBFTGRSOL PRODILTGTETFGRFSAMAHALGDLNQOGYNDIAIGVPSAGKFGTTVV VSDVNSDGLDDVLVGAPLFPKETCGYWAJHAVSGFFGFTLKGD SIDIRNDYDDLIVGAPGTGKVAVYRAPPVOTDIAIGVPSAGK QRGKVLIYNGNKDGLINTKPPFKFCQGVWASHAVPSGFFGTLKGD SIDIRNDYDDLIVGAPGTGKVAVYRAPPVOTDIAIGVPSAGK QRGKVLIYNGNKDGLINTKPPFKFCQGVWASHAVPSGFFTLKGD SIDIRNDYDDLIVGAPGTGKVAVYRAPPVOTDIAIGVPFAGKD QRGKVLIYNGNKDGLINTKPPFKFCQGVWASHAVPSGFFTLKGD SILDKNCQVPDSMTSAACFSLKVCASVTGGSIANTIVLMREVQLD SLKQKALIKRTLFLDNIQAHRVPFLVIKRKGSBQCQDFTVYLRD ETEFROKLSPINILNYSLDESTF KEGLEVKYE LINTYRENUVG QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NBGGGAYBRELFVWIPEERADYVGIERNNKFRFLSCEYKMENVT PMVCCLGNPWYGGTNYSLLGLEFFYPORBLESCEYKMENVT	ŀ		1	SPDGSKILATIPSAVFRVWEAQMWICERWFILISGRCQIGCNSFD
5955 1705 139 GVGWRGARAMATVQEKARALINISALHSPAHRPFGFSVAQKPFGA TYVWSSIINTLQTQVEVKKRRHRLKRHDCFVGSEAVDVIPSHL IQNKYFGDVDIPRAKVVRVQALMDYKVFEAVPTKVPGKDKKRT FEDSSCSLYRFTTIPNQDSQLGKERKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINDEWQGETIGRL LQLVDLPLLDSLLKQQEAVPKTPQPKRQSTWNNSNYLDRGILK AYSDSQEDEMISAAIDCSEYLPDQWVSEISRFFEQPFTTLUK ELLFDAIGRYYSSREPLLAHRLSDVINGIAELLUNGKTEIALEAT QLLKKLLDFONREFRRLLYFMAVAANDSEPKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFFLWHDQKDVEKIPGTL\HKI US\VK\LMAIQNGRDPNRDBGYIYCQRIDQRDYSNNTEKTTKDE LLINLKTLDEDSKLSAKEKKK\LLGQPYKCHPDIFIBHFGD 5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKUVALKKPYGVLYKKNNITRFFEDOTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIBLGIRNFV SLKDIKNSKCPEGTKFMLIFAGDDFVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEVYLHFTAINGKIYFRSYKLLLKESGCRTPRIE LEEMGPSLDLVLRTHLASDDLYKLSMKMPKALKRPAKRILEDFRK KRIKKKLMELSQPLJFHCVLLKRIKHQSIQSFL 5958 1 3138 AAALGMLNFFACQAFMLDVEKLTVYSGPKGSYFGYAVDFHIPD TTNNRKIRVNGTKEPIEFKSNOWFG\ATVKA\HKGKSCGPVAP LLFTRRNFLKPTPEKGPVGTCYVAIONFSAVAEFSPCONSNADP EQGYCQAGFSLDFYKNGDLIVGGPGSFYWGGQVTTASVADIA BATASVUNGAKKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNOWFG\ATVKA\HKGKSCGPVAP LLFTRRNFLKPTPEKGPVGTCYVAIONFSAVAEFSPCONSNADD EQGYCQAGFSLDFYKNGDLIVGGPGSFYWGGQVTTASVADIA BATASVUNGAKANTSQPILGTFYKNGDLIVGGTSVAAGEFTGDSQ ELVAGIPRGAONFGYVSIINSYDMTFIQNFTGEQMASYFGTTVV VSDVNSDGLDDVLVGAPLFMERFFESNPREVGGIVXYLCONSSLL FEDPOILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLITNGNKDGLINTKPPFKFCQGVMASHAVPSGFGFTLRGI SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLHHMIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNIQAHRVPFLVIKRQKSCQCDPTVTLRG PETFFROKLSPINISLNYSLDESTERSELEVKETLINYRRNIVSE QAHILVDGGEDNLCVPDLKLSARPDKHQVIIGDENHLMLINAR NEGEGGYERELFVMIPEGRAPVGIERNMSINFPLGCETKMENVT PMVCOLGNPWINGSTNYSLLGLRFAVPRIBESCETKMENVT	1		Į	GSRLLFTVLGEPLIYSLSFPERCGEGRG\ALEVQSQQRDWQICD
TYWSSIINTLOTQVEVKKRRHRLKRHNDCFVGSEAJDVIFSHL IQNKYFGDVDIPRAKVVRVQQALMDYKVFEAVPTKVPGKKRPF FEDSSCSLYRFTTIPNDSQLGKENKLYSPARYADALFKSSDIR SASLEDLMENLSLKPANSPHYNISATLSPQVINEVWGEETIGRL LQLVDLPLLDSLLKQQEAVELPQFKRGSTWANSSNYLDRGILK AYSDSQEDEMISAAIDCSEYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLINHLSDVHNAIARLLUNGKTEIALEAT QLLKKLLDFONREFFRRLLYMAVAAMPSEFKLQKESDNRVVK RIFSKAIVDNKNLSKGKTDLLVLFI\MDHQKDVFKIFGTL\HKI VS\VK\LMAIQNGRDPRRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLKKTLDEDSKLSAMEKKK\LLGQFYKCHPDIFIEHFGD 5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENTKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKNITRPFEDQTSLEFF SKKSDCSLFMGSHNKKRPHNILVIGRNYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFUTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKTYFRSYKLLLKKSCGTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKISHD TFGTTYGRIHMGKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKLMELSQPLLHFUKRIKIKHGYGSFL ARTASULVGAPKANTSQPDIVEGGAVYCPWPABGSAQCRQIPF DTTNNKIR KINGTKSPIEFSNGWFG\ATVKA\HKGKSCGFVAP LLFTWRNFLKPTPEKGPVGTCYVATQNSAVAEFSPCGNSNADP EQGGYCQAGFSLDFYKNGDLIVGGGSFYWQGVITASVADIIA NYSFKOILRKLAGERQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGTTVV VSDVNSDGLDDVLVGAPLFMERFEFSNPREVGQIYLYLQVSSLL FRDPOILTGTETTGRFGSAMAHLGDLNQDGYNDIAIGYPFAGKD QRKVLIYMGNKDGLNTKPFPKFCCGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFTGTKWAVYRARPVVTUDAGLLLHPMIIN LENKTCQVPDSNTSAACFSLRVAVYRARPVVTUDAGLLHPMIIN LENKTCQVPDSNTSSACFSLRVAVYRARPVVTUDAGLLHPMIIN LENKTCQVPDSNTSSACFSLRVAKSHCGNASHQUPIVVLRN SLKQKGAIKRTLFLDNHQARPFPLVIRQKSHCCQDFIVVLRD SLKQKGAIKRTLFLDNHQARPFPLVIRQKSHCCQDFIVVLRD SLKQKGAIKRTLFLDNHQARPFPLVIRQKSHCCQDFIVVLRD SLKQKGAIKRTLFLDNHQARPFPLVRURGKSHCCQDFIVVLRD PMUVCDLGRPMVGSTNYSLGLEFFAVPRLEKYFILNYKRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NBEGGGYBEALEFWNIPEEADYVGIIGRNKKGFRPLSCETKMENNY PMUVCDLGRPMVGSTNYSLGLEFFAVPREKKTNMSINFIDLQIRSS	ļ		Ĭ	RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL
IQNXYFGDVI PRAKVVRVCQALMDYKVFEAVPTKVFGKDKRFT FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVMQEETIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDWLSAAIDCSEYLPQDWVBISRSFPEQDBRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIARLLUNGKTEIALEAT QLLLKLLDFQNREEFRRLLYFMAVAAMPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\MX VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFISHFGD 5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLMEN KNAMLIK GGNANATTKVLKDVYALKKFYGVLYKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSKMPKRALKPKKKNISHD TFGTTYGRIHMQKQDLSKLGYMM\KGLKKRPARITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL AAALGMULWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPPEKGPVGTCYVALGVSAVADIIA NYSFKDILKKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGTVSIINSYDMTFLQNFTGSQMASYFGTVV VSDVNSDGLDDVLVGAPLFMRREFESNPREVGGTYLYLQVSSLL FRDPGILTGTETFGRFGSAMAHLGDLNQDGYNDLAIGVPFAGKD QRGKVLIYMGNKDGLNTKFFFKFCQGVWASHAVPSGFGFTLRGD SLIVAGIPRGAQNFGTVSIINSYDMTFLQNFTGSQMASYFGTVV VSDVNSDGLDDVLVGAPLFMRREFESNPREVGGTYLYLQVSSLL FRDPGILTGTETFFGRFGSAMAHLGDLNQDGYNDLAIGVPFAGKD QRGKVLIYMGNKDGLNTKFFFKFCQGVWASHAVPSGFGFTLRGD SLIKMIYMGNKDGLNTKFFFKFCQGVWASHAVPSGFGFTLRGD SLIKMIYMDLUGAPLFULVGRGSKAVYARAFVVTDAGLLLHMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIRQKSHCQOPIIVYTRR ETFFFRKLS PINISLNYSLDSSTFKEGLEVKPLINYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADVGIERINKGFRPLSCEYKMENV PMWVCDLGRPMVGTNYSLGLEFFAVPRLEKYTMSINFDLQIRSN	5956	1705	139	GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA
FEDSSCSLYRFTTIPQDSQLGKENKLYSPARVADALFKSSDIR SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDSLLKQQEAVEKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSBYLPQDMVVEIGRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLINLLSVHNGIAELLUNGKTEIALEAT QLLLKLLDFORREFERRILLYFMAVAAMPSEFKLQKESDNEMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIFGTL\HKI VS\VK\LMAIQNGRDPRRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLKTLDEDSKLSAMEKKK\LLGQFYKCHPDIFIEHFGD LLNLKTLDEDSKLSAMEKKK\LLGQFYKCHPDIFIEHFGD SKKSDCSLFFRGSINKKRPHNIVTGRWYDYMLDMIELGIENFV SKKSDCSLFFRGSINKKRPHNIVTGRWYDYMLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFALMGKIYFRSYKLLLKKKSGCRPFRIE LBEMGPSLDLVLRRTHLASDLYKLSNKWRALKFKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPAERITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRILKIGSIQSFL SFSS 1 3138 AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPLIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\KKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCVYAIQNFSAVAEFSPCONSMADP EQQGYCQAGFSLDFYKNGDLIVGGGSFYWGGQVITASVADIIA NYSFKDLIRKLAGEKQTEVAPASVDDSYLGYSVAAGFFTGDSQQ ELVAGIPRGAQNFGVVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVQAPLFMREFESSNPREVGQITLYLQVSSLL FRDPQILTGTETFGFRGSAMAHLGDLNQGYNDIAIGVPFAGKD QRGKVLIYNGNRDGLDVLVQAPLFMRREFFSSNPREVGQITLYLQVSSLL FRDPQILTGTETFFRGSSAMAHLGDLNQGYNDIAIGVPFAGKD QRGKVLIYNGNRDGLDVLVQAPLFVCQSVWASHAVPSGFGFTLRGD SDIDKNDYPPDLVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGGSINNTTVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVYFPLVIKRQKSHQCQDFIVYLRD ETFFRNKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NGEGGAYEAELEVMIPEEADVGIERNKGFRPLSCEYKENNY PMWVCDLGRPMVSGTNYSLGLEFFAVPRLEKTMMSINFDLQIRSS			1	TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL
SASLEDLMENISLKPANSPHVNISATLSPQVINEVNOEBTIGEL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDGEILK AYSDSQEDEWLSAATLOESTYLPDQMVVETSRSPPEQPDRTDLVK ELLFDAIGRYYSSRSPLLNHLSDVINGIAKLLUNGKTEIALBAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEPKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\W\LMAIQNGRPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKK\LLQPYKCHPDIFIEHFGD LLNLLKTLDEDSKLSAKEKK\LLQPYKCHPDIFIEHFGD SEKSDCSLFMTGSHNKKRPNRUVIGRMYDYHVLDMIELGIENFV SKKSDCSLFMTGSHNKKRPNRUVIGRMYDYHVLDMIELGIENFV SKKSDCSLFMTGSHNKKRPNRUVIGRMYDYHVLDMIELGIENFY SKKSDCSLFMTGSHNKKRPNRUVIGRMYDYHVLDMIELGIENFY SLKDIKNSKCPBGTRFMLTAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLBYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMSPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDBEKKS KRIKKLMBLSQPLJFHCVLLKRIIKHQSIQSFI AAALGMLLWFPACQAFNLTVSGPKGSYFGYYAVDFHIPD ARTASVLVAGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNOWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKSPVGTCYVAIQNFSAYAEFSPCGNSNADP EGGGYCQAGFSLDFYKNGDLIVGGRGSFYWGGVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQ ELVAGIPRGAQNFGYVSIINSYMTFIQNFTGEDMASYFGYTVV VSDVNSDGLDDVLVGAPLFWERFFESNPREVGQIVLTLIQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGYPFAGKD QRGKVLIYMGNKDGLNTKFPFKFCQGWASHAVPGFFTLRGD SDIDKNDYYDPLIVGARFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVOLD SLKQKGAIKRTLFLDNHQAHRVPFLVTKRGKSHQCQDFIVYLRD ETTEFRRKLSPINISLHYSLDESTFKEGLEVKPILNYYKENIVSE GAHILVDCGEDNLCVPDLKLSARPDVHQVIIGBENHLMLIINAR NGEGGAYEARLFFWIPEBEADYVGLIERNNKGFRPLSCEYKMENVT PMWVCDLGIRNNSGTTYSLGERNNKGFRPLSCEYKMENVT	1		İ	IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT
SASLEDLMENISLKPANSPHVNISATLSPQVINEVNOEBTIGEL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDGEILK AYSDSQEDEWLSAATLOESTYLPDQMVVETSRSPPEQPDRTDLVK ELLFDAIGRYYSSRSPLLNHLSDVINGIAKLLUNGKTEIALBAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEPKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\W\LMAIQNGRPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKK\LLQPYKCHPDIFIEHFGD LLNLLKTLDEDSKLSAKEKK\LLQPYKCHPDIFIEHFGD SEKSDCSLFMTGSHNKKRPNRUVIGRMYDYHVLDMIELGIENFV SKKSDCSLFMTGSHNKKRPNRUVIGRMYDYHVLDMIELGIENFV SKKSDCSLFMTGSHNKKRPNRUVIGRMYDYHVLDMIELGIENFY SKKSDCSLFMTGSHNKKRPNRUVIGRMYDYHVLDMIELGIENFY SLKDIKNSKCPBGTKPMLTFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLBYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMSPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDBEKKS KRIKKLMBLSQPLJFHCVLLKRIIKHQSIQSFI AAALGMLLWFPACQAFNLTVSGPKGSYFGYAVDFHIPD ARTASVLVAGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNOWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKSPVGTCYVAIQNFSAYAEFSPCGNSNADP EGGGYCQAGFSLDFYKNGDLIVGGRGSFYWGGVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQ ELVAGIPRGAQNFGYVSIINSYMTFIQNFTGEMASYFGYTVV VSDVNSDGLDDVLVGAPLFWERFFESNPREVGGIYLTLIQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGYPFAGKD QRGKVLIYMGNKDGLMTKFPFKFCQWWASHAVPSGFGFTLRGD SDIDKNDYYDPLIVGARFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIAMTIVLMAEVOLD SLKQKGAIKRTLFLDMHQAHRVPFLVTKRGKSHQCQDFIVYLRD ETTEFRRKLSPINISLHYSLDESTFKEGLEVKPILNYYKENIVSE GAHILVDCGEDNLCVPDLKLSARPDVHQVIIGDENHLMLIINAR NGEGGAYEARLFVMIPEBADYVGLIERNNKGFRPLSCEYKMENVT PMWVCDLGIRNWSGTTYSLOERTRAGFFRLSCEYKMENVT			1	FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR
LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWSAAIDCSEYJPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSREPLLNHLSDVINGIAELLUNGKTETALEAT QLLLKLLDFQNREEFRRLLYFMAVAANPSEPKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLULF,MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRYSNNYEKTKDE LLNLKTLDEDSKLSAKEKKK\LLGQPYKCHPDIFIEHFGD 1479 151 ELQVAVAMDTLDRVVKPKTKRAKFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDOTSLEFF SKKSDCSLFMFGSHHKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYPRSYKLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKLMELSQFLLFHCVLLKRIIKHQSIQSFL AAALGMLLWFPACQAPNLDVEKLTVXSGPKGSYFGYAVDFHIPD DTTNNRKIRVNGTKEPIEFKSNWFG\ATVKA\HKGKSCGPVAP LLFTWRFIK,PTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EQQGYCQAGFSLDFYKNGDLIVGGPGSFYWGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQ ELVAGIPRGAQNFGYVSIINSYMMTEJONFTGEGMASYFGTTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPOILTGTETFGRFGSAMAHLGUNQDGYNDIAIGVPFAGKD QRKVLIYMGNKDGLNTKPFPKFCQQWASHAVFGFFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVPPLVIKRQKSHQCQDFIVYLRD ETTFRRKLSPINISLNYSLDESTFKEGLEVKPLLNYKENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NGEGGAYEAELFWNIPEEADYVGLERNNKGFRPLSCEYKMENVT PMWVCDLGRDNMVSGTIYSLGIERNNKGFRPLSCEYKMENVT			}	SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL
AYSDSQEDEMLSAAIDCSEXLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSREPLLNHLSDVHNGIAELLUNGKTEIALEAT QLLLKILDFQNREFERLLYFMAVAAMPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYQGRIQQBYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHEDIFIEHGD ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVIYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKFWLIFFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDLIYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTKMYKAKKKPABERITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL S958 1 3138 AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVIVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRK IR VNGTKEP IEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGGGYCQAGFSLDFYKNGDLIVGGGGSYFWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGFFTGDSQ ELVAGIPRGAQNRGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMREFESNPREVGGIYLTLLOYSLL FRDPQILTGTETFGRFGSAMHLDDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLINTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFILDNHQARRVPDLVIKRQKSIQCOPFIVYLRD ETTEFRKLSPINISLNYSLDSSTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NGGEGAYEABLFVWIPEEADYVGIERNNKGFRPLSCEYKMENVT BMVVCDLGDNPMVSGILGRFAVPFLEKTNNSINFDLQTRSS				LOLVDLPLLDSLLKOOEAVPKIPQPKRQSTMVNSSNYLDRGILK
ELLFDAIGRYYSSREPLLNHLSDWHNGIAELLUNGKTETALEAT QLLLKILLDFQNEEFERLLYFMAVAANPSEPKLQKESDNRMVVK RIFSKAIVDNKNLSKGKTDLLUTEI\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK,LLGQFYKCHPDIFIEHFGD 5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNEHFGD SKSDCSLFMFGSHNKKRPKNLVTGRMYDYHVLDMIELGIENFY SKSDCSLFMFGSHNKKRPKNLVTGRMYDYHVLDMIELGIENFY SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEVVLHFTALNGKTYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFCULKRTIKHQSIQSFL 5958 1 3138 AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVIVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKKSCGPVAP LLFTWRNFLKPTERKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGGSYFWQGOVITASVADIIA NYSFKDILRKLAGEKQTEVAPAYDDSYLGYSVAAGEFTGDSQQ ELVAGIFRGANNFGVYSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPOILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPFKFCGSWANSHAVPSGFFTLRGD SSIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQARRYPLVIKRQKSHQCQDFIVYLRD SLKQKGAIKRTLFLDNHQARRYPLVIKRQKSHQCQDFIVYLRD SLKQKGAIKRTLFLDNHQARRYPLVIKRQKSHQCQDFIVYLRD FTEFFRKLSFINISLNYSLDSSTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NGGEGGAYEAELFVWIPEEADVYGIERNNKGFRPLSCEYKMENVT PMVVCDLGNPMVSGILDRPWSGLERFRYDGIERNNKGFRPLSCEYKMENVT	1		į.	AVSDSOEDEWISAAIDCSRYLPDOMVVEISRSFPEOPDRTDLVK
QLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESIDNRMVVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGIIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD 5957 1479 451 ELQVAVAMDTLDRVVKPKTKRARGFLEKREPKLMENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKRRPNNLVIGRNYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVI.HFFALNGKIYFRSYKLLLKKSGCRTPRI LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIEMQKQDLSKLQTKKM\KGLKKRPAERITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL AAALCMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD DTTNNKKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVALQNFSAVAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGERQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSBGLDDVLVGAPLFWREFFESNPREVGQITYLYLQVSSLL FRDPOILTGTETFGFRGSAMAHLGDLNQDGYNDIAIGVPFAGKD QBGKVLIYNGKKDGLNTKPFPKFCQGWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRAPPVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQL SLKQKGAIKRTLFLDNHQAHRVPFLVIKRQKSHQCQDFIVYLRD SLKQKGAIKRTLFLDNHQAHRVPPLVIKRQKSHQCQDFIVYLRD SLKQKGAIKRTLFLDNHQAHRVPPLVIKRQKSHQCQDFIVYLRD ETEFRIKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NBGEGAYAEAELFVMIPEEADVYGIERNNKGFRPLSCEYKMENVT			1	FLIEDATGRYVSSPEDIJNHISDVHNGIAELLVNGKTEIALEAT
RIFSKAIVDNKNLSKGKTDLLV-FL\MDHQKDVFKIPGTL\HKI VS\VK\LMATQNGRDPNRAGYIYQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLDFFRG PTVSNIRLAGLEYVLHFTALINGKTYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTTGRIHMQKQDLSKLQTRKM\KGLKKRPABERITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL AAALGMLLWFPACQAFNLDVEKLTVYSGFKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRKNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGGGYCQAGFSLDFYKNGDLIVGGGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDEDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRGSAMAHLGDLNQDGYNDIAIGVFFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRCD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHEMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHILMIINAR NEGEGAPCAEALFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT	1			OLIT VI I DEONDEREPRI I VEMAVAANDSERKLOKESDNRMVVK
VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKK\LLGQFYKCHPDIFIEHFGD 5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKEPKLNENI KNAMLIK GGNANATVTKVLKDVYALKKPYGVIYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKR PNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTEPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTAINGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVIRRTHLASDDLYKLSMKMPKALKPKKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKLMBLSQPLLFHCVLLKRILKHQSIQSFL AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIJVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGFGSFYMQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHEMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD GTEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NBGEGAYAEALEFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT				DIRECTA TUDNICAL EXCLUDITATION OF THE CONTROL OF TH
LINLIKTLDEDSKLSAKEKKK\LLGGPYKCHPDIFIEHFGD 5957 1479 451 ELQVAVAMDTIDRVVYRKTKRAKRFLEKREPKINENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNIVIGRNYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLIKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMOKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL AAALGMLLNFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPPTEKGPVGTCVVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGGIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGWWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFILDNHQAHRVPPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT PMWVCDLGNPWSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS				KIPSKAI VOKKUBSKIKIDDI ZVIVCOPIDODDVSNNTEKTTKDE
5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNITRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPAERITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL ARALGMLLMFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQMFSAYABFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQMFGYVSIINSYMMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKCQVWASHAVPSGFFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADVVGIERNKGFRPLSCEYKMENVT RMWVCDLGNPWSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	i		1	VS VK \IMATQNGKDPNRDAGITICQRIDQRDIDIRTERECD
GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF SKKSDCSLFMFGSHNKKRPNNLVTGRMYDYHVLDMTELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALINGKTYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABERITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRILKHQSIQSFL AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCDWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCCEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGRPMVSGTNYSLGLRFAVPRLEKTMNSINFDLQIRSS		<u> </u>		LUNDERTHOEDSKISARERRR (HEIGHT IRCHTOTT THIT CO
SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRIKSLLIDFFRG PTVSNIRLAGLEYVLHFTALMGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL S958 1 3138 AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYVCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILKKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMWVCDLGRPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	5957	1479	451	ELQVAVAMDTDDKVVKPKTKKAKKIDEKKEPKDNENIKMAMDIK
SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALINGKTYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKKMELSQPLLFHCVLLKRIIKHQSIQSFL KRIKKKMELSQPLLFHCVLLKRIIKHQSIQSFL AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVFFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLIGNPMVSGTNYSLGLEFAVPRLEKTNNS INFDLQIRSS	1		1	GGNANATVTKVLKDVYALKKPYGVLYKKKNTTKPFEDQISLEFF
PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTTKMKKGLKKRPAERITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQMFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPFCCGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVPPLVIKRQKSHQCQDFIVYLKD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGGDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNNSINFDLQIRSS	1	1		SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVDDMIELGIENFV
LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPAERITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL AAALGMLLWFPACQAFNLDVEKLTYYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1	1		SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG
TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPAERITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL 5958 1 3138 AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHEMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLERFAVPRLEKTNMSINFDLQIRSS	1	1		PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE
KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL 5958 1 3138 AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLERAVPRLEKTNMSINFDLQIRSS		1		LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKNISHD
KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL 5958 1 3138 AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLERAVPRLEKTNMSINFDLQIRSS	1	1		TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPAERITEDHEKKS
AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGTTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1			KRIKKKLMELSOPLLFHCVLLKRIIKHQSIQSFL
ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	EGER	 	3138	AAALGMLLWFPACOAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD
DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	2956	•	1 3130	ARTASVI,VGAPKANTSOPDIVEGGAVYYCPWPAEGSAQCROIPF
LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	Į			DOTANDER TOWNGTKED TREKENOWEG LATVKA HKGKSCGDVAP
EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPFFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS				TI DEMONET ADADEAUDICACAMA LONEGA ASEES DOGNANADO
NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPFFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS				PROGRADA DESI DEVISIONI TRACOCCEVANOCOLITA CUANTITÀ
ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPFFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS				EGOGICOVERSPOR I UNIONDITA CRESCI I MAGGATIVO AUDITA
VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETTEFRDLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1			NYSEKDILRKLAGEKQTEVAPASYDDSYLGISVAAGEFIGDSQQ
FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVPPLVIKRQKSHQCQDFIVYLRD ETTEFRULSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS				ELVAGIPRGAQNFGYVSIINSYDMTFTQNFTGEQMASYFGYTVV
QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1		l	VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL
SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1		1	FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD
SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS		Ì		ORGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD
LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1	<u> </u>	1	SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN
SLKQKGAIKTTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS			1	LENKTCOVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD
ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1			SIKOKGAIKRTLFLDNHOAHRVFPLVIKROKSHOCODFIVYLRD
QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS				PERPORT OF THE STAY STORE OF STEREOLEV KPILNYYRENIVSE
NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS				CAUTI UDGCEDNI CUDDI KI CAD DDKHOVI I GDENHI MI I TNAR
RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1		Į.	QARITUVUCGEDRUCYPULUSARPULIQVITTODDRILDIDITIVIT
RMVVCDLGNPMVSGTNYSLGLKFAVPKLBKTNMSINFDLQIRSS NKDNPDSNFVSLQINITAVAQVEIRGVSHPPQIVLPIHNWEPEE	1			NEGEGATEAELE VMITAEEDI AGTERANKOLKLUSCE I KALINA I
NKDNPDSNFVSLQINITAVAQVEIRGVSHPPQIVLPIHNWEFEE	1	j		RMVVCDLGNPMVSGTNYSLGLKFAVPKLBKTNPSLTVFDDQTKSS
	L	<u> </u>		NKDNPDSNFVSLQINITAVAQVEIRGVSHPPQIVDFIHMWEPEE

r		T = 17	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			EPHKEEBVGPLVEHIYELHNIGPSTISDTILEVGWPFSARDEFL
	Ī		LYIFHIQTLGPLQCQPNPNINPQDIKPAASPEDTPELSAFLRNS
1	Ì	ľ	TIPHLVRKRDVHVVEFHROSPAKILNCTNIECLOISCAVGRLEG
			GESAVLKVRSRLWAHTFLQRKNDPYALASLVSFEVKKMPYTDQP
İ		ł	AKLPEGSIAIKTSVIWATPNVSFSIPLWVIILAILLGLLVLAIL
			TLALWKCGFFDRARPPQEDMTDREQLTNDKTPEA
5959	1	1166	GTSGYAAQQLPSLLKEREFHLGTLNKVFASQWLNHRQVVCGTKC
3939		1100	
j			NTLFVVDVQTSQITKIPILKDREPGGVTQQGCGIHAIELNPSRT
1	1		LLATGGDNPNSLAIYRLPTLDPVCVGDDGHKDWIFSIAWISDTM
ŀ			AVSGSRDGSMGLWEVTDDVLTKSDARHNVSRVPVYAHITHKALK
ľ			DIPKEDTNPDNCKVRALAFNNKNKELGAVSLDGYFHLWKAENTL
			SKLLSTKLPYCRENVCLAYGSEWSVYAVGSQAHVSFLDPRQPSY
Į.	1		NVKSVCSRERGSGIRSVSFYEHIITVGTGQGSLLFYDIRAQRFL
	1		BERLSACYGSKPRLAGENLKLTTG\KGWLNHDETWRNYFSDIDF
	<u></u> .		FPNAVYTHCYDSSGTKLFVAGGPLPSGLHGNYAGLWS
5960	2853	870	FVWSDGGPRPRRGPAVGAGAAHLSDPWAMTPGTANRATNPLNKE
			LDWASINGFCEQLNEDFEGPPLATRLLAHKIQSPQEWEAIQALT
	1		VLETCMKSCGKRFHDEVGKFRFLNELIKVVSPKYLGSRTSEKVK
	·		NKILELLYSWTVGLPEEVKIAEAYQMLKKQG\IVKSDPKLPDDT
	1		TFPLPPPRPKNVIFEDEEKSKMLARLLKSSHPEDLRAANKLIKE
	1		MVQEDQKRMEKISKRVNAIEEVNNNVKLLTEMVMSHSQGGAAAG
	1		SSEDL\MKEL\YQRCBRMRPTLFPTGRVDTEDND\EALAEILQA
ì	1	İ	NDNLTQVINLYKQLVRGEEVNGDATAGSIPGSTSALLDLSGLDL
			PPAGTTYPAMPTRPGEQASPEOPSASVSLLDDELMSLGLSDPTP
		·	PSGPSLDGTGWNSFQSSDATEPPAPALAQAPSMESRPPAQTSLP
1			ASSGLDDLDLLGKTLLQQSLPPESQQVRWEKQQPTPRLTLRDLQ
1			NKSSCSSPSSSATSLLHTVSPEPPRPPQQPVPTELSLASITVP
			LESIKPSNILPVTVYDOHGFRILFHFARDPLPGRSDVLVVVVSM
1	1		1
ł	ŀ		LSTAPQPIRNIVFQSAVPKVMKVKLQPPSGTELPAFNPIVHPSA
	· ·		ITQVLLLANPQKEKVRLRYKLTFTMGDQTYNEMGDVDQFPPPBT WGSL
5961	100	2147	1
2361	198	3147	SGEPRPEPGNMATCIGEKIEDFKVGNLLGKGSFAGVYRAESIHT
	:		GLEVAIKMIDKKAMYKAGMVQRVQNEVKIHCQLKHPSILELYNY
			FEDSNYVYLVLEMCHNGEMNRYLKNRVKPFSENEARHFMHQIIT
			GMLYLHSHGILHRDLTLSNLLLTRNMNIKIADFGLATQLKMPHE
	1		KHYTLCGTPNYISPEIATRSAHGLESDVWSLGCMFYTLLIGRPP
			FDTDTVKNTLNKVVLADYEMPTFLSIEAKDLIHQLLRRNPADRL
ŀ			SLSSVLDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAITASS
		'	STSISGSLFDKRRLLIGQPLPNKMTVFPKNKSSTDFSSSGDGNS
1	•		FYTQWGNQETSNSGRGRVIQDAEERPHSRYLRRAYSSDRSGTSN
1	1		SQSQAKTYTMERCHSAEMLSVSKRSGGGENEERYSPTDNNANIF
			NFFKEKTSSSSGSFERPDNNQALSNHLCPGKTPFPFADPTPQTE
			TVQQWFGNLQINAHLRKTTEYDSISPNRDFQGHPDLQKDTSKNA
			WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF
			GSDPLSEQSKTRGMEPPWGYQNRTLRSITSPLVAHRLKPIRQKT
			KKAVVSILDSEEVCVELVKEYASOEYVKEVLOISSDGNTITIYY
			PNGG\RGFPLA\DRPPSPT\DNISR\YSF\DNLPEKYWRKYQYA
	l		SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVWFYDGVKI
			HKTEDFIQVIEKTGKSYTLKSESEVNSLKEEIKMYMDHANEGHR
ļ i			ICLALESIISEEERKTRSAPFFPIIIGRKPGSTSSPKALSPPPS
			VDSNYPTRDRASFNRMVMHSAASPTOAPILNPSMVTNEGLGLTT
	!		TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGWATQ\LTSGAVW
			· · · · · · · · · · · · · · · · · · ·
			VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLPDYIKQ
F252			KLQCLSSILLMFSNPTPNFH
5962	20	2447	RVCSSSASTASQAVMADAWEEIRRLAADFQRAQFAEATQRLSER
	Į		NCIEIVNKLIAQKQLEVVHTLDGKEYITPAQISKEMRDELHVRG
			GRVNIVDLQQVINVDLIHIENRIGDIIKSEKHVQLVLGQLIDEN
]			YLDRLAEEVNDKLQESGQVTISELCKTYDLPGNFLTQALTQRLG
1 1			RIISGHIDLDNRGVIFTEAFVARHKARIRGLFSAITRPTAVNSL
, ,			ISKYGFQEQLLYSVLEELVNSGRLRGTVVGGRQDKAVFVPDIYS
			RTQSTWVDSFFRQNGYLEFDALSRLGIPDAVSYIKKRYKTTQLL

PCT/US00/34263

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	\=possible nucleotide insertion)
	sequence	<u> </u>	TLKAACYGOGLVDOVEASVEEAISSGTWVDIAPLLPTSLSVEDA
	ł)	
ļ			AILLQQVMRAFSKQASTVVFSDTVVVSEKF\INDCTELFRELMH
		}	QKAEKEMKNNPVHLITEEDLKQISTLESVSTSKKDKKDERRRKA
}	1	1	TEGSGSMRGGGGGNAREYKIKKVKKKGRKDDDSDDESQSSHTGK
ŀ			KKPEISFMFQDEIEDFLRKHIQDAPEEFISELAEYLIKPLNKTY
1			LEVVRSVFMSSTTSASGTGRKRTIKDLQEEVSNLYNNIRLFEKG
			MKFFADDTQAALTKHLLKSVCTDITNLIFNFLASDLMMAVDDPA
			AITSEIRKKILSKLSEETKVALTKLHNSLNEKSIEDFISCLDSA
l]	AEACDIMVKRGDKKRERQILFQHRQALAEQLKVTEDPALILHLT
			SVLLFOFSTHSMLHAPGRCVPQIIAFLNSKIPEDQHALLVKYQG
1	1		LVVKQLVSQSKKTGQGDYPLNNELDKEQEDVASTTRKELQELSS
	ļ.		SIKDLVLKSRKSSVTEE
			
5963	62	1130	PWNPQDFPGNRGLMG\QKGEIGPP\GQQGKKGAPGMP\GLMGSN
1	}		GSPGQPGTPGSKGSKGEPGIQGMPGASGLKGEPGATGSPGEPGY
1	1		MGLPGIQGKKGDKGNQGEKGIQGQKGENGRQGIPGQQGIQGHHG
[AKGERGEKGEPGVRGAIGSKGESGVDGLMGPAGPKGQPGDPGPQ
1	1		GPPGLDGKPGREFSEQFIRQVCTDVIRAQLPVLLQSGRIRNCDH
ļ		1	CLSQHGSPGIPGPPGPIGPEGPRGLPGLPGRDGVPGLVGVPGRP
}	'	j	GVRGLKGLPGRNGEKGSQGFGYPGEQGPPGPPGPEGPPGISKEG
l		1	PPGDPGLPGKDGDHGKPGIQGQPGPPGICDPSLCFSVIARRDPF
1			RKGPNY
5964	3	2147	SCRTRGRLSPLOPREAGSSRGSRARSEPPRPGGMEEACQVQTTK
3904		1 223.	RGDPHELRNIFLOYASTEVDGERYMTPEDFVQRYLGLYNDPNSN
		i	PKIVOLLAGVADOTKDGLISYQEFLAFESVLCAPDSMFIVAFQL
	1		FDKSGNGEVTFENVKEIFGQTIIHHHIPFNWDCEFIRLHFGHNR
1	ļ	i	
1		Í	KKHLNYTEFTQFLQELQLEHARQAFALKDKSKSGMISGLDFSDI
1			MVTIRSHMLTPFVEENLVSAAGGSISHQVSFSYFNAFNSLLNNM
l]	1	ELVRKIYSTLAGTRKDAEVTKEEFAQSAIRYGQATPLEIDILYQ
	,	1	LADLYNASGRLTLADIERIAPLAEGALPYNLAELQRQQSPGLGR
ł	1	ļ	PIWLQIAESAYRFTLGSVAGAVGATAVYPIDLVKTRMQNQRGSG
ļ	1	1	SVVGELMYKNSFDCFKKVLRYEGFFGLYRGLIPQLIGVAPEKAI
			KLTVNDFVRDKFTRRDGSVPLPAEVLAGGCAGGSQVIFTNPLEI
ļ	1		VKIRLQVAGEITTGPRVSALNVLRDLGIFGLYKGAKACFLRDIP
1	1		FSAIYFPVYAHCKLLLADENGHVGGLNLLAAGAMAG\VPAASLV
l .	1	1	TPADVIKTRLOVAARAGOTTYSGVIDCFRKIL\REEGPSAFWKG
1			TAARVFRSSPQFG\VTLVTYELLQRGFYIDFGGLKPAGSEPTPK
1	1	1	SRIADLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSVA
1		1	VVOPKAAVAATO
	 	 	MVTWLYRFLPTSNMAAKLRSLLPPDLRLQFWLHARLQKCFLSRG
5965	1	1498	
1			CGSYCAGAKASPLPGKMAMGLMCGRRELLRLLQSGRRVHSVAGP
1		ľ	SQWLGKPLTTRLLFPAAPCCCRPHYLFLAASGPRSLSTSAISFA
			EVQVQAPPVVAATPSPTAVPEVASGETADVVQTAAEQSFAELGL
1			GSYTPVGLIQNLLEFMHVDLGLPWWGAIAACTVFARCLIFPLIV
İ			TGQREAARIHNHLPEIQKFSSRIREAKLAGDHIEYYKASSEMAL
	1	1	YQKKHGIKLYKPLILPVTQAPIFISFFIALREMANLPVPSLQTG
1			GLWWFQDLTVSDPIYILPLAVTATMWAVLELGAETGVQSSDLQW
			MRNVIRMMPLITLPITMHFPTAVFMYWLSSNLFSLVQVSCLRIP
1			AVRTVLKIPQRVVHDLDKLPPREGFLESFKKGWKNAEMTRQLRE
1			REQRMRNQLELAARGPLRQTFTHNPLLQPGKDNPPNIPSS\SSS
			SSKPKSKYPWHDTLG
F055	 	1005	RSKQVMARLTKRRQADTKAIQHLWAAIEIIRNQKQIANIDRITK
5966	102	1925	
		j	YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQE
		1	GYWLPGDEIDWETENHDWYCFECHLPGEVLICDLCFRVYHSKCL
			SDEFRLRDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE
		, ,	RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE
			FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC
1			KNCFYLANARPDNWFCYPCIPNHELDWAKMKGFGFWPAKVMQKE
1	}		DNQVDVRFFGHHHQRAWIPSENIQDITVNIHRLHVKRSMGWKKA
1			CDELELHQRFLREGRFWKSKNEDRGEEEAESSISSTSNEQLKVT
	1]	QEPRAKKGRRNQSVEPKKEEPEPETEAVSSSQEIPTMPQPIEKV
1		Į.	SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF
İ	1	1	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide _	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine.
1	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
Ì	sequence		\=possible nucleotide insertion)
			KDRMKSDHKRETERVVREALEKLRSEMEEEKRQAVNKAVANMQG
	İ		PMDDYCYOUVEYCYERENEET MAT A TOTAL TO THE TOTAL T
1		i	BMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISQTKKKQWCYNC
5967	102	1925	BEEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
1 330.	102	1925	RSKQVMARLTKRRQADTKAIQHLWAAIEIIRNQKQIANIDRITK
			YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQE
	İ		GYWLPGDRIDWETENHDWYCFECHLPGEVLICDLCFRVYHSKCL
I			SDEFRLRDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE
İ			RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE
1	[·		FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC
Ĭ			KNCFYLANARPDNWFCYPCIPNHELDWAKMKGFGFWPAKVMQKB
	1		DNQVDVRFFGHHHQRAWIPSENIQDITVNIHRLHVKRSMGWKKA
1			CDELELHQRFLREGRFWKSKNEDRGEEEAESSISSTSNEOLKVT
			QEPRAKKGRRNQSVEPKKEEPEPETEAVSSSQEIPTMPOPIEKV
			SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF
1			KDRMKSDHKRETERVVREALEKLRSEMEEEKRQAVNKAVANMQG
	,		EMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISQTKKKQWCYNC
1	}		EEEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
5968	81	1288	VRFPRRGGAPPTVLTPGRQQGVFLGPQRPGSEPDIPARGQPHPP
]			RPVGVSTSAQAQVQPPAMHRRRLALGLGFCLLAGTSLSVLWVYL
1	•		ENWLPVSYVPYYLPCPEIFNMKLHYKREKPLQPVVWSQYPQPKL
ı			LEHRPTQLLTLTPWLAPIVSEGTFNPELLQHIYQPLNLTIGVTV
			FAVGN/HFLESAEEFFMRGYRVHYYIFTDNPAAVPGVPLGPHRL
			LCCIDIOCUCUMPERCADDAETICOUTA PRANTONIA DEL S
			LSSIPIQGHSHWEETSMRRMETISQHIAKRAHREVDYLFCLDVD
			MVFRNPWGPETLGDLVAAIHPSYYAVPRQQFPYERRRVSTAFVA
			DSEGDFYYGGAVFGGQVARVYEFTRGCHMAILADKANGIMAAWR
1			EESHLNRHFISNKPSKVLSPEYLWDDRKPQPPSLKLIRFSTLDK
5969	1106		DISCLRS
3303	1126	503	DVGFNIKRKRCDLDVFLESPRKPSGRRDRAPEKQRRIAANKCLC
1			TGVREGEPPS/TTSQKVKEAGRDFTYLIVVLFGISITGGLFYTI
			FKELFSSSSPSKIYGRALEKCRSHPEVIGVFGESVKGYGEVTRR
1	•	•	GRRQHVRFTEYVKDGLKHTCVKFYIEGSEPGKQGTVYAQVKENP
		* *	GSGEYDFRYIFVEIESYPRRTIIIEDNRSQDD
5970	316	4712	SQDNIGHRLLQKHGWKLGQGLGKSLQGRTDPIPIVVKYDVMGMG
	• • 1	•	RMEMELDYAEDATERRRVLEVEKEDTEELRQKYKDYVDKEKAIA
1 1	1		KALEDLRANFYCELCDKQYQKHQEFDNHINSYDHAHKQRLKDLK
			QREFARNVSSRSRKDEKKQEKALRRLHELAEQRKQAECAPGSGP
1	1		MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG
1			GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF
1 . 1		·	SFAKKAPVKLESIASVFKDHAEEGTSEDGTKPDEKSSDQGLQKV
			GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE
/			PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES
1			KKGSSPKPKSCIKAAASQGAEKTVSEVSBQPKETSMTEPSEPGS
1 1	ļ		KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA
, 1	ļ	J	GKESQEGPKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS
		ļ	YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE
į į		İ	DMKCKEACGERTINGCCCOMDADAGCCCCCOMDADAGCCCCCCOMDADAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
į į			PNKSKEVGGBKIVRSSGGRMDAPASGSACSGLNKQBPGGSHGSE
		•	TEDTGRSLPSKKERSGKSHRHKKKKKKKKKKSKKKKKKHKADTEEK
			SSKAESGEKSKKRKRKRKKKKKSSAPADSBRGPKPEPPGSGSPA
			PPRRRRAQDDSQRRSLPAEEGSSGKKDEGGGGSSSQDHGGRKH
[KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ
)			KSPSQYSEEEEEEDSGSEHSRSRSRSGRRHSSHRSSRRSYSSSS
			DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS
	1	ľ	SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSRS
i	1	J	SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR
	1	Ì	KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK
l			DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL
	j	İ	EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPOGYFGPKLPPS
			LGNKPVLPLIGKLPATRKPNKKCEESGLERGEBOEOSETEEGPP
1		İ	GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG
	į		PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSOPGPVESSL
		1	The state of the s
	I	I	LPIAPDLEHFPSYAPPSGDPSIESTDGAEDA\SLAPLESQPITF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į.	amino acid		S=Serine, T=Threonine, V=Valine,
[residue of	
l .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
!	amino acid	sequence	Codon, /=possible nucleotide deletion,
ŀ	sequence	1 -	\=possible nucleotide insertion)
			TPEEMEKYSKLOOAAOOHIOOOLLAKOVKAFPASAALAPATPAL
l	1	l.	OPIHIOOPATASATSITTVOHAILQHHAAAAAAAIGIHPHPHPQ
ŀ		ļ	PLAQVHHIPQPHLTPISLSHLTHSIIPGHPATFLASHPIHIIPA
			SAIHPGPFTFHPVPHAALYPTLLAPRPAAAAATALHLHPLLHPI
!		1	FSGQDLQHPPSHGT
5971	53	2149	SFLYFVGVDMDNPIGNWDGRFDGVQLCSFACVESTILLHINDII
3911)	2143	PESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDPGNRN
			_
			RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTD
			FDRSSPPLQPPPVNSLTTENRFHSLPFSLTKMPNTNGSIGHSPL
ł			SLSAQSVMEELNTAPVQESPPLAMPPGNSHGLEVGSLAEVKENP
	ſ		PFYGVIRWIGQPPGLNEVLAGLELEDECAG\CTDGTF/REGTRY
1			
1			FTCALKKALFVKLKSCRPDSRFASLQPVSNQIERCNSLAIWEAY
,	1		LSEVVEENTPTQKWEKEGLEIMIG\KKKGIQGHYNSCYLDSTLF
1			CLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRIYG
ĺ	1		YVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRV
l			EPLLKIRSAGOKVODCYFYOIFMEKNEKVGVPTIQQLLEWSFIN
1	1		SNLKFAEAPSCLIIQMPRFGKDFKLFKKIFPSLELNITDLLEDT
İ	I	i	
	1	1	PROCRICGGLAMYECRECYDDPDISAGKIKOFCKTCNTQVHLHP
	1	j	KRLNHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHY
	1		VAFVKYGKDDSAWLFFDSMADRDGGQNGFNIPQVTPCPEVGEYL
			KMSLEDLHSLDSRRIQGCARRLLCDAIYVPCTQSPTMSLYK
5050	 	1761	ILLAGSPSPRDOCSORQSSGGDKELVTRGCTFSTAVVSPSAMTQ
5972	440	1/61	
	1	ŀ	EPFREELAYDRMPTLERGRQDPASYAPDAKPSDLQLSKRLPPCF
i	İ	1	SHKTWVFSVLMGSCLLVTSGFSLYLGNVFPAEMDYLRCAAGSCI
	į		PSAIVSFTVSRRNANVIPNFQILFVSTFAVTTTCLIWFGCKLVL
			NPSAININFNLILLLLELLMAATVIIAARSSEEDCKKKKGSMS
ļ	1		DSANILDEVPFPARVLKSYSVVEVIAGISAVLGGIIALNVDDSV
1	1		L = -
1		ļ	SGPHLSVTFFWILVACFPSAIASHVAAECPNKCLVEVLIAISSL
l	l .	1	TSPLLFTASGYLSFSIMRIVEMFKDYPPAIKPSYDVLLLLLLLV
ļ	İ	Į.	LLLQA/GPQHGHRHPVRALQGQCKAAGCILGHPERPAGAPGWGG
		1	GOEPPEGVROGESLESRRGANGPVTPRRGNRVAAPSLAPGMETH
	1	ł	NP.
5973	 	-2007	NGDGKDLFGHIWAWRSNGIISNFRRSPHAGMAEDEPDAKSPKTG
59/3	65	- 2007	
		1	GRAPPGGAEAGEPTTLLQRLRGTISKAVQNKVEGILQDVQKFSD
l	1	ĺ	NDKLYLYLQLPSGPTTGDKSSEPSTLSNEEYMYAYRWIRNHLEE
		1	HTDTCLPKQSVYDAYRKYCESLACCRPLSTANFGKIIREIFPDI
Į.		1	KARRLGGRGOSKYCYSGIRRKTLVSMPPLPGLDLKGSESPEMGP
ĺ	1		EVTPAPRDELVEAACALTCDWAERILKRSFSSIVEVARFLLQOH
1			
l	1	1	LISARSAHAHVLKAMGLAEEDEHAPRERSSKPKNGLENPEGGAH
1	1	1	KKPERLAQPPKDLEARTGAGPLARGERKKSVVESSAPGANNLQV
1	1	,	NALVARLPLLLPRAPRSLIPPIPVSPPILAPRLSSGALKVÄTLP
1	1	1	LSSRAGAPPAAVPIINMILPTVPALPGPGPGPGRAPPGGLTQPR
1	1		GTENREVGIGGDOGPHDKGVKRTAEVPVSEASGOAPPAKAAKOD
1	1		
1	1	1	IEDTASDAKRKRGRPLKKSGGSGERNSTPLKSAAAMESAQSSRL
ļ		1	PWETWGSGGEGNSAGGAERPGPMGEABKGAVLAQG\QGDGTVSK
i			GGRGPGSQHTKEAEDKIPLVPSKVSVIKGSRSQKEAFPLAKGEV
1		1	DTAPOGNKDLKEHVLQSSLSQEHKDPKATPP
5974	4293	2200	LGLOMHTTSGRIHOAMVTSLNEDNESVTVEWIENGDTKGK\BID
33/4	1433	4200	LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR
1			
1			TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNGSV\S
1	1		DISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKREKRRLQQQELR
1		1	EKRAODVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC
İ	1		VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDLTRYL
	1		
	1		ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG
}		1	QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK
1	1		LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVGLQE
	-	1	REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR
	1	1	KGKLHGKFSLIDLAGNERGADTSSADRQTRLEGAEINKSLLALK
1			NUMBER STATES OF THE PROPERTY
1	1	1	ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATISPG
1	1		MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPPNQI\DD
1]	LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM
	1	t .	

SEQ	Predicted	Dwodd - bod ond	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
"""	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			EEQVVEDHRAVFQESIRWLEDEKALLEMTEEVDYDVDSYATQLE
			AILEQKIDILTELRDKVKSFRAALQEEEQASKQINPKRPRAL
5975	4293	2200	LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\EID
1	· .		LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR
			TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNGSV\S
1			DISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKREKRRLQQQELR
			EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC
			VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDLTRYL
1			ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG
			QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK
			LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVGLQE
			REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR
1			KGKLHGKFSLIDLAGNERGADTSSADRQTRLEGAEINKSLLALK
1			ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATISPG
1			MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPPNQI\DD
1	,		LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM
1			BEQVVEDHRAVFQESIRWLEDEKALLEMTEEVDYDVDSYATQLE
L_			AILEQKIDILTELRDKVKSFRAALQEERQASKQINPKRPRAL
5976	20	2949	VHHLHLTRVSVVVNLDIILRIAQQMGIKTLNLVLG\LKRA\LEF
			PEVSWMEVKDPNMKGAMLTNTGKYAIPTIDA\EAYAIGKKEKPP
			FLPEEPSSSSEEDDPIPDELLCLICKDIMTDAVVIPCCGNSYCD
			BCIRTALLESDEHTCPTCHQNDVSPDALIANKFLROAVNNFKNE
İ			TGYTKRLRKQLPSPPPPIPPPRPLIQRNLQPLMRSPISRQQDPL
			MIPVTSSSTHPAPSISSLTSNQSSLAPPVSGNPSSAPAPVPDIT
			ATVSISVHSEKSDGPFRDSDNKILPAAALASEHSKGTSSIAITA
1			LMEEKGYQVPVLGTPSLLGQSLLHGQLIPTTGPVRINTARPGGG
			RPGWEHSNKLGYLVSPPQQIRRGERSCYRSINRGRHHSERSQRT
		\$	QGPSLPATPVFVPVPPPPLYPPPPHTLPLPPGVPPPOFSPOFPP
	•	•	GQP\PPAGYSVPPPGFPPAPANLSTPWVSSGVQTAHSNTIPTTQ
			APPLSREEFYREQRRLKEEEKKKSKLDEFTNDFAKELMEYKKIQ
			KERRRSFSRSKSPYSGSSYSRSSYTYSKSRSGSTRSRSYSRSFS
		•	RSHSRSYSRSPPYPRRGRGKSRNYRSRSRSHGYHRSRSRSPPYR
	:		RYHSRSRSPQAFRGQSPNKRNVPQGETEREYFNRYREVPPPYDM
1 1			KAYYGRSVDFRDPFEKERYREWERKYREWYEKYYKGYAAGAOPR
			PSANRENFSPERFLPLNIRNSPFTRGRREDYVGGQSHRSRNIGS
; I			NYPEKLSARDGHNQKDNTKSKEKESENAPGDGKGNKHKKHRKRR
]			KGEESEGFLNPELLETSRKSREPTGVEENKTDSLFVLPSRDDAT
·	. 1		PVRDEPMDAESITFKSVSEKDKRERDKPKAKGDKTKRKNDGSAV
	1		SKKENIVKPAKGPQEKVDG\DVRDLLDLNL\QLKKPKEETPKDL
]	Ī		TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRNKTSQRGKSE
<u> </u>	1		EGLFQRCQIRKANN
5977	1363	1336	FLEDRGQVLSHFQCLSLHSINHILHPGAGVAAGPATGW/REYLT
	1	·	PVLKESKFKETGVITPEEFVAAGDHLVHHCPTWQWATGEELKVK
			AYLPTGKQFLVTKNVPCYKRCKQMBYSDELEAIIEEDDGDGGWV
	ļ		DTYHNTGITGITEAVKEITLENKDNIRLQDCSALCEEEEDEDEG
1			EAADMEEYEESGLLETDBATLDTRKIVEACKAKTDAGGEDAILQ
1 1	ļ		TRTYDLYITYDKYYQTPRLWLFGYDBQRQPLTVEHMYEDISQDH
	ľ		VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIETVAEGGGEL
			GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM
5978	160	3213	RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ
]	100	2613	= 1
1			RPRREPEAMDEQSVESIAEVFRCFICMEKLRDARLCPHCSKLCC
j l	1		FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWAEEVTQQLDTLQ
[LCSLTKHEENEKDKCENHHEKLSVFCWTCKKCICHQCALWGGMH
		i	GGHTFKPLAEIYEQHVTKVNEEVAKLRRRLMELISLVQEVERNV
			EAVRNAKDERVREIRNAVEMMIARLDTQLKNKLITLMGQKTSLT
			QETELLESLLQEVEHQLRSCSKSELISKSSEILMMFQQVHRKPM
[ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP
			LQVSGLCWRLKVYPDGNGVVRGYYLSVFLELSAGLPETSKYEYR
]			VEMVHQSCNDPTKNIIREFASDFEVGECWGYNRFFRLDLLANEG
			YLNPONDTVILRFQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ
L		<u>-</u>	INNLKERLTIELSRTQKSRDLSPPDNHLSPQNDDALETRAKKSA

ID		- 71	This said magment containing gignal nontide
	Predicted	Predicted end	Amino acid segment containing signal peptide
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1		residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	W=Tryptopnan, Y=Tyrosine, X=Unknown, ~=Scop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	ł	\=possible nucleotide insertion)
-			CSDMLLER\GPYSAS\VREAKEDEEDEEKIQNEDYHHELSDGDL
		i	DLDLVYEDEVNQLDGSSSSASSTATSNTEENDIDEETMSGENDV
		ł	BYNNMELEEGELMEDAAAAGPAGSSHGYVGSSSRISRRTHLCSA
i		ĺ	
]	ATSSLLDIDPLILIHLLDLKDRSSIENLWGLQPRPPASLLQPTA
ĺ		ļ	SYSRKDKDQRKQQAMWRVPSDLKMLKRLKTQMAEVRCMKTDVKN
į]	TLSEIKSSSAASGDMQTSLFSADQAALAACGTENSGRLQDLGME
			LLAKSSVANCYIRNSTNKKSNSPKPARSSVAGSLSLRRAVDPGE
			NSRSKGDCOTLSEGSPGSSQSGSRHSSPRALIHGSIGDILPKTE
i		•	DROCKALDSDAVVVAVFSGLPAVEKRRKMVTLGANAKGGHLEGL
· · · · · · · · · · · · · · · · · · ·			
l			QMTDLENNSETGELQPVLPEGASAAPEEGMSSDSDIECDTENEE
- 1		Ĺ	QEEHTSVGGFHDSFMVMTQPPDEDTHSSFPDGEQIGPEDLSFNT
[*	•	1	DENSGR
5979	212	3665	LPDMTMYLWLKLLAFGFAFLDTEVFVTGQSPTPSPTDAYLNASE
22,2	6- ± 6-		TTTLSPSGSAVISTTIATTPSKPTCDEKYANITVDYLYNKETK
1			LFTAKLNVNENVECGNNTCTNNEVHNLTECKNASVSISHNSCTA
1			PDKTLILDVPPGVEKVPVHCCS\QVEQPDSTIWLKWKNIETSTC
			DTQNITYRFQCGNMIFDNKEIKLENLEPEHEYKCDSEILYNSHK
			FTNASKIIKTDFGSPGEPQIIFCRSEAAHQGVITWNPPQRSFHN
i		1	FTLCYIKETEKDCLNLDKNLIKYDLQNLKPYTKYVLSLHAYIIA
1			KVQRNGSAAMCHFTTKSAPPSQVWNMTVSMTSDNSMHVKCRPPR
i		1	DRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKDLQYSTDYTFK
			AYFHNGDYPGEPFILHHSTSYNSKALIAFLAFLIIVTSIALLVV
. 1			LYKIYDLHKKRSCNLDEQQELVERDDEKQLMNVEPIHADILLET
		1	YKRKIADEGRLFLAEFQSIPRVFSKFPIKEARKPFNQNKNRYVD
			ILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPR
. 1		1	DETVDDFWRMIWEQKATVIVMVTRCEEGNRNKCAEYWPSMEEGT
ĺ			RAFGECCCKDLTKHKRCP\DYIIQKLNIVNKKEKATGREVTHIQ
		l	
		ì	FTSWPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR
		1	TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQYI
			LIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE
			FQRLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE
·		1 .	LEMSKESEHDSDESSDDDSDSEEPSKYINASFIMSYWKP\EVMI
1	ľ	· .	AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG
· •			
		1	EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ
			YTNWSVEQLPAEPKELISMIQVVKQKLPQKNSSEGNKHHKSTPL
	ļ	1	LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP
		i	GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD
		1	KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP
			ASPALNOGS
		2262	DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI
5980	3	2363	
		1	PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR
	1		PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP
	<u> </u>		VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN
			CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN
		}	LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN
	1		IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP
	1	1	
}	1		VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL
!	1		ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR
, ,	1		MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK
Į ,	1		SICSOFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK
Į l			DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN
}		1	WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG
 	}		SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL
			DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA
h	1	1	MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK
			LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG
		I .	
		1	DDI.KRDI.I.GIVODMI.OGIMNRI.CKS\NSROPNRGLDDST
			DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST
5981	1	2519	GRRHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL
5981	1	2519	GRRHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP
5981	ì	2519	GRRHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL

SEO	Predicted	Predicted end	I Amino agid seemest combail to deal
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Clutamia Acid Raphonalalaria a car
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first		L=Leucine, M=Methionine, N=Asparagine,
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
``	sequence	i	\=possible nucleotide insertion)
			TEFGMAIGPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVQTD
1	ł.		LPFHPLTQMMYSPQNSDYLLALSTENGLWVSKNFGGKWEEIHKA
] .	J	[VCLAKWGSDNTIFFTTYANGSCKADLGALELWRTSDLGKSFKTI
l l	-		GVKIYSFGLGGRFLFASVMADKDTTRRIHVSTDQGDTWSMAQLP
İ	•		SVGQEQFYSILAANDDMVFMHVDEPGDTGFGTIFTSDDRGIVYS
			KSLDRHLYTTTGGETDFTNVTSLRGVYITSVLSEDNSIQTMITF
1			
]		DQGGRWTHLRKPENSECDATAKNKNECSLHIHASYSISQKLNVP
	İ		MAPLSEPNAVGIVIAHGSVGDAISVMVPDVYISDDGGYSWTKML
1			EGPHYYTILDSGGIIVAIEHSSRPINVIKFSTDEGQCWQTYTFT
			RDPIYFTGLASEPGARSMNISIWGFTESFLTSQWVSYTIDFKDI
1	ĺ		LERNCEEKDYTIWLAHSTDPEDYEDGCILGYKEQFLRLRKSSVC
			QNGRDYVVTKQPSICLCSLEDFLCDFGYYRPENDSKCVEQPELK
1		·	GHDLEFCLYGREEHLTTNGYRKIPGDKCQGGVNPVREVKDLKKK
1			CTSNFLSPEKQNSKSNSVPIILAIVGLMLVTVVAGVLIVKKYVC
			GGRFLVHLYSVLQQH\AEA\NGVDGVDALDTASHTNKSGYHDDS
· .			DEDLLE
5982	56	2316	ATRPPRGSSWCRQFSRTASAAPGRSNMLRIPVRKALVGLSKSPK
1			GCVRTTATAASNLIEVFVDGQSVMVEPGTTVLQACEKVGMQIPR
1			FCYHERLSVAGNCRMCLVEIEKAPKVVAACAMPVMKGWNILTNS
			EKSKKAREGVMEFLLANHPLDCPICDQGGECDLQDQSMMFGNDR
			SRFLEGKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDD
1			LGTTGRGNDMQVGTYIEKMFMSELSGNIIDICPVGALTSKPYAF
1 .			TARPWETRKTESIDVMDAVGSNIVVSTRTGEVMRILPRMHEDIN
1			EEWISDKTRFAYDGLKRQRLTEPMVRNEKGLLTYTSWEDALSRV
1			AGMLQSFQGKDVAAIAGGLVDAEALVALKDLLNRVDSDTLCTER
1	1		VFPTAGAGTDLRSNYLLNTTIAGVEEADVVLLVGTNPRFEAPLF
1	٠ ا		NARIRKSWLHNDLKVALIGSPVDLTYTYDHLGDSPKILQDIASG
	·		SHPFSQVLKEAKKPMVVLGSSALQRNDGAAILAAVSSIAQKIRM
	* *		TSGVTGDWKVMNILHRIASQVAALDLGYKPGVEAIRKNPPKVLF
			LLGADGGCITRQDLPKDCFIIYQGHHGDVGAPIADVILPGAAYT
1 1			EKSATYVNTEGRAQQTKVAVTPPGLAREDWKIIRALSEIAGMTL
			PYDTL\DQVRNRLEEVSPNLVRYDDIEG\ANYFQQANELSKLVN
1 .1			QQLLADPLVPPQLTMKDFYMTDSISRASQTMAKCVKAVTEGAQA
1 :1	, 1		
5983	248	1862	VEEPSIC
2703	248	1763	EARGDGGRRHRASGRRAGRGEP\AGLKSQGQRAVPKRAVARGG
1 1	*		RQ\YSAAIALLEPAGSBIADDLSILYSNRAACYLKEGNCSGCIQ
1 1	ľ		DCNRALELHPFSMKPLLRRAMAYETLEQYGKAYVDYKTVLQIDC
	İ		GLQLANDSVNRLSRILMELDGPNWREKLSLIPAVPASVPLQAWH
]			PAKEMISKQAGDSSSHRQQGITDEKTFKALKEEGNQCVNDKNYK
1	}		DALSKYSECLKINNKECAIYTNRALCYLKLCQFEEAKQDCDQAL
[QLADGNVKAFYRRALAHKGLKNYQKSLIDLNKVILLDPSIIEAK
	I		MELBEVTRLLNLKDKTAPFNKEKERRKIEIQEVNEGKEEPGRPA
] [GEVSTGCLASEKGGKSSRSPEDPEKLPIAKPNNAYEFGQIINAL
]	1		STRKDKEACAHLLAITAPKDLPMFLSNKLEGDTFLLLIQSLKNN
į l	ļ	1	LIEVODELUVOULI VI CVAEDEVANI DI POVOCCO PER PER CONTE
	ł		LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL
5984	765	1100	SDTPNNHFTLEDIQALKRQYEL
2504	755	1193	SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSFVL
1	ļ		TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG
	Í		SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY
L!			FHHSLRSISRFSSG
5985	22	1408	RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR
·	J		RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE
			FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDRVADAK
j l			
			GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEBEEDTDPRVI
[HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD
		j	EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG
			ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM
			FESFIESVPLLKSLEVSERMKIVDVIGEKIYKR/DGERIITQGE
			K\ADSFYIIESGEVSILIRSRTKSNKDGGNQEVEIARCHKGQYF
			GELALVTNKPRAASAYAVGDVKCLVMDVQAFERLLGPCMDIMKR
			NISHYEEQLVKMFGSSVDLGNLGQ

PCT/US00/34263

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į.			
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
,	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
5986	1806	484	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP
3300	1000	10-2	SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED
Į.	1		
1		·	GLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI
	1		LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGQHSPLRE
i	ŧ	k .	EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFQQEFSTP
İ	1	1	SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG
		i	QNWLNDQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG
1	1		VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ
1	1	1	
l	1		RTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN
		1	DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL
l			TV
5987	1806	484	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP
1		1	SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED
1		1	GLRWTPKSPLDPDSGLLSCTLPNGFGGOSGPEGERSLAPPDASI
1			
1	1	1	LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGQHSPLRE
i			EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFQQEFSTP
1		1	SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG
1			QNWLNDQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG
	İ		VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ
			RTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN
	1	İ	<u> </u>
l		ł.	DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL
1	f .	f	TV
5988	1292	410	FKKYFLSFLGLLESSHSRDRIHNLVLMFLLATHNLVWWFTCRFQ
1		1	RLDCIYLNAGIMPNPQLNIKALLFGLFS\AEGLLTQGDKITADG
	l ·	}	LOEVFETDVFGHFILIRELEPLLCHSDNPSQLIWTSSRNARKSN
1 .	-		FSLEDFOHSKGKEPYSSSKYATDLLSVALNRNFNQQGLYSNVAC
		İ	PGTALTNLTYGILPPFIWTLLMPAILLLRFFANAFTLTPYNGTE
1	1		l control of the cont
1			ALVWLFHQKPESLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAE
1		1	KFYQKLLELEKHIRVTIQKTDNQARLSGSCL
5989	194	2610	AMDFPQHSQHVLEQLNQQRQLGLLCDCTFVVDGVHFKAHKAVLA
]	į į	ACSEYFKMLFVDQKDVVHLDISNAAGLGQVLEFMYTAKLSLSPE
	1		NVDDVL\AVATFLQMQDIITACHALKSLAEPATSPGGNAEALAT
1		•	EGGDKRAKEEKVATSTLSRLEQAGRSTPIGPSRDLKEERGGQAQ
			SAASGAEQTEKADAPREPPPVELKPDPTSGMAAAEAEAALSESS
1	ł		
1	1		EQEMEVEPARKGEEEQKEQEEQEEGAGPAEVKEEGSQLENGEA
1.	1		PEENENEESAGTDSGQELGSEARGLRSGTYGDRTESKAYGSVIH
1			KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDPAACK
1			AHEKTHSPLKPYGCEECGKSYRLISLLNLRKKRHSGEARYRCED
1			CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE
1			THOTOKEHKCPHCDKKFNQVGNLKAHLKIHIADGPLKCRECGKQ
1			FTTSGNLKRHLRIHSGEKPYVCIHCORQFADPGALQRHVRIHTG
1		ļ	
1			EKPCQCVMCGKAFTQASSLIAHVRQHTGEKPYVCERCGKRFVQS
Ι .			SQLANHIRHHDNIRPHKCSVCSKAFVNVGDLSKHIIIHTGEKPY
1	1.		LCDKCGRGFNRVDNLRSHVKTVHQGKAGIKILEPEEGSEVSVVT
1			VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA
			VKOVOEEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM
1		1	FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGAEGQPALAE
1			T control of the cont
		<u> </u>	TSPTAPECPPPAE
5990	2	4700	FGPGPDSGGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD
1	1		SGFVSLSRLGPSLRDKDLEMEELMLQDETLLGTMQSYMDASLIS
	İ		LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR
Į.	1	1	PRWGOSPPPOORSDGEEEEEVASFSGQILAGELDNCVSSIPDFP
1		1	MHLACPEEEDKATAAEMAVPAAGDESISSLSELVRAMHPYCLPN
1		1	
1	1		LTHLASLEDELQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV
1		1	VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL
1	1	1	CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP
1	1	1	GSORARKGRKKKSKEOPAACVEGYARRLRSSSRGQSTVGTEVTS
ı	Į	1	QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN
1		1	LERSAGOSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS
	1	1	PEVSWG7SSAWVEGATINFIANTATATION AND ANSWGWS
1		l .	
	ļ		PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA EPVLINPVLADSAAVDPAVVPISDNLPPVDAVPSGPAPVDLALV

eptide d, E= ine, ine, "Stop LVESES SEYRR PPAPAK SPTEQV LGMPPS SSTCTY SRGTPA ASPHPK ETRPRE RTQGSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSQ RSLSPP RSRSRS VVFIGK
LIVESES SEYRRR PPAPAK SPTEQV LIGMPPS SPSGYP SSTCTY SRGTPA ASPHPK ETRPRB RTQGSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
LVESES SEYRRR PPAPAK SPTEQV LIGMPPS SPSGYP SSTCTY SRGTPA ASPHPK ETRPRE RTQGSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
LVESES SEYRRR PPAPAK SPTEQV LIGMPPS SPSGYP SSTCTY SRGTPA ASPHPK ETRPRE RTQGSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
LVESES SEYRRR PPAPAK SPTEQV LIGMPPS SPSGYP SSTCTY SRGTPA ASPHPK ETRPRE RTQGSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
LVESES SEYRRR PPAPAK SPTEQV LGMPPS SPSGYP SSTCTY SRGTPA ASPHPK ETRPRE RTQSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
LVESES SEYRRR PPAPAK SPTEQV LGMPPS SPSGYP SSTCTY SRGTPA ASPHPK ETRPRE RTQSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
LVESES SEYRRR PPAPAK SPTEQV LGMPPS SPSGYP SSTCTY SRGTPA ASPHPK ETRPRE RTQSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
LVESES SEYRRR PPAPAK SPTEQV LGMPPS SPSGYP SSTCTY SRGTPA ASPHPK LETRPRE RTQSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
SEYRRR PPAPAK SPTEQV LGMPPS SPSGYP SSTCTY SRGTPA ASPHPK LETRPRE RTQSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
SEYRRR PPAPAK SPTEQV LGMPPS SPSGYP SSTCTY SRGTPA ASPHPK LETRPRE RTQSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
SPTEQV LGMPPS SPSGYP SSTCTY SRGTPA ASPHPK ETRPRB RTQGSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
ELGMPPS SPSGYP SSTCTY SSRGTPA ASPHPK ETRPRB RTQGSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
SPSGYP SSTCTY SRGTPA ASPHPK ETRPRB RTQGSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
SPSGYP SSTCTY SRGTPA ASPHPK ETRPRB RTQGSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
SRGTPA ASPHPK ETRPRE RTQGSE ADSLAV LWKPLA GVHGPS KRHQDI .PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
ASPHPK ETRPRE RTQGSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
ETRPRE RTQGSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
RTQGSE ADSLAV LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
ADSLAV LLWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
LWKPLA GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
GVHGPS KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
KRHQDI PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
PCLAPS ASPSSQ RSLSPP RSRSRS VVFIGK
ASPSSQ RSLSPP RSRSRS VVFIGK
RSLSPP RSRSRS VVFIGK
RSRSRS VVFIGK
VVFIGK
YRYAEE
SNREDF
LGLQAR
RNLNLK
TLQGKL
ELETDI
DHAEEM
HRNVMM
WLITGI
VEGL KLRRVL
AICFVC
LMGPVK
LFCILO
Dr CIDQ
FCFPGS
RLDLEM
TEFLSO
IHRDLK
YRAPEI
Q\LFRI
NLEPEG
YVLORF
SCTWPL
PEPAGG
PEKRLT
SKFIKV
RGRSKA
ADMWTT
GGVPPT
LHTYSS
LMTQVD
SLVPTL
LDLDMY
RRLPGR
RRLPGR AAAAAA

CEO I	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ISDYFERRVEQPLYGLDGSAAKEATEEQSALPTLMSVMLAKPRL
			DTEQLAQRGAGLCFTFVSAQQNSPSSTGSGNTEHSCSSQKQISI
			QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLLRANCDLR
			RQI\DEQQKMLEKYK\ERLNRCFDNEPRNFLIEKSKQEKMACRD
		,	KSMQDRLRLGHFTTVRHGASFTEQWTDGYAFQNLIKQQERINSQ
			REEIERORKMLAKRKPPAMGOAPPATNEOKORKSKTNGAENETL TLAEYHEOEEIFKLRLGHLKKEEAEIOAELERLERVRNLHIREL
			TLAEYHEQEETFKLKLGHLKKEEAETQAELEKVKNLHTKEB KRIHNEDNSQFKDHPTLNDRYLLLHLLGRGGFSEVYKAFDLTEQ
			RYVAVKIHOLNKNWRDEKKENYHKHACREYRIHKELDHPRIVKL
			YDYFSLDTDSFCTVLEYCEGNDLDFYLKQHKLMSEKEARSIIMQ
			IVNALKYLNEIKPPIIHYDLKPGNILLVNGTACGEIKITDFGLS
			KIMDDDSYNSVDGMELTSQGAGTYWYLPPECFVVGKEPPKISNK
	1		VDVWSVGVIFYQCLYGRKPFGHNQSQQDILQENTILKATEVQFP
			PKPVVTPEAKAFIRRCLAYRKEDRIDVQQLACDPYLLPHIRKSV
			STSSPAGAAIASTSGASNNSSSN
5996	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
ا ا			LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
	1		AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
			FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
			FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5997	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
			LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
j			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
	İ	1	FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
i e			
ļ			FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5998	1612	981	FFSIFTWSLTAALAVRRPKDLSFQEEYSTLPP\ASAQP DOOACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB
5998	1612	981	FFSIFTWSLTAALAVRRPKDLSFQEEYSTLPP\ASAQP DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
5998	1612	981	FFSIFTWSLTAALAVRRPKDLSFQEEYSTLPP\ASAQP DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
5998	1612	981	FFSIFTWSLTAALAVRRPKDLSFQEEYSTLPP\ASAQP DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
			FFSIFTWSLTAALAVRRPKDLSFQEEYSTLPP\ASAQP DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP
5998 5999	1612	981	FFSIFTWSLTAALAVRRPKDLSFQEEYSTLPP\ASAQP DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP
			FFSIFTWSLTAALAVRRPKDLSFQEEYSTLPP\ASAQP DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNBGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG
			PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS PFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG
			FFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWOYSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS
			FFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWOYSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG
			FFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS CVYLGLSPRDLVLHFRHKGLTLFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD
			FFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS CVYLGLSPRDLVLHFRHKGLTLFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS
			FFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGHMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE OLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE
			FFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGHMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI
			PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS PFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQBSNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQOKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL
			PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQBSNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTERRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV
			PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQBSNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTERRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK
			FFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWOYSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQOHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP
			PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWOYSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNYMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP
5999	2	1790	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWOSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLFITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR
5999	2	1790	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLPP\ASAQP DQQACLIGHMTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK
5999	2	1790	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGHMTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLTLFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIFGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNYAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KABELIQQEHADQAEIRSLVTWGMYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK
5999	2	1790	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLPP\ASAQP DQQACLIGHMTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLPPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTTSRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD
5999	2	1790	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGHMTTEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP RPPMEKARRGGDGVPRGPVTHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMISSLGGASLEGS QVYLGLSPRDLVLHFRHKGLTLFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNYAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEPTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NOYLKVLLALKLHKMREEGEEEGGEK\LVEEALEKAPG\VTDV
5999	2	1790	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYOEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVWAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVWTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFKTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEPTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY
5999	2	1790	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQBSNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVWTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLAIKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKKALBYIP\NNAYLHCQIGCCY RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR
5999	2	1790	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWOYSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCOVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQBSNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVWTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNERALECLR KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGGEEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN
5999	2	1790	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWOYSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCOVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNERALECLR KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRIESPELDCEGGWTLKCGGNQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGGEEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKVFQVMMLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL
5999	2	1790	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQBSNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTERRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVWTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS
5999	101	1790	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWOYSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNYMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQAEIRSLVTWGNYAWVYHMGRLSDVQIYVDK VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERARVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKTAKMRL SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS SWNGE
5999	2	1790	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWOYSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL NAHSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL KAEELIQQEHADQAEIRSLVTWGNYAWVYHMGRLSDVQIYVDK VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEPTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS SWNGB AFAHSPSRGHRHTHIHTPRHTPRCTMAESHLQSSLITASQFFEI
5999	101	1790	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPTTVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEPTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS SWNGE AFAHSPSRGHRHTHIHTPRHTPRCTMAESHLQSSLITASQFFEI WLHFDADGSGYLEGKELQNLIQELQQARKKAGLELSPEMKTFVD
5999	101	1790	PFSIFTWSLTAALAVRRPKDLSFQEEYSTLFP\ASAQP DQQACLIGIMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCB LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA FWAFLWFTGDSCYL\ANQWOYSKPKDNPLNEGTDASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG LLQAKLQLITHAYFEEKDFSQISILKELYEHMISSLGGASLEGS QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL NASSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEPTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALBYIP\NNAYLHCQIGCCY RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS SWNGB AFAHSPSRGHRHTHIHTPRHTPRCTMAESHLQSSLITASQFFEI

- 000	15.1.		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
I.	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
)	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
			LKLFDSNNDGKLELTEMARLLPVQENFLLKFQGIKMCGKEFNKA
ł			FELYDQDGNGYIDENELDALLKDLCEKNKODLDINNITTYKKNI
1	l .	}	MALSDGGKLYRTDLALILCAGDN
6002	977	81	LAPPGGGLHIPPRTPLSHSRPPPSHHAPHPSPLPLPPADLHPHS
""]	"	1
1			SMAQRSDLLELDCQLTRDRVVVVSHDENLCRQSGLNRDVGSLDF
	j		EDLPLYKEKLEVYFSPGHFAHGSDRRMVRLEDLFQRFPRTPMSV
1	1		EIKGKNBELIREQ/VLVRRYDRNEITIWASEKSSVMKKCKAANP
			EMPLSFTISRGFWVLLSYYLGLLPFIPIPEKFFFCFLPNIINRT
			YFPFSCSCLNQLLAVVSKWLIMRKSLIRHLEERGVQVVFWCLNE
			ESDFEAAFSVGATGVITDYPTALRHYLDNHGPAARTS
6003	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP
			APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA
1	Į.		FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR
	1		SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA
1	1		HLSTVLGNKFDHGARAIVPTLFNLVPNSAKVMATSGCAAIRFII
	1.		RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE
1	1		RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY
1			NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSQESLNRPFSS
1	1		KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDVNAAAGAK
1	l·		AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV
	1		RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT
			TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSREASPSRLSV
	ļ. J		ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS
	1 1		TOAL VARIETICA CORCUCTION CONTRACTOR CONTRAC
1	} !		TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVEEA
			VADALLIGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS
1	1 1		YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGLQN
			LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI
	!		QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES
1 .] ·		FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD
1	1		FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFBLNTPE
			FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP
1	1		RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLRG
]	•		VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA
		*	GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSIS
İ		•	PFNKSALKEAMFDDDADQFPDDLSLDHSDLVABLLKELSNHNER
	·	•	VEERKIALYELMKLTQEESFSVWDEHFKTILLLLLETLGDKEPT
]	[·		IRALALKVLREILRHOPARFKNYABLTVMKTLEAHKDPHKEVVR
1			SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMOT
	l .		KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV
		•	HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS
			GQS
6004	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP
		1050	
	i i		APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA
j l	ļ	·	FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR
1 1			SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA
	1		HLSTVLGNKFDHGABAIVPTLFNLVPNSAKVMATSGCAAIRFII
	[RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE
<u> </u>			RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY
[NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSQESLNRPFSS
Į į		,	KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDVNAAAGAK
} [1		AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV
			RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT
[TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSREASPSRLSV
		ļ	ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS
			TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVEEA
			VADALLLGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS
1	1		YSSRNGSIPTYMRQT\EDV\ABVLNRCASSNWSERKEGLLGLQN
			LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI
			QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES
			FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD
	1	İ	FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE
			

Degiming corresponding to first anino acid amino acid residue of amino acid amino acid amino acid sequence sequ				
No: nucleotide corresponding to first mains acid residue of mains acid residue of amino acid residue of amino acid sequence seque	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cocation Corresponding Coffresh Coff	, ,		1	
to first amino acid residue of amino acid residue of amino acid sequence Percline, Gedludmaine, R-Aspaine, sequence Secrine, T-Threonine, W-Valine, w-Tryptophan, Y-Tyrosine, X-Unknown, *-stop Codon, /=possible nucleotide deletion, \-possible nucleotide insertion) PTMLIGALPRIFOCATELLERHIRANICONGTOSSINGS PLITEP RSPAMMS PLITEPITS (NILE PREPENDIS PRESIDENT SERVING PROPERTION) FTMLIGALPRIFOCATELLERHIRANICONGTOSSINGS PLITEPI RSPAMMS PLITEPITS (NILE PREPENDIS PRESIDENT SERVING PLITEPI RSPAMMS PLITEPITS (NILE PREPENDIS PRESIDENT PLITEPITS (NILE PREPENDIS PRESIDENT PLITEPITS (NILE PREPENDIS PRESIDENT PLITEPITS (NILE PREPENDIS PRESIDENT PLITEPITS (NILE PREPENDIS PRESIDENT PLITEPITS (NILE PREPENDIS PRESIDENT PLITEPITS (NILE PREPENDIS PRESIDENT PLITEPITS (NILE PREPENDIS PRESIDENT PLITEPITS (NILE PREPENDIS PRESIDENT PLITEPITS (NILE PREPENDIS PRESIDENT PLITEPITS (NILE PREPENDIS PRESIDENT PLITA PLITEPITS (NILE PREPENDIS PRESIDENT PLITA PLITEPITS (NILE PREPENDIS PRESIDENT PLITA PLITEPITS (NILE PREPENDIS PRESIDENT PLITA	NO:		· ·	
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acquence #TYPICOPAIN, Y=TYTOSINE, X=UNKNOWN, *=SCO, Codon, /=possible nucleotide deletion, 'possible nucleotide deletion,' 'possible nucleotide insertion) #TYPICALALPRITOGRATULARHIRATINGGROSSMGSPLTEP RESPANMSSPLTSPTNTSONTLSPSAFDYDTENMSSEDIYSGL #TRALALALPRITOGRATULARHIRATINGGROSSMGSPLTEP RESPANMSSPLTSPTNTSONTLSPSAFDYDTENMSSEDIYSGL #TRALALALVAREILEMBUTTSSPSRSONTPYNYNSDE GGDATDSSGTALALDRIKAGLANDSPTBASSPSRSONTPYNYNSS PFMKSALKEAMFDDADAPSTWALKELSINN VERKKIALVERLIMKLTOESSPSWODEHFKTILLLISTLODKGRUN SABEAASVALATSI\SPECCIKUCPITGTADVPINLASHEN KYLENVSKETINLILLISTMOLIGOTHOMESSSVKRACVPICAV HAVIGDELKPHLSGLTGSKRKKLALNIYIKRAGTGSGADPTTD GOS ### SSGGRRODGOFFGRERKOMASGLGSPSPCSAGSSEEDIMAS RESIGNEROLOGFFGRERKOMASGLGSPSPCSAGSSEEDIMAS RESIGNEROLOGFFGRERKOMASGLGSPSPCSAGSSEEDIMAS RESIGNEROLOGFFGRERKOMASGLGSPSPCSAGSSEEDIMAS RESIGNEROLOGFFGRERKOMASGLGSPSPCSAGSSEEDIMAS RESIGNEROLOGFFGRERKOMASGLGSPSPCSAGSSEEDIMAS RESIGNEROLOGFFGRERKOMASGLGSPSPCSAGSSEEDIMAS RESIGNEROLOGFFGRERKOMASGLGSPSPCSAGSSEEDIMAS RESIGNEROLOGFFGRERKOMASGLGSPSPCSAGSSEEDIMAS RESIGNEROLOGFFGRERKOMASGLGSPSPCSAGSSEEDIMAS RESIGNEROLOGFFGRERKOMASGLGSPSPCSAGSSEEDIMAS RESIGNEROLOGFFGRERKOMASGLGSPSPCSAGSSEEDIMAS RESIGNEROLOGFFGRERKOMASGLGSPSPCSAGSSEEDIMAS RESIGNEROLOGFFGRERKOMASGLGSPSPCSAGSSEEDIMASGLGSPSCSAG RESIGNEROLOGFFGRERKOMASGLGSPSTAGSSEEDIMASGLGSPSTAGS RESIGNEROLOGFFGRERKOMASGLGSPSTAGSSEEDIMASGLGSPSTAGS RESIGNEROLOGFFGRERKOMASGLGSPSTAGSSEEDIMASGLGSPSTAGSS		location		
amino acid residue of amino acid sequence Sequence FYMIJSCHORY TYPYOSIAN, X-UNKNOWN, *-Stop Codon, /=possible nuclectide deletion, \possible nuclectide deletion,		corresponding		L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence W*Tryptophan, Y=Tryrosine, X=Unknown, *=Stor continue acid sequence V=Tryntophan, Y=Tryrosine, X=Unknown, *=Stor continue acid sequence V=Tryrosine, v=Tryrosine,	i	to first	amino acid	
amino acid sequence Codom, /=possible nucleotide deletion, -possible nucleotide insertion) FYRHLIGALPRIFOCATELIRAHILAPITOROGYGSSNGSPLTEP! RSPANMSSPLTSPTTTSONLSPASSPOTDYENNASSED:PLTEP! FSTANMSSPLTSPTTTSONLSPASSPOTDYENNASSED:PLTEP! GGDATDSOTALJANDAGLHSMSPTTSSPSRSDPTNYPTDYENNASSED:PSTANDAGGGGOPG MSDF GGDATDSOTALJANDAGLHSMSPTTSSPSRSDPNYPTYPTSSPSPSPSPNYPTYPTSSPSPSPSPNYPTYPTSSPSSPSPSPNYPTYPTSSPSPSPSPNYPTYPTSSPSPSPSPNYPTYPTSSPSPSPSPNYPTYPTSSPSPSPNYPTYPTSSPSPSPNYPTYPTSSPSPSPNYPTSTANDAGGGGATAGLARIAPITATAGLASSPSPSPNASSPSSPSPNYPTYPTSSPSPSPNASSPSSPSPNASSPSSPNASSPSSPNASSPSSPSPNASSPS	1	amino acid	residue of	
Sequence A-possible nucleotide insertion		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence Sequence		amino acid	sequence	Codon, /=possible nucleotide deletion,
FTHILIGALIPETPODATELLINIHLENTINOTYSSING PLITER REPARMS SPILTPTITE QOTILIS PRAPTOTYDEMISED LYSELI VTERATORS FREQUENCE PLEASE PLOT PLANSES DELY SELI VTERATORS FREQUENCE PLEASE PLANSES DELY SELI VTERATORS FREQUENCE PLEASE PLANSES DELY SELI VTERATORS FREQUENCY PLANSES PRODUCT PLANSES PREVENTINO PROVIDED TO THE PROPERTY PLANSES PRODUCT PLANSES PRODUCT PLANSES PROVIDED TO THE PROPERTY PLANSES PRODUCT	Ì	secuence	1 -	\=possible nucleotide insertion)
RSPANNSSPITSPINTSQNTLSPSAFDVIDTEMMISBELTYSSELL VTEATQNFSFSRGEDNNEPLERSKENDGENSKEDGENSGPL(MSDE) GGDATDSSQTAL/DNKASLLHSMPTHSSPSSDVNPYNYSDS: PFKKSALKEAMPODADOP PODLSCHSTULGHSUNDTHASPEN VERKLALYSLEKLTORSSFSVNDEHKTILLLLETLGDUKE IRALALKYLEKLHOPASFKYNASLTVMTLEARLKEJENNI VERKLALYSLEKLHOPASFKYNASLTVMTLEARLKEJENNI VERKLALYSLEKLHOPASFKYNASLTVMTLEARLKEJENNI RALALKYLEETLHOPASFKYNASLTVMTLEARLKEJENNI RYTERVSKETLALLLEPLUPGLIGVTNSSSSVYRAGVELUX AREASSV/LATS1\SPECIKVLCPI1QTADVFINLAALKKE RYTERVSKETLALLEPLUPGLIGVTNSSSSVYRAGVELUX AREASSV/LATS1\SPECIKVLCPI1QTADVFINLAALKKE RYTERVSKETLALLEPLUPGLIGVTNSSSSVYRAGVELUX LINDIGELKPHLSQLTGSKMKLINLYTKRAQTGSGADPTDI GOS 83SGRRGBOLAGPFGERKKASSGAGGSSSTCAGGSEEDMAD RANGKERPHLLCQLLDDSSGDEFFYELKKKKKPKPKPDKTP KROKKERPHLLCQLLDDSSGDEFFYELKKKKKPKPKPDKTP KROKKERPHLLCQLLDDSSGDEFFYELKKKKKPKPKPDKTP KROKKERPHLLCQLLDDSSGDEFFYELKKKKKPKPKPDKTP KROKKERPHLLCQLLDDSSGDEFFYELKKKKKPKPPDKTP KROKKEKRHLLCQLLDDSSGDEFFYELKESVALLSDSGSSYV KROKKKKKRJDKKKKKKSSKCRUKERESEDDDDDVSSEKPKSSAGG KROKKEKRJDKYRKENSSSERDDDDVSSEKPENSSAGGENSADAAAAAAVANAVSSWY TYAPPSPPYWPEIKAKTKGKKOPNARRYKKSSFRYPDAKK TYAPPSPPYWPEIKAKTKGKKOPNARRYKKSSFRYPDAKK TYAPPSPPYWPEIKAKTKGKKOPNARRYKKSSFRYPDAKK TYAPPSPPYWPEIKAKTKGKKOPNARRYKKSSFRYPDAKK TYAPPSPYWPEIKAKTKKKKKGEEDYADGYKTDHDOVC CQGGSEIILCDCCPRATHWYCLDPDMERAPEGNOSCHEKKE CQGGSEIILCDCCPRATHWYCLDPDMERAPEGNOSCHEKKE CQGGSEIILCDCCPRATHWYCLDPDMERAPEGNOSCHEKKE CQGGSEIILCDCCPRATHWYCLDPDMERAPEGNOSCHEKKE KKYRKTRALINGSFRYBADPATAGYKTDHDOWNER SANGKREGEFFANDAWAY WKKSMYSELQLELICCQUMFRAYGRRUNDGPPSODPOGDES S\KRKKNOBPKPARAMERAPTYRATUPGTYKTERSPFTLADAM ERGRFFAKLKKYNGKARPKTYTTDPTYKTERSPFTLADAM ERGRFFAKLKKYNGKARPKTYTTDPTYKTERSPFTLADAM ERGRFFAKLKYNGKARPKTYTTDPTYKTERSPFTLADAM ERGRFFAKLKYNGVARRABERTYRATUPGTYTTDPTYKTERSPFTLADAM ERGRFFAKLKYNGVARRABERTYRATUPGTYTTATATATATATYTTYTDPTYKTARATATATATATATATATATATATATATATATATATAT				FTMLLGALPKTFODGATKLLHNHLRNTGNGTQSSMGSPLTRPTP
VTEALQNESSTROUGHMEDLERDSKKDDGDSKCGOPOLMSDIG GGDATDSGOTALDNKSLLIMSPTHSSPRESDRYPNYNSDSS PFKKSALKEAMPTDDADQPDDLSLDHSDLWAELLKELSNNN VERKKLALYSLAKUTOSESFSVADFHKSTILLLILETLGUESE IRALALKVLETLHHOPARFKYTASITVMKTLEAHKDPHIKSV SAERAASVLATST SSECKIKUTOSESTSTANGKTUTAATKM KVIERVSKETLIALLIPEINPGLIQOYDNSSSVKRACVECTUM HAVISGDLKPHLSQLTGSKMKLINLYKKRAQTGGGAAPTTO GQS RSSGRRQBOLGGFPGRERKGMASALGSSSVKRACVECTUM KRUKGDELKPHLSQLTGSKMKLINLYKKRAQTGGGAAPTTO GQS RSSGRRQBOLGGFPGRERKGMASALGSSSPCGAGSEEEIMDAD NNSLPPHPHRSEDPEEDLSSTETTYKLKKKKKYPKKPRDPXIPI KROKKERHILLCRQLIDISSGEDFFVEREERVALKSDSGOSDY GKKKKKKLIJKKKKKKSKSKRREERDDDLDDUSSEDPDATIO GKKKKKKLIJKKKKKKSKSKRREERDDDLDUSSEDPDATIO GKKKKKKLIJKKKKKKSKSKRREERDDDLDUSSEDPDATIO GKKKKKKLIJKKKKKSKSKRREEDDDLDUSSEDPDATIO GKKKKKKLIJKKKKKSKSKRREEDDDLDUSSEDPDATIO GKKKKKLIJKKKKKLIJKKKKGSEVITAVGVETDHDUTCI CQGGGEILLCTCPATHWALDDPBERAPECKNSCHCHEKE GWARKEDNSGGEILBEVGGDLEREDDDLINSSCHCHEKE COMBAKEDNSGGEILBEVGGDLEREDDLINSSCHCHEKE GWARKEDNSGGEILBEVGGDLEREDDLINSSCHCHEKE GWARKENSSGGLEILBEVGGLEEDDHAMPECRAVCKOGGEIL CDTCPSSYHHCLUNPLPLPEINGRMCGRCTPALKKVQKI WKMGQPBSPTPVRRPERDADPHTSPKPLBGRBERGFFVKNGG YMKCSNVSEQLELLCYQMFRAYGKKOMDEBPSGDFGGGBE S\RRKNNSEGLELLEC\QVMFRAYGKKOMDEBPSGDFGGGBE S\RRKNNSEGLELLCQVMFRAYGKKOMDEBPSGDFGGGBE S\RRKNNSEGLELLCQVMFRAYGKKOMDEBPSGDFGGGBE S\RRKNNSEGLELLCQVMFRAYGKKOMDEBPSGDFGGGBE S\RRKNNSEGLELLCQVMFRAYGKKOMDEBPSGDFGGGBE S\RRKNNSEGLELTCQVMFRAYGKKOMDEBPSGDFGGGBE S\RRKNSSGLELLCQVMFRAYGKKOMDEBPSGDFGGGBE S\RRKNSSGLENCYGNFAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKA	I			
GGDATDSSQTAL\DNKASLLISHMPTISSPRSDYNPYNYSDS PFKKSALKRAMPDDADQP PDDLSLISHBUMVELLISHNIN VERKIALYSLIKLTORSSFSVNDEHKTILLLLETLGUESE IRALALKYLEKLHORDSPSVNDEHKKTILLLLETLGUESE IRALALKYLEKLHORDSPSVNDEHKKTILLLLETLGUESE RADAGSV\LATSI\SPECTKVLCPIIQTADYPINLAALKM RVIERVSKETLALLIPERVBGLIQGYMENSSSVSKRAVQVELW RAVIGDELKPHLSQLTGSKMKLINLYIKRAQTGSGGADPTTD GQS RSSGGROBOLGGFFGRERKGMASGLGSPSPCSAGSEEEUHDA NNSLPPHPRNEEDPEDLSSTETFKLKKKKKPKKPRDFXTPI KROKKKKKLIGSSKEEPEFVELTHTKNAFSGFVRLLAARNKLA KMMMULGAKKERLICGIDSSGEEPEFVEREEVALARSSGSSDY GKKKKKKLIGSKKEKKSKSKREEEEEDDDDDDCKEPKSSSONY TEVAPPPPPVEVFIKAKTKGGKOMARNEPKSGSFRVDAKK KMMMULGAKKEFSTNNIPFKGSGAASVAAAAAAVVVSSWY TEVAPPPPPVEVFIKAKTKGGKOMARNEPKSGSFRVDAKK KMMMULGAKKEFSTNNIPFKGSGAASVAAAAAAAVVVSSWY TEVAPPPPPVEVFIKAKTKGGKOMARNEPKSGSFRVDAKK KMMMULGAKKEFSTNNIPFKGSGAASVAAAAAAAVVVSSWY TEVAPPPPPVEVFIKAKTKGGKOMARNEPKSGSFVPADAKK KMMMULGAKKEFSTNNIPFKGSGAASVAAAAAAAVVVSSWY TEVAPPPPPVEVFIKAKTKGKGKOMARNEPKSGSFVPADAKK KMMVLGAKKRETIKKKKHLETKKKKKOMARNEPKSGSFVPADAK PKKVAPLIK ILIGGFGSKRKRSSEDDDLDUEDDFDDAS INSY SDGSTSRSSRSKKKHLETKKKKKOMARNEPKSGFVPADAAVVSSWY TEVAPPPPPVEVFIKAKTERGKOMARNEPKSGFVPAVGG QKARKSNSGELBEVGGDLEEEDVINHEEYCKCKGGEL CDTCPSSYHHCLINPPLPBINNERGKCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		1	į.	
PFKKSALKEAMPODDADO PDDISLICHSDUVAELLKELSINNIN VERKIALYSLIKUTOSES FSVORDHEYTILLILIETIGDEEL IRALALKVILETLEHIOPAR FRIVABLITUMTURAHKOPHIKKVI. SABEAASV\LATSI\S PECKINLOTI 1QTAYD YBLIALATKM RVIENVSKETILLILEEINFOLIQYDNSESSVRKACVFCLW ENVIENVSKETILLILEEINFOLIQYDNSESSVRKACVFCLW ENVIENVSKETILLILEEINFOLIQYDNSESSVRKACVFCLW ENVIENVSKETILLILEEINFOLIQYDNSESSVRKACVFCLW ENVIENVSKETILLILEEINFOLIQYDNSESSVRKACVFCLW ENVIENVSKETILLILEEINFOLIQYDNSESSVRKACVFCLW ENVIENVSKETILLILEEINFOLIQYDNSESSVRKACVFCLW ENVIENVSKETILLILEEINFOLIQYDNSESSSVRKACVFCLW ENVIENVSKETILLILEEINFOLIQYDNSESSSPSPCSAGSEEEDMAD SSSS RSSGRRDGUGGFGERKEMASGLSSSSPSPCSAGSEEEDMAD NSLPPHPRIBEEDEEDLSESTETPKLKKKKPKPRDPKTPI KROKKERHLCQGLOSSSGOPEFVEEEEVALRSDSGOSDY GKKKKKLIGHTKKKKKGSKORNABEREDHADDSSGOSDY GKKKKKLIGHTKKKKKGSKORNABEREDHADDSSGOSDY GKKKKKLIGHTKKKKKGSKORNABEREPKSSSRVPDAKK KOMMULGAKWEESTINNPKSSSGAVAAAAAAAVAWVSSWV TEVAPPPPVEVPIRKAKTKGKKONABEREPKSSSRVPDAKK PKWAPLKIKKGKGONABEREPKSSSRVPDAKK PKWAPLKIKKKKGEEVTAVOGYTETDHODY CQCGGGSIILCTOPAHWALCIDEMEKABEKKNSCHCHER CWEAKEDNSGOSSILEEVGGOLEEEDDHADESPODASINSY SDSSTSRSSSKKKHETTKKKKKGEEVTAVOGYTETDHODY CQCGGGSIILCTOPAHWALCIDEMEKABEKKNSCHCHER CWEAKEDNSGOSSILEEVGGOLEEEDDHADESPODASINSY SDSSTSRSSSKKKHETTKKKKKGEEVTAVOGYTETDHODY CQCGGGSIILCTOPAHWALCIDEMEKABEKKNSCHCHER CWEAKEDNSGOSSILEEVGGOLEEEDDHADESPODASINSY SDSSTSRSSSKKKHETTKKKKKGEEVTAVOGYTETDHOON KKRONICAR HANDEN SOSIALIKEN SOSIALIKEN STANDAM STANDAM VERNOON KKRONICAR SOON SOSIALIKEN STANDAM VERNOON KKRONICAR SOON SOON SOON SOON SOON SOON SOON SOO	1	1	1	
VERRKIADYELMKLTOGESES WWDEHFKTILLILLIETIGERICH IRALAKAURELIKHOPHEKU SABEASAY LATSI'N SPECITUTCHI IGTADYE INLALAKUREN KU ERWISETIINLIJPER IMGOLOGYDNESSE SVERACYPCIW. RVI ERWISETIINLIJPER IMGOLOGYDNESSE SVERACYPCIW. HAVI GDELKPHLSQLTGSKMKLLNI'L KRAQTGSGADPTTDI OGS SSEGROBQLGQFPGRERKGMASGLGSF SPCSAGSEEEDMDAI NNSLPPHEREDEREDLSETETPKLKKKKEKERPAPPH KROKKERHLLCGLGUSSGEGEFFFEREEDLAKERSE SCSIV. GKKKKKCIG PKKEKKSKSKKEEEEEDDDDDDDS ER PKSES BOMMEDDIAMYSEEDVRITTINKAFGQVFRELTAKURENSE SCSIV. KROMMULGAKWREFSTINDF KGSGASVAAAAAAAVAVVENTE ENGMEDDIAMYSEEDVRITTINKAFGQVFRELTAKURENSE SCSIV. TEVAPPPPPEVEVIRKATKEKGEEVTANDAGTDHODDOS ER PKSES SDGSTSRSSRSKKKRTTKKKKKGEEVTANDAGTDHODY. GOGGEI ILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCEKEE QWEAKSDAS BEGEI LIEBVGGIDEEDDHHERGSPEVORGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL CDTCPSSYHIHCLINPPLETPNISELLCPRCTCPALIKS KVOCKOGGEL SYNRHILLING BEGELILBERVGGERPTIVLTVITY TIKHGOPPLEN KANTAKURAL KROCKAASMKKEASVKFHVILLTS LITIDAGLISI DWACLITURGERPTTURTVITYON VANDILKS KKYNKYLTILARS KVACKOGGEN SKOCKORINICATERALIKAN KKYNKYKYLTHARATOVYLTYSDSDMAHUNTATATATATATATATATATATATATATATATATATATA	l			T
IRALALKVLREILRIDPAREKWYAELIVWKTLEAHIOPHEKWY SABRASWY LATST) SPROCIEVUCPI (1970-11AATIKW KVIERVSKETAILLIPE IMPOLICOYDNOSESSURKACUPCIW HAVIGDELKPHLSQLTGSKMKLLALYI KRAQTGSGAPTTD' GQS RSSGRQBQLGOFFGRERKMASGLGSF SFCSAGSEEEDMDA NNSLPPHIPENEEDEEDLESETETPKLKKKKKPKKPRDPKTPI KROKKERMILCRQLEDSSGEGEFVEBEEVALRSDSEGSDY GKKKKKKGLGF KKKKKSKKSKKEREBEEDDDDDS KEPKSSKO) GKKKKKKGLGF KKKKKSKKSK KREKEREEDDDDDS KEPKSSKO) GKKKKKKGLG FKKKKSKSK KREKEREEDDDDDDS KEPKSSKO) GKKKKKKGLG FKKKKSKSK KREKEREEDDDDDDS KEPKSSKO) GKKKKKKGLG FKKKKSKSK KREKEREEDDDDDDS KEPKSSKO) GKKKKKKGLG FKKKKSKSK KREKEREEDDDDDDS KEPKSSKO) GKKKKKKGLG FKKKKKSK KREKEREEDDDDDDS KEPKSSKO) GENOMMULGAKWEFSTINEP KREKEREEDDDDDDS KEPKSSKO) GKKKKKKGLG FKKKKKSK KREKEREEDDDDDDS KEPKSSKO) GKKKKKKGLG FKKKKKSK KREKEREEDDDDDDS KEPKSSKO) GENOMMULGAKWEFSTINEP KREKEREEDDDDDDS KEPKSSKO) GENOMMULGAKWEFSTINEP KREKEREEDDDDDS KEPKSSKO) GENOMMULGAKWEFSTINEP KREKEREEDDDDDS KEPKSSKO) GENOMMULGAKWEFSTINEP KREKEREEDDDDDS KEPKSSKO) GOGSTILCHOPPORTHANTIK KREKEREEDDDDS KREKERSPENDEDDDS GOGSTRONG FTALKER GENOMMULGAKWEFSTINEP KREKEREEDDDDDS KREKER GENOMMULGAKWEFSTINEP KREKEREEDDDDS KREKER GENOMMULGAKWEFSTINEP KREKERSPENDE GOD FORDE S\RRENNEDDE SEILBEVGGDLEEEDDHIMEEC VICKORGE WHICH KROOD FYDRAMEET FAR TO FENNING FERNING FOR FALKER HUHT HILLING FERNI	1		j	<u> </u>
SABEASY\LATSI\SPECIEVUCEPIIQTADYFINLANDER RVIERVISETAILLIPEIMOGIQSYNESSEVRACOYPCIW HAVIGDELRPHLSQLTGSKMKLLNIYIKRAQTGSGGADPTTDI CQS SSEGRRQBQLGGPFGRERKGMASGLGSFSPCSAGSEEEDMDAI NNSLPPHPERREDPEEDLSETETPKLKKKKPKERPDFYL KROKKERNLLCRLOLDSSGGEFEVFEREEWLALESDSGSDY GKKKKKLGPKRKLGALDSSGGSFEVFEREEWLALESDSGSDY GKKKKKLGPKRKLGALDSSGGSFEVFEREEWLALESDSGSDY GKKKKKLGPKRKLGALDSSGGSFEVFEREEWLALESDSGSDY GKKKKKLGPKRKLGALDSSGGSFEVFEREEWLALESDSGSDY TEVAPPPPPEVEVPIRKATKERGEPTEDDDDDDSTBPKSGSGS BDMGMEDIDHYFSEDVRITYNKAPGGVFRPLIAKANFKIA KDMMVLGAKMBEFSTNIPFKGSGGSVARAAAAAAVAVVE TEVAPPPPEVEVPIRKATKERGKGPNARRKRSPSRVPDAKK KDMMVLGAKMBEFSTNIPFKGSGGSVARAAAAAAAVAVVE TEVAPPPPEVEVPIRKATKERGKGPNARRKAPGFETHODYCI CQGGEIILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCHER QWEAKEDNSGGEILLEWGDLEEEDDHIMBFCRVCKGGGEL CDTCPSSYHIHCLINFPLEETINSWELCPRETCPALKGKVQKI WKMGQPPSPTTVDRPPDADDNTTSFKELGRERGPFVVGVGGGEL CDTCPSSYHIHCLINFPLEETINSWELCPRETCPALKGKVQKI WKMGQPPSPTTVDRPPDADDNTFSFKELGRERGPFVVGVGGGEL CDTCPSSYHIHCLINFPLEETINSWELCPRETCPALKGKVQKI WKMGQPPSPTTVDRPPDADDNTFSFKELGRERGPFVVGVGGGEL CDTCPSSYHIHCLINFPLETINFVGGGGGDUSCHANDATATATATATATATATATATATATATATATATATATA	1			1
EVIERVSETIALLIPELMOLIGOTINSESSVEKACVPCLVV HAVIGDELXPHLSQLTGSKMKLLNYIKRAQTGSGADPTDI GOS		[
HAVIGDEKPHLSQLTGSKMKLLNLYLKRAQTGSGABPTTD' GOS 133 5955 RSSGRRØBOLGOPFGRERKGMASGLGSPESPCSAGSEESDMDA NNSLPPPHPENEDPEEDLSETETPLKKKKKPKPRDYKTJ KROKKERHLLCRQIGDSSGEDEFVEESEEVALRSDSGSDY- GKKKKKKLJPKKEKSKSKREBEEBDDDDDDS KEPSSROJ GKKKKKKLJPKKEKSKSKREBEEBDDDDDDDS KEPSSROJ GKKKKKKLJPKKEKSKSKSKREBEEBDDDDDDDS KEPSSROJ GKKKKKLJPKKEKSKSKSKREBEEBDDDDDDS KEPSSROJ EDMOMBDIDHVFSEDPYRTLINKKAPGOPPHLIAKKPKLAR KMMVLJGAKWREFSTNIPFKGSGASVAAAAAVAVESMV TEVAPPPPPVEVPTIRAKTKRGKOPMARRKPKGSPPVAKK PKVAPLKI KLJGGFGSKRKRSSSBDDLDVSSDPDDAS INSY SDGSTSRSSRSKLITTKKKKGEBDYADGYETDHGDVI QOGGBITLCDTCPRAYHHVCLDPDMEKAPBGKNSCPHCKER OMERAKDDNSGEBILGBEVGDLBEDDHBERGCVCKDOGGLI CDTCPSSYHIHCLMPPLPBIPNGSWLCPPCTCPALKGKVQKT WKMQPPSPTVVRPPDADDNTPSPKPLEGRPFCYCHAGKSVQKT WKMQPPSPTVVRPPDADDNTPSPKPLEGRPFCYVKQGG YMCSWVSSLGLEHC\COMPRTYQKKNDMDEPPSGDPGGDE S\RRKNKDPKFARMERFYRYGIKFEN\MMHIRILINSVDK HVHYLIKMDLPYQGASWEGDVEICPPTVKYGSOPVIKAGG S\RRKNKDPKFARMERFYRYGIKFEN\MMHIRILINSVDK HVHYLIKMDLPYQGASWEGDVEITJADGYTLJKYSLQ LILTYDHAILGSIDBACLIUDEAHBLKNONGKFFVLINGSLQ LLLTYGTHGJANLESLEHLINFLTPEBFRINGSVTVQTAVFLY YKEGHSKGPFLVSNPLSTIIN\MBEFFENMAPDMYV\VYYVG DSRAIT REMERSY\FWNINGSTGDTILALGERAYFHVLITS LITTUMAILGSIDBACLIUDEAHBLKNONGKFFVLINGSLQ LLLTYGTHGJANLESLEHLINFLTPEBFRINGSVTVQTAVFLY YKEGHSKGPFLVSNPLSTIIN\MBFFENMAPDMYV\VYYVG DSRAIT REMERSY\FWNINGSTGDTILATVTMLKYCLSPM KKYYK\YILHSKFIKALN\ARGGGOVSILAVVTMLKKCNH LFFVANMERAPKMYMGYTDSALIRATSGETTVQTAKKKMUTHL RPGIGSKTGSMSKOELDILLIKFTTBETFTOTYI IYDSDMRHMD AFSRAHRIGQNKKVMIYRFVTRASVERITTOVAKKKMUTHL RPGIGSKTGSMSKOELDILLIKFTTBETFTOTYI IYDSDMRHMD AFSRAHRIGQNKKVMIYRFVTRASVERITTOVAKKKMUTHL RPGIGSKTGSMSKOELDILLIKFTBETFTOTYI IYDSDMRHMD AFSRAHRIGGNRKMIYRFVTRASVERITTOVAKKKMUTHL RPGIGSKTGSMSKOELDILLIKFTBETFTOTYI IYDSDMRHMD RSGLEVENDERSKESSESPOTTVTTSTGGTI NTRAPVPPAEDGII KRGVGBSTDDAWGNISTIKK GEBEURGEBEVERII IKGESSTGHNATATOVI IYDSDMRHMD RSGLEVENDERSKESSESPOTTTTSTTGGTI NTRAPVPPAEDGII KERSBLKGBESSPOTTTTSTTGGTI NTRAPVPPAEDGII KIERSBLKGBESSPOTTTTSTTGGTI NTRAPVPPAEDGII KIERSBLKGBESSPOTTTTTSTTGGTI NTRAPVPPAEDGII KRENGURGGSVOTTARATINIBPKG AADVEKVERKSAI DLTTUVEDKBEKEESE		1		
6005 133 5955 RSSGRRØBOLGOFFGRERKGMASGLGSPSPCSAGSEEEDMDAI NNSLPPPHPEMEDPEEDLSETETPKLKKKKPKKPRDPKTPI KROKKERMLLCRGLGDISSGEOPEFVEEEEVALRSDSKGSDY GKKKKKGLSPKKEKKKSKSRKEEEEEDDDDDISKSPKSSAGS GKKKKKGKGPKEPKKEKKSKSRKEEEEEDDDDDDSSKSPKSSAG EDMMMDIDHVFSEEDYRTLINYKARSQFVRPLIARKOPKIA KMMMULGAKMEFSTNNPFKSSGASVARAAVAVVESWY TEVAPPPPPVEVPTRAKTKEGKGSPARRKPKGSPRVPAKK PKKYAPLKIKLGAGGGKRKRSSSEDDLDVSSDFDDASINSY, SDGSTSRSSRSRKKLRTTKKKKKGEEVTANDGYETDHODYC CQQGEIILCDTCPRAYHMVCLDPDMKKAPGGKSCPHCEKE QWEAKEDNSEGEBILBEVGGDLEEEDDHEMBFCRVCKDGGEL CDTCPSSYHIHCLNPPLPSIPNGBWLCPRCTCPALKGVQKI WKWGQPPSSTPVPRPDADDAPWTSPPPLEGBFERQFFVKWQG YMHCSWVSSLQLELHC\QVMFRNYQRKDDMBEPSGDGGDE S\RRRKNKDPKFABMEEFFYRGIKPEN\MIHRILMSSVGK HVHYLIKMGDLPYDOASWSSEDVBLQDYDLFKGSYVAPHYLDA THPYQMEGLWILRSWAGGTDTILADENGGGKTVQTAVFLY YKEGHSKGPFLVSAPLSTIN\WERFEMMADDMYVV\YTVYU DISRAITRENESS\FENDALTGGKKASRKKRASKVRHVILITS LITIDMAILGSIDMACLIVDEAHELNNQSKFFFXUHILST LITIDMAILGSIDMACLIVDEAHELNNQSKFFFXUHILST LITIDMAILGSIDMACLIVDEAHELNNQSKFFFXUHILST LITIDMAILGSIDMACLIVDEAHELNNQSKFFFXUHILST LITIDMAILGSIDMACLIVDEAHELNNQSKFFFXUHVULSFM KKYYKY\THILKTTPEPFHAHLGFFLESFADIKK KKYYKY\THILKTTPEPFHAHLGFFLESFADIKK KKYYKY\THILKTTPEPFHAHLGFFLESFADIKK KKYYKY\THILKTTPEPFHAHLGFFLESFADIKK KKYYKY\THILKTTPEPFHAHLGFFLESFADIKK KKYYKY\THILKTTPEPFHAHLGFFLESFADIKK KKYYKY\THILKTTPEPFHAHLGFFLESFADIKK KKYYKY\THILKTSFFKADIKATATADTYIITDSDWINDHND AFSRARIGOGNKTMALDLEDFLEHEGYKYERTELGGTTGMNRGBAL FNAPGAQOFCPLLSTRRGGLOINLATADTYIITDSDWINDHND AFSRARIGOGNKTMALDLEDFLEHEGYKYERTELGGTTGMNRGBAL FNAPGAQOFCPLLSTRRGGLOINLATADTYIITDSDWINDHND AFSRARIGOGNEFHANGWARDSALATARGCHURHTYSQQGDLO NGGKSFFRAPKYKGMANDAVERKKKMUTHVTRAVEERITYOVSLIKK SVIHYDDKAIERKWANYNDGSGEDDWDDOSDNGSDYSVSSEG DPDRESSEPRPSRKGGRAPKROKPADAVEKKMUTHV REEMMGEBEEVERSIKGESPODPWERLURHTYSQQGDLO NGGKFFRANTYTHADGGFTELLARGVGNEBVLGFW MHILCEFGADGAFTTADGVFRGLSGNYCHAWENGST DLNDEKKKNIKNIKGFFKMIDAGGFTGHAGYKATA REHUGDNADVYTRUPARTILARIDGGTTELLARGVMSLTRAVSHARD AADVEKVERKSAIDLTTUVEDKEBKKEEEEKKVYNAPTATE SADARGVETETKIKLGGLANTERUGSTNOTATATIRGVFRANGOLORDATATIRGFFK NGGMFLETKIKNIAGGFTRILARGMANDAVALHKVIK				
S955 ### SSGRROEDLOGPERERGMASGLOSPSPCSAGSEEEDMAN NNSLPPPHPENEDPEEDLSETETPLIKKKKYKKPKRPDEVTY KROKKERHLLCRCIGISSGEDEFVEEEEVALRSDSEGSDY GKKKKKKILGPKKEKKSKSRREEEEEDDDDDDDS KEPSAGO GKKKKKKILGPKKEKSKSKREEEEEDDDDDDDDS KEPSAGO GKKKKKKILGPKKEKSKSKREEEEEDDDDDDDDDDDS KEPSAGO GKKKKKKILGPKKEKSKSKREEEEEDDDDDDDDS KEPSAGO GKKKKKILGPKKEKSKSKREEEEEDDDDDDDS KEPSAGO ENDOWMDELD HUFSEEDVERLITNYKARSGCYPPLAKKE KMMVILGAKMEFSTNIPKGSGASVAAAAAAVVENV TEVAPPPPVEVPTIKKKIKGKGEPVARKEKSESPVPLAKK PKWAPLKI KLIGGPGSKRKRSSSEDDDLDVSSPDEDASINSY. SDGSTSRSSRSKKLRTTKKKKCEEEVTANDGYETDHODVC CQGGGILTLCTCTCPATYHIVCLDPDMEKAPEGKNSCPHCEKE GWEAKEDNSEGEELLEEVGGBLEEEDDHHMSFCRVCKOGGEL CDTCPSSYHIHCLMPPLEPINOEMUCTPAUDGYETDHODVC CQGGGILTLCTCTCPATYHIVCLDPDMEKAPEGKNSCPHCEKE GWEAKEDNSEGEELLEEVGGBLEEEDDHHMSFCRVCKOGGEL CDTCPSSYHIHCLMPPLEPINOEMUCTCCTCALKGKVQKI. WKWGQPPSPTVPRP PDADPNTPS PKPLEGRPERGPFVKWGG YWHCSWVSSLOLELHCYQWFRYNYKKKOEESVTANDGYETDHODVC YWHCSWVSSLOLELHCYQWFRYNYKKKOESVTANDGYETDHODVC YWHCSWVSSLOLELHCYQWFRYNYKKKOESVTANDGYETDHOD ***GYRKINKDPFAEMER***PYRGIKPENDFATGCTCALKGKVQKI.** WKWGQPPSPTVPRP PDADPNTPS PKPLEGRPERGPFVKWGG YWHCSWVSSLOLELHCYQWFRYNYKKKOESVTANDGYTANDFXC ***HCSWVSSLOLELHCYQWFRYNYKKKOESVTANDFXCHOPTVKYERQPFYLDAT** TILHFYQMBGLAWLRFSWAGGTOTILADEMGLAKTYATYVLTY YKKGHKKGFFVXAPAGATTILNVBREFERBAPSKOGYSYNTHELM** EEGRPKKKLKKVKLRKLERPPETPTVDTYVKYERQPFYLDATY YKKGHKKGFFYLOTATATATATATATATATATATATATATATATATATATA	1			
NNSLPPEHEREEDPEPLESTETPKLKKKKYKKKKYKRPENDYLPI KROKKERMILCROIGDISGEOPEPVEEREEVALRSDSGSDY GKKKKKKLOLPKYERKSKSKREBEEDDDDDDDSKPSSGO GKKKKKKLOPKYSEEDPTTLINYKAPSGPVPPLIAAKNPKIA KOMMULGAKWEFSTNNPKSSSGASVAAAAAAAVVUESWY TEVAPPPPPVEVPIRAKTKEGKOPMARRKRKSSPRUPAKK PKKVAPLKIKLIGGGGSKRKRSSSEDDDLDVSSDPDDASINSY; SDGSTSRSSRSRKKLITTKKKKKGEEVIAVDGYETDIGDVC CQGGGILLICDTCPRAYHVULDPDMEKAPGKNSCPHCERE OWARKEDNSGEBILEBVGGDLEBEDDHHMEFCRVCKOGEL CDTCPSSYHHICLIPPLEPIDRGBULCPDCTOPALKGKVQKI, WKWGQPPSPTPVPRPDADPTPSPKPLEGRPERGFFVKWQG YWHCSWSSLGLELHC\QWMFRHYQRKNDMDEPSGDTGGDE S\RRRKNKDFKFABMEERFYRYGIKEPW, MMHRILINHSVKK HVHYLIKMBDLPYDQASWSSEDVBIQDYDLFKGSYWHRELM EEGRPGKKKKKKKKKKKKLKRLEPPFTTVDTYKYERQPEYLDAT THEPYQMECLANLERSWAGGTOTILADENGGGKTVAYFLY YKEGHSKGFFVVSAPLSTIIN WERFEFRAPDVY\VTYVG DERAITRENEPS\PTDNATLTDWRFEFRAPDVY\VTYVG DERAITRENEPS\PTDNATLTDWRFEFRAPDVY\VTYVG DERAITRENEPS\PTDNATLTDWRFEFRAPNOTLYNFLY CKCHSKGFFVVSAPLSTIIN WERFEFRAPDVY\VTYVG DERAITRENEPS\PTDNATLTDWRFEFRAPNOTLYNFLY YKKCHSKGFFVVSAPLSTIIN WERFEFRAPNOTLYNFLY CHICHTURALLGSIDWACKLAVARDAWALAN GIKKLHDMG,PHAHRRLEADVFKMPSKTELLV\KVELSFM KKYYK,YILHSKFKKALN,ARSGGNOTSLAVMADLKKCCHH LFPVAAMEAPKMPMGWTGGSALTRAGGKLINLAVMADLKKCCHH LFPVAAMEAPKMPMGWTGGSALTRAGGKLINLAVMADLKKCCHH LFPVAAMEAPKMPMGWTGGSALTRAGGKLINLAVMADLKKCCHH LFPVAAMEAPKMPMGWTGGSALTRAGGLINLATADTVIITNSDWIPHND AAPSAHH LGOKKKWATYRFVTAASVEERITQVAKKKMMTHL RPGIGSKTGSMSKQELDDILKFGTBELFKDEATDGGDNKGG SVIHYDDRAIERLERNGDETTELLQCMMSPLISFKVAQY REEBMGEEBEEVEREITKGESVOPDVWERLICHHYSQQEDIK GRKAFLMATMARGMPPGDAFTTGAUVRDLRGKSEKFFKAYVS MHILCEFGAAGAFTFABORDKKPH PLARVGWSISSEC DPDERSSAPRSRKGLINDKKCHP PLARVGWSMSELS GRAFANATMARGMPPGDAFTTGAUVRDLRGKSEKFFKAYVS MHILCEFGAAGAFTFABORDKKPH PLARVGWSTELLY EFEHVNORMSMELABURGERSKEFKAYVS MHILCEFGAAGAFTFABORDKKPH PLARVGWSTELLEPTALE QAPAPAS EDEKVVEPPEGEBKVSKAGPSSPFTFPTFBGDT NTTADAVPAPAPADGIKTRIGENSKAGRONGANAVLHKVLK EFELLSDNKADVTRIDATTATPDOGTELLARIGNAMERAATVT YEINHRHDYMLLAGIINGGAARANDOJONDPRVAILINEPKG NGGMFLE KINKKLARRFKLEGAUVIEGENGANGNANAVLHKVLK EELLSDNKADVTRIDATTATPPVAVRLGERSKEFKENGANGHANAVLHKVLK EELLSDNKADVTRIDATTATPPVAVRLGERFT		1	1	
RROKKERM,LCQLOBSGEGPFVEEREEVALRSDSGSDY GKKKKKLOPKKEKKS KSKEKEREEDDDDDDSKEPKSSAQ) EDMEMBD I DHVPSEED YRTLTNYKAFSQFVRPLI AAKNPKIA KMMMVLGAKWREFSTNNPFKGSGSASVAAAAAANAVVESMV TEVAPPPPPVEVPTRKAKTEGKGRONARRYKKGSPRVPDAKK PKWAPIKI KLAGFGSKRKESSGSDDLDVESDDASINSY SDGSTSRSSRSKKKITKKKKKGEEVADOYEDTHODYC CQGGBI ILCTCPPAYHMVCLDPDMEKAPGKROCHCERE QWEAKEDNSEGESI LEEVGGDLEEEDDHMEFCRVCKOGGSL CDTCPSSYHIHCLBPPLPEI DNGEHLCPRCTCPALKGKVQKI WKWGQPPSTPVPRR PDADDNTPSFKPLEGREPF FVKWGG YWHCSWVSELQLELKCYQWFRNYGKNDMDEPSGDFCGGE S\RRKKNDPKFAEMEERFYRYGI KPEW\MMIHRILINSVDK HVHLI KWRDLP YDQASWSEGVEL GDLFKGSYMNIRELM EEGROKKLKKVKLEKLERPPETPTVDPTVKYEROPEYLDAT TLHPYQMEGLIWLRFSWAQGTDTI LADEMGLGKTVCTAVPIX YKGHSKGFFLVSAPLSTI IN WERE FFMMAPDMYV\VTVG DSRAI I RENEFS\FFDANA I RGGKKASRNKKRASKKFHVLLTS LITIDMAILGSTDWACI TUPBAHRIKKNQSKFFFVLNGVSL LLITGTPLQNNLEELFHLLMFITPERFHNLEGFLEEFADI LK GIKKLHUMG.S\PHMERIKADVFKINGSKFFFVLNGVSL LLITGTPLQNNLEELFHLLMFITPERFHNLEGFLEEFADI LK KYYK\YLILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCHH LFPVAMEAPKMPNGMYDGSALIRASGKLLLQKMKKNLKKCCHH LFPVAMEAPKMPNGMYDGSALIRASGKLLLQKMKKNLKKCCHH LFPVAMEAPKMPNGMYDGSALIRASGKLLLQKMKKNLKCCHH RRGGGSKTGSMSKQELDD I LKFGTEELFKODEATOMGCAI FNAPGAQQFCFLLSTRAGGIG INLATADTVI I YDSIMPHHOD APSRAHI GQNKKWUTKPYTRASVEERI TQVAKKKMMITHL RRGGSKTGSMSKQELDD I LKFGTEELFKODEATOMGCAI FNAPGAQGFCFLLSTRAGGIG INLATADTVI I TOSIMPHHOD APSRAHI GGNKKWUTKPTTRASVEERI TQVAKKKMMITHL RRGGSKTGSMSKQELDD I LKFGTEELFKODEATOMGCAI FNAPGAQGFCFLLSTRAGGIG INLATADTVI I TOSIMPHHOD APSRAHI GGNKKWUTKPTTRASVEERI TQVAKKKMMITHL RRGGSKTGSMSKQELDD I LKFGTEELFKODEATOMGCAI FNAPGAQGFCFLLSTRAGGIG INLATADTVI I TOSIMPHHOD APSRAHI GGNKKWUTKPTTRATOTY TOSIMPHHOD APSRAHI GGNKKWUTKPTTRATOTY TORIVAKKMMITHL RRGGSKTGSMSKQELDD I LKFGTEELFKODEATOM RRGGSTGSTSMSKQELDD I LKFGTEELFKODEATOM RRGGSTGSTSMSKQELDD I LKFGTEELFKODEATOM RRGGSTGSTSMSKQELDD I LKFGTEELFKODEATOM RRGGSTGSTSMSKQELD I LKGGSGVFTTTTGGVSLAFKVAQ REEBMGEEEVERE FREGGERVENGERPTTTTGTUT MTPAVPP PAPADOI KIEBERSIKLEEGES I EGKESVKSTAPFTATE OAPPAPAS EDEKVVVPPPGGBEKVERKGERFTPTSTFGDT MTPAVPP PAPADOI KIEBERSIKLEEGES I EGKESVKSTAPFTA	6005	133	5955	
GKKKKKKLOPKKEKSSKSKRKEREEEDDDDDDSERPESSAU, EDMGMEDIDHYFSEEDYRTLTNYKAFSQFVRPLIAAKNFKIA KOMMOVLGAKWREFSTNNFFKGSSGSVAAAAAAVAVVESMV TEVAPPPPPVEVPTRKAKTEGGKGFNARRFKGSSGRVDAAKK PKKVPJK KLAGFGSSKKRSSSEDDDDVESSFDDAS INSY SDGSTSRSSRSKKKRTTKKKKKGEEVTAVOETDIGDVC COQGELILCDTCPPALMWCLDPDMERAPEGKWSCPHCKEE QWEAKEDNSEGEILERVGDDLEEEDDHMEFCRVCKDGGEL CDTCPSSYHIHCLAPPLDEIPMSEALCPRCTCPALKGKVOKT. WKWGQPPSFTVPVRPPDDADNTTSFKPLEGRERGFFVKWGG YWHCSWVSLGLELKC\QVWFRNYQRKDDMEPPSGDFGGGE S\RRKKNKDPKAEMEERFFYRYGIKED\KOPPGDTGGGEL S\RRKKNKDPKAEMEERFFYRYGIKED\KOPPGDTGGGEL S\RRKKNKDPKAEMEERFFYRYGIKED\KOPPGDTGGGEL S\RRKKNKDPKAEMEERFFYRYGIKED\KOPPGDTGGGEL S\RRKKNKDPKAEMERFFYRYGIKED\KOPPGDTGGGEL S\RRKKNKDPKAEMERFFYRYGIKED\KOPPGDTGGGEL S\RRKKNKDPKAEMERFFYRYGIKED\KOPPGDTGGGEL S\RRKKNKDPKAEMERFFYRYGIKED\KOPPGDTGGGEL S\RKKNKLKKKKKKKKKKKKAEVKHPULLTS HVHYLIKWDLEPJOASWSSBUEIODVDLFKGSYMNHRELM EBGRFGKKKKKKKKKKKKAEVKHPULLTS TLHPYQMEGLANNLERSWAGGTDTILADEMGIGKTVUTAVFLY YKEGHSKGFFLVSAFLSTIIN\WEREFERMAPDMYV\VTYVG DSRAIIEREPS\FENDAIGGKGKFRVLNGSSLC ULLTGTTDLQNINEELFELHLMFTJPBRINGGKFFRVLNGYSLG ULLTGTTDLQNINEELFELHLMFTJPBRINGGKFFRVLNGYSLG LLLTGTTDLQNINEELFELHLMFTJPBRINGGKFFRVLNGYSLG GIKKLHDMLG\PHALRIKADVFKNMPSKTELIV\RVELSPM KKYYK\YILHSKFLKALN\ARGGGGGVSLLNVMDLKKCCHM LFFVAAMEAPKMPNOMYGSALIRAGGGGNVSLLNVMDLKKCCHM KKYYK\YILHSKFLKALN\ARGGGGGVSLLNVMDLKKCCHM LFFVAAMEAPKMPNOMYGSALIRAGGGGINLAATADTVIIVDSDWIPHND AFSRAHEIGGNKKVMIYRFVTRASVEERITQVAKKKMMLTHL RPGIGSKTTSMKKGELDLILKFGTBELFKDEATDGGGDNKBG SSVIHYDDKAIBRLLDRNQDETEDTLAGMBYLSFKVAGY REEBMGEEEEVREIIKGESVDPDYWEKLLRHYPQQGED MAGNKRI KRQNYMYDDGSGDRDWODDSDNGSDYSVASEBE DFDBRSSAPRRFSRKGLENDKOKFPLECANTUPTSTGGT NTGAVUPPAADOLKIERKEREFEKMAVV MHLCEFGADGAETFAGCVPREGLSRQHVLTRIGVMSLIRKK EFEHVNORMSMELAEVSBKKKESDEERKESVETPTSTTGGT NTGAVUPPAADOLKIEREBKESKESEERENTEPTSTGGT NTGAVEPSPAADOLKYCERESTATUTY VUPBCRGKSEKEFKAVV MHLCEFGADGAETFAGCVPREGLSRGHVLTRIGVMSLIRKK EFEHVNORMSMELAEVSBKAKENGGGSGSPSKYTTPSTTGGT NTGAVEPPAADOLKIELERILAGENEKEEEEKKEVALLONGET DLNDEKQKKNIKQFFPPNIADGGFTELHSLWORDERAATUTK YESIMRRHUPMILAGIINGKERFFLLEGALUFUERLGLERAAY LUMSED PSMALNTYFFE		1		NNSLPPPHPENEEDPEEDLSETETPKLKKKKKPKKPRDPKIPKS
BDWGMEDIDHVESGEDVRITATYKAPSGYRPALAANAPAVVESMY KMMAVLAGAMREPSGYNDPPKGSGSGAVAAAAAAVAVVESMY TEVAPPPPPVEVPIRIAKTKEGKGPNARRKPKGSPRVPDAKK PKKVAPIKIKLGGGGSKRKESSEDDDLDVESDPDASINSY SDGSTSRSSRKKLETKKKKKGESEVTAVDGYETDGDYC CQGGEIILCDTCPRAYHMYCLDPBMEKAPGKRSCPHCEKE OWARKEDNESGEELLEKUGUBEEDDUHMEFCRVCKDGGEL CDTCPSSYHIHCLAPPLDEIPMGEKLCPRCTCPALKGKVOKT. WKWGQPPSPTPVPRPPDADPNTPSPKPLEGPPERQFPVKQG YWHCSWVSELGLELIC\QVWFRNYQRKNDHDEPPSGDFGGDE S\RRKKNKDPKPAEMEERFYRYGIKPEN\MINITALINISVDK HVHYLIKWRDLPYDAGAMSSEDVEIQDTLFKGSYMNIRGELM EBGRPGKKLKKVKLKKLERPPETPTVDPTVKYRRQFYLDAT THEPYGMEGIANLERSWAGGTDTILANGLGKTVQTAVFLY YKEGHSKGPFLVSAPLSTIIN\WEREFEMAPDMYV\VTYVG DSRAIIREBFS\FEDNAIRGGKKASRNKKESVKFHVLLTS LLITGTPLQNNLEELFHLLMFLTPERFHNLEGFLEEFADIAK QIKKLHMMGJ\PHLMRIKADVFKIMGKEFFVLNYSIQ LLLTGTPLQNNLEELFHLLMFLTPERFHNLEGFLEEFADIAK KKYYK\TLHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCHH LEPVAAMBAPKMPNGMYDGSALIRAGGGNGVSLLNVVMDLKKCCHH KKYKK\TLHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCHH LEPVAAMBAPKMPNGMYDGSALIRAGERITUVBCMNUKKCCHH RRAGAQQPCFLLSTRAGGIGINLATADTVIIVDSDMPHND AFSRAHIGGNKKWMIKPFVTRASVERITQVGNKKMLIKEG SVIHYNDKAIBFLIKONGNOETDTELGOMBVLSKGKMAITH RRGIGSSTGSMSKQELDDILKFGTEELFKDEATGGGDNKGS SVIHYNDKAIBFLIKONGNOETDTELGOMBVLSSFKVAQY REEMMGEEEEVEREIIKGESVPDPYWEKLLINHYRQQGDL MIGKKRI RRKQNYNYDDSGADDNOGDSTSVASEGG SVIHYNDKAIBFLAGUVBCHDETTURLVRDLRIKSKERFAYYS MRHLCEFGADGAETTRAGVPRELISERGHVLTRIGVMSLIRK EFFHNGRWSMELAEVERNKKMSQCGS SPSKYTPTSTFGGT NTPAVPD PAAGOIG TENSKLEEGSIEGKSVKSTAPBTAIE QAPAPAS EDEKVVVPPPGEBEKVEKAEGIEGKSVKSTAPBTAIE QAPAPAS EDEKVVVPPPGGBEKVEKAEVERTEEPMETPIKG AADVEKVEEKSAIDLTPIVVEDKERKKEEKEENKIPSTPSTGGT NTPAVPD PAAGOIG TENSKLEEGSIEGKSVKSTAPBTAIE OAPAPAS EDEKVVVPPPGGBEKVEKAEWICHERTEPMETPSTGGT MTRADVP PAAGOIG TENSKLEEGSIEGKSVKSTAPBTAIE OAPAPAS EDEKVVPPPGGBEKVEKAEMILERLERKLUSGLILLERLERGE BELLSGMKADVTELAEIT INHGTARMQOIONDPRTALILEFFRA REHHENDYNLAGIINKTIARRFLLEGALUSEGNAUNGERNAULHKVLK EBLLSGMKADVTELAEIT INHGTARMQOIONDPRTALILBFEFRA REHLEGERGEVEKAENTIELGALUSERGERATAVTIK SEHLIGDWROGLEKSTVCRUEGSFPTESVTCKUSETUVSYKU CRUPRGKOKPCETVFOKGEFPTESVTC		1		KRQKKERMLLCRQLGDSSGEGPEFVEEEEEVALRSDSEGSDYTP
MMMVLGAWREFSTNNPFKGSSGASVAAAAAAVAVVESNV TEVAPPPPVEVPIKAKTKEGKGPNARKEKSGRPVARKE PKKVAPLKIKLGGFGSKRKSSBEDDLDVESDFDDASINSY. SDGSTSRSSRSKKLRTTKKKKKGEEEVTAVOGFTDHDOYC. CQQGGEIILDCTCPRALMWCLDPDMEAPEGKWSCPHCEKER. OWEAKEDNSGEBLIBEVGGDLBEEDDHHMEFCRVCKDGGEIL. CDTCPSSYHIHCLNPPLPETPMGENCTCPALKGKVOKT. WKWGQPPSPTPVPRPPDADPNTPSPKPLEGPPERGFFVKWQG- YWHCSWVSELQLEIHC\QVWFRNYQRKNDMBPPSDGFGGDE- S\RRKKKNKDFKAEMERFFYRYGIFVEN\MMIRTLINISVOK- HVHYLIKWRDLPYDQASWBSEDVEIQDYDLFKQSYMNIRELM- EBGRPGKKLKKVKLKKLEKLERPPETPTVYTYKRFQPEYLDAY- TLHPYQMEGLINILRSPARQGTDTILADEMGLGKTVQTAVFLY- YKKGHSKGPFLVSAPLSTIINWEREFFMWADDMYVVTYTVQ- DSRAILREBFFS\FEDDANIRGGKKASRKKEASVKFHYLLTS- LITIOMATIGSIDWACTLIVDEAHRIKNNQSFFPYLLOFSIG. OIKKLHDMG\] PHMLRRIKADVFKMMPSKTELTV\AVELSPM- KKYYK\YILISKFLKAIN\ARGGGROVSLLIVVMDLKKCCMH- LFPVAAMEAPRMPMMYDGSALIRASGKLLLIQKMLKHILKG RVLIFSGMTKMLDLLEDFLEHEGYKYERIDGGITGMMQEAI- PARGAGOGCFFLLSTRAGGIGINLATADTVIITDSDWMPHMD APSRAHRIGGNKVMIYRFVTRASVEELTQVAKKKMMITHL- RRGIGSKTGMSKQBLDIIKGTEREDEATDGGODNKIG SSVIHYDDKAIERLKQUSSGEDRUDGDSDNGSDYSVASEG DFDRSSAPRRPSRGGLGNDKDFLPETLQCMBEYLSSFKVAQY REEBMGEEEVEREIIKQESVDFDYWSKLLRIKTPQQCEBDL NIGKKKRIRKQVNYNDOSQEDROWODDSDNGSDYSVASEG DFDRSSAPRRPSRGGLENDKDFLPFLAKWGNIEVLGFW QRKAFLHAINTXGMPDOAFTTGHUVDLIKGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSROHVLTRIGVMSLIRKK EFEHVNGRWSMBELAEVERKKNSGPGGPSPSPKTPTPSTPGDT NTPAPVPADGOIK LEENSLKEESEIEGKEKVXSTAPETAIE OAPAPASEDEKVVVPPPGGERKVERKEREKEFWITTPSKQ BLADUKKVERKSAJDTIVVPDKEKEKKENEVERTEEPMETTPSKQ AADVEKVERKSAJDTIVTVVDKDEKSKEEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSROHVLTRIGVMSLIRKK EFEHVNGRWSMBELAEVERKENKSGPGGPSPSPKTPTPSTPGDT DLADEKQKKNIKQRFMFNIADGGFTELHSLMONEBERATVTK TSTHURRHDYWLLGGITNHGYARMDDIONDPYAILINEPFKG BAADVEKVERKSAJDTIVTVVDKEEKERBEEKKSVALORGET DLADEKQKNIKQRFMFNIADGGFTELHSLMONDERRALTVTK TSTHURRHDYWLLGGITNHGYARMDDIONDPYAILINEPFKG GRFRINTYIFILIGKHQLAKEHJLKEERMANNAPHANALHHVKL BELLSDMKADVTRLPATTARTPPVAVRLQMSENNILSRLANN EPTPQUAQQQ DNDFLRNTVHRHPPVTAEPSPLALAENEDVVVVAKCREBERATVTK GRFRINTYIFILIGKHQLKSHGHLKHLDRLTSGVLMFAKTAA BRIHGOVRDROLEKEFVURNDEGFPTEVTCKEBTULVVSYK CZVUPRGKO	j	1		GKKKKKKLGPKKEKKSKSKRKEEEEEDDDDDDDSKEPKSSAQLL
TEVAPPPPPUVDIKANTKEGKGPNARREPKGSPRVPDAKK PKKVAPLKIKLGGFGSKRKRSSSEDDLDVVSDFDDASINSY. SDGSTSRSSRSKKKLETTKKKKKGEEEVTAVDGYETDHQDYC CQGGEIILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCEKE OWEAKEUNSGGEIILEBUVGGLEEDHHMEYCRVCKGGGLI CDTCPSSYHHICINPPLPBIPNGEWLCPRCTCPALKGKVGKT. WKWGQPPSPTPVPRPPDADDNTPSPKPLEGRPERQFPVKWQG YWHCSWYSELQLEHC\QWMPRHYQRGWDMDBPPSGDPGGDE S\RKKKNKDPFPPPRPPPDADDNTPSPKPLEGRPERQFPVKWQG YWHCSWYSELQLEHC\QWMPRHYQRGWDMDBPPSGDPGGDE S\RKKKNKDPFPPPRPPTVDPTVKYERQPEYLDAY HYNTIL KRNDLPYDOADSWESEDVJDDLFKGSYSWRRELM EEGRPGKKLKKVKLRKLERPPETPTVDPTVKYERQPEYLDAY TILHPYQMEGIMWIRFSWAQGTDTILADEWGLKKTVQTAVFLY YKEGHSKGSPFLVSSPLSTIIN\WBEFERWAPDMYV\VTYVG DSRAIIRENBFS\FEINAIRGGKKASRWKKEASVKFHVLLIS LITIOMAILGSIDWACLIVDERHKNOSKFFPVLNGYSLQ GKKHLHDMLG\PHMIRRIKADVFKNMPSKTBLIV\RVELSPM KKYYK\YILHSKFLKALM\ARAGGOQVSLLNVVMDLKKCCHH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKMLKECHH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKMLKCCHH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKMLKCCHH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKMLKCCHH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKMLKEC RVLITSGMTKMCLLEDFLEHEKYRETIGGTCHMRQEAI FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWMPHAD AFSRAHRIGGNKKVMIYRPVTRASVERITQVSKKKMLITHL RRGLGSKTGMSKGGLEDDILKGTEELFKDEATDGGGDNKBG SSVIHYDDKAIERLLDRNQDFTEDTELQKMSVMSLSFKVAQV BEEMGEEEBVEREIIKQBESVPDEWELLIRHTVEQQGEL NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDYSVASBES DFDERSSAPRPSRKGLRNDKNELPFLLARVGGNIEVLGFN QRKAFLNAINKYGMPPOQAFTTQUVVRDLKGKSEKKFKAYVS MHLCEPGADGAFTFADGYPRGLSRQDGDVRTIGGWSLIRKK BEEHLBURGRWBMELEABVERNKKWAGOGSPBPKTPTPSTGDT NTPAPVPPAEDGIKIEGESEVEKKEVKSTAPETAIE QAPAPASEDEKVVVEPPBGEEKVEKABVKRTERPMETPSTGDT NTPAPVPPAEDGIKIEGRSEEKEESEKEWALDNGET DLNDEKKKKNIKQRFMFNLADGGTELHSKOMBERAATVIK BEEHLBURGRWBMELLADTINGTARRQDIONDPRYALLINGFE NGMYLEIKKKLARRFKLLEQALVIEEQLRRAAYLINMSEDP PSMALNTTFAEVECLAESGHLSKKSMAGNKPANAVLHKVLK BELLSDMKADVTRIADTAIRIPPVAVRLQWSENNILSRLAND EPTPQQVAQQQ DDFLRNTVHRHEFPVTAEPIRLAENEDVVVVDKPSSIPVE GRFRNTVIFILGKEHGLKELBPLHRLDRLTSGVLMFAKTAR ERIHBOVERGRLEEVYCZWEGEPFTEEVTCKSPILVVSKYK CCVUPRGKPCETVFORLISNINGGSSVVCRPLTGRTHQINVH		1		EDWGMEDIDHVFSEEDYRTLTNYKAFSQFVRPLIAAKNPKIAVS
PKKVAPI.KI KLGGFGSKRKRSSEDDDLDVESDFDDAS INSYSDSTRSSRSRKKLRTTKKKKGEEVTAVDGYETDHQDYC CQGGEILLCDTCPRAYHMVCLDPDMEKAPECKWSCPHCEKE QWEAKEDNSSGEILEBVGGDLEEDDHHMBYCRVCKDGGELL CDTCPSSYHHTCLNPPD.PEJ PIDEURCPRCTCPALKGVOKI. WKWGQPPSTPVPRPDDADPNTPSPKPLEGRPERQFFVKWQG YWHCSWVSELQLELHC\QWMFRNYQRGUNDMEPPSGDFGGLE S\RKKKKNEPKFAPMERFYRYGIKFDWDMEPPSGDFGGLE S\RKKKKNEPKFAPMERFYRYGIKFDWDMPPSGAPGGLE S\RKKKKNEPKFAPMERFYRYGIKFDWDMPPSGAPGGLE DSRAI IRENBFS\PEDINATGGKKASMKKEASVKFAVWFLINS THHPYQMEGLNWLRFSWAQGTDTILLADEMGLKTVQTAVFLY YKEGHSKGPFLVSAPLSTI IN\WEREFEMWAPDMYV\TYYG DSRAI IRENBFS\PEDINATGGKKASMKKEASVKFHVLLTS LITIDMAILGSIDWACLIVDBAHRLKNINQSKFPRVLNGYSLQ LLLTGTFLQNNLEELFHLLINFLTFERFHNLEGFLEFFADIAK QIKKLHMUG\PHMLRRIKADVFRNMPSKTELIV\RVELSPM KKYYK\YILHSKFLKALN\ARGGGNQVSLLINVVMDLKKCCHH LFPVAMADEAPKMPGNYDGSALIRASGKLLLLQKMLKNLKSC RVLIFSQMTKMLDLLEDFLBHEGYKYERIDGGITGNMRQEAI FNAPGAQQFCFLLSTRAGGLGINLATADTVIJTDSDNWPHHDD APSRAHRIGQNKYMIYNFVTRASVERITQVAKKKMLMIKE RVLIFSQMTKMLDLLEDFLBHEGYKYERIQGGDNKSC SSVIHYDDKAIERLLDRNQDETEDTELQGMBYLSFKVAQY REBEMGEEEVEREIIKQESVDEDYWEKLLHHHTEQQGBDL NLGKKKIRKQVMYNGSGEDRDWQDDQSNOSDYSVASEG DFDERSSAPRPSKGLIRDINKDKLPFLLARVGGNEVLGFN QRKAFLNAIMRYGMPPQDAFTTOWLVRDLIGKSEKEFKAYVS MHHLCEPGADGATFFADGYPRGUSRGHVUTTRIGVMSLIRK BEFHUNGRSWPBLABVERNERWQPGSPSPKTPTPSTTGDT NTPABVPPABGGIKIERBISKBESIBGEKVKSTAPBTAIE QAPAPASEDEKVVVEPPBGGEKVERVERKTEEPHETEPK QAPAPASEDEKVVVEPBGGEKVERVERKTERFERPTETPFODT NTPABVPPABGGIKIERINGDANGDONDPRYAILINEFFKG DLNDEKKKKNIKGRFMFNIADGGFTELHSLUMGERAATVYK YEINHRRHDWALLGIINIGVARMQDIONDPRYAILINEFFER NRGNFLEIKNRHDWALLGIINIGVARMQDIONDPRYAILINEFFER PSMALNTRFAEVECLAESHQHLSKESBARANVKNANAVLIKVLK BELLSDWKADVTRIAGTINGTARMQDIONDPRYAILINEFFER PSMALNTRFAEVECLAESHQHLSKESMARNARANAVLIKVLK BELLSDWKADVTRIAGTINGTARMQDIONDPRYAILINEFFER PSPMALNTRFAEVECLAESHQHLSKESMARNARANAVLIKVLK BELLSDWKADVTRIAGTINGTARMQDIONDPRYAILINEFFER PSPMALNTRFAEVECLAESHGLLEEPHERDRUKWDRARASILIKSLAMR EPTPQOVAQQQ DNDFLENTVHRHEPPVTAEPIRLLAENEDVVVDKPSSIPVF GRFRINTVIFILGKEHQLKERHPHRLDRLTSGVLMFAKTAR BEHHBQVERGRLEEVVCRUGEPFTEEVTCKSPILVVSKYC CVUPRGKPCETVFOLISNINGGSSVVCRUPLTG				KMMMVLGAKWREFSTNNPFKGSSGASVAAAAAAAVAVVESMVTA
SDGSTSRSSRSKKLRTYKKKKGEEVTJAVJOYSTDHODYC CQQGGEIILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCEKEE QWEAKEINSEGEEILEEVGGLEEEDDHHMEYCRYCKDGGEL CDTCPSSYHHHCINPPLEBIPNGWLCPRCTCPALKGKVQKI. WKWGQPSPTPVPVPRDADPMTSPLEGRERGPFGFFVKWGG YWHCSWVSELQLELHC\QVMPRNYQRKNDMBBPSGDFGGEE S\RKRKNKDFFAEMEERFYRYGIKFEW\MMHRILINHSVDK HVHYLIKRNDLFYDGASWESEBUSIQYDLFKQSYWNRRELM EBGRPGKKLKKVKLRILBEPPSTPTVDPTVKYERQPEVLDAT THYPQMEGLMURISFWAGGTDTIADEMGLKTVOTAVFLY YKEGHSKGPFLVSAPLSTIIN\WEREFEMMAPDMYV\VTYVG DSRAIIRENBFS\FEDNAIRGGKKASRMKKEASVKFHULITS LITIDMAILGSIDMACLIVDBAHKNOSKFFRLNGYSLQ LLLTGTFLQNNLEELFHLLINFLTERFHNLEGFLEEFADIAK QIKKLHDMALQ\PUMLERLEADVFHNSKTELIV\YAVELSPM KKYYK\YLHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKHLKHLKEAD RKYYK\YLHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKHLKHLKEAD RKYYK\YLHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKHLKHLKLAKEA RKYYK\YLHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKHLKHLKALKEA RKYYK\YLHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKHLKHLKLAKEA RSGLGSKTGSMSKQELDDILKRGTEELFKDEATDGGDNKKG SSVJHYDDKAIERLLDFRNDGTEETDELQGMNSYLSSFKXQAX PREEMGEEEVEREITKQESVYDVEKLLRHHYEQQQEDL NLGKKKIRKQWYNNOGSQEDRDWQDDQSDNSDYSVASEES DFDERSEAPRRPSRKGLDDILKRGTEELFKDEATDGGDNKKG SSVJHYDDKAIERLLDRNDGTEETDELQGMNSYLSSFKXQAX MEHLCEPGADGATFADGVPRGGLSRQHVLTTRGVWSLIRKK PEFHUNGRWSMPELAEVENKKMSQOGSPSPKTPTPSTGGT ONTAAVVPABEDGIKIERDSLKEESSIBGBEKVKSTAPETALE EFEHUNGRWSMPELAEVENKKMSQOGSPSPKTPTPSTTGGT NTPAPVPABEDGIKIERNESSIBGEKEVKSTAPETALE OAPAPASEDEKVVVEPPEGEEKVERKEEEKKEVMLONGET DLNDEKKVKNIKQRFMFNIADGGFTELHSLKMORERAATVIK VEINBRRIDVELLGALGINGGYARDONDPNYALLINDFFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRAAYLINMSEDP PSMALNTRFAEVECLAESSGHLSKESMAGNKPANAVLIKVIK BELLSDWKADVTRIAGTINGTANGLONDPRYALINSPEKG PSMALNTRFAEVECLAESSGHLSKESMAGNKPANAVLIKVIK BELLSDWKADVTRIAGTINGTANGLONDPRYALINSPEKG BELLSDWKADVTRIAGTINGTANGLONDPRYALINSPERA EFITEQOVAQQQ DDTARNTVFRIEFPVALEEPRILLAENEDVVVDKDRSSIPVE GRFRINTVIFILGKEHQLKELHPHRLDRLTSGVLMFAKTAB ERIHBOVADRQLEKEVVCEVBGEFFTEEVTCKSPILUNGSF	1	,		TEVAPPPPPVEVPIRKAKTKEGKGPNARRKPKGSPRVPDAKKPK
CQQGBILLCDTCPRAYHWYCLDPDMEKAPEGKMSCPHCEKER QWEAKENNSEGEILBEVGGDLEEDDHHMEFCRVCKDGGEL CDTCPSSYHHRCLMPPLPEIPNGEWLCPRCTCPALKGKVQKL WKWGQPPSPTPVPRPDADDTTSPRPLBGRPERQFFVKWGG YWHCSWYSELOLEHC\QVMFNYQRKDINDBPPSGPFGGDE \$ \text{RRKNKDPKFAEMEERFYRYGIKPERQFFVKWGG} \\ YWHCSWYSELOLEHC \text{RVKPMPYQRKDINDBPPSGPFGGDE} \\ \$ \text{RRKNKDPKFAEMEERFYRYGIKPEW\mMIHRILNHSVDK} \\ HVHYLIKWRDLPYDQASWSEDVEIQDYDLFKQSYWNHRELM BEGRPGKKLKKVKLKKLERPPTTDPTVYKYREQPELDAT TLHPYQMBGLMWLRFSWAQGTDTILADENGLGKTVQTAVFLY YKEGHSKGPFLVSAPLSTIIN\WERFEMWADDMYV\VYVG DSRAIIRENBFS\\FEDMAIRGGKKASRMKKEASVKFHYLLIS LITIDMAILGSIDWACTIIVDEAKRLKNNQSKFFRVLNGYSLQ LLLTTPLQNNLEELFHLLMFTBFFHNLEGFLEEPADIKK QIKKLHDMLG\\PHMLRRLKADVFKNMPSKTELIV\RVELSPM KKYYK\YLHSKFHKALN\\ARGGGNQVSLLNVWDLKKCCNH LFPVAMEAPRMPMGMYDGSALTRASGKILLLQKMLKKLKCCNH LFPVAMEAPRMPMGMYDGSALTRASGKILLLQKMLKNLKKCCNH LFPVAMEAPRMPMGMYDGSALTRASGKILLLQKMLKNLKKCCNH RFADAGQCFCFLLSTRAGGIGINLATADTVIIYDDWNPHND AFSRAHRIGGNKKMIVRFTVRASVEERITGGITGNMRGEAI FNAPGAQQFCFLLSTRAGGIGINLATADTVIIYDDWNPHND AFSRAHRIGGNKKMIVRFTVRASVEERITGGGITGNMRGEAI FNAPGAQQFCFLLSTRAGGIGINLATADTVIIYDDWNPHND AFSRAHRIGGNKKMIVRFTVRASVEERITGGGITGNMRGEAI FNAPGAQQFCFLLSTRAGGIGINLATADTVIIYDDWNPHND AFSRAHRIGGNKKMIVRFTVRASVEERITGGGITGNMRGEAI FNAPGAQQFCFLLSTRAGGIGINLATADTVIIYDDWNPHND AFSRAHRIGGNKKMIVRFTVRASVEERITGGGITGNMRGEAI GREBMGEEEVEREIIKQESVDPDYWEKLLRHHYEQQGDL NIGKKRIKRQVVYNNDGSGEDRWQDDDSDNSSYSSEG GREBMGEEEVEREIIKQESVDPDYWEKLLRHHYEQQGDL NIGKKRIRKQVVYNNDGSGEDRWQDDGSDSSYNSSEG GRESEAPRRFSPKGLRNNOKRPLPPLLAGRIGWSELVIGFN QRKAFLNAIMMYGMPPCDAFTTOWLVRDLGKSEKEFKAYS MRHLCEPGADGAETFADGVPRGGISRGNVLTRIGWSLIRK EFEHNGRWSMPELAEVERKKMSQPGSPSPTPTPSTPGTFGT NTPAPVPPAEDGIIKIERNSLKEESISGEKVKSTAPBTAIE QAPAPASBEBEKVVVPPPEGEKVEKABVERTEEPMFTEPR AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVMLONGBT DLNDEKGKKNIKQRFMFNIADGGFTELHSLWNBEDD PSMALNTRFAEVECLAESHQLISKESMAGNKPANAVLHKVIK EELLSDMRADVTRLPATTARIPPVAVLLQMSENILSLLAINE EPTPQQVAQQQ DDDFLRNTVHREPPVTAEPTRLLAENEDVVVDKDESSIPVF GRFRNNTVIFIIGKEHQLKSLHPLHLDRLTSGVLMFAKTAA ERIHBQVRDRQLEKYVCRVEGEFPT	1			PKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSYSV
CQQGGEILLCDTCPRAYHWYCLDPDMEKAPEGKMSCPHCEKEI QWEAKENNSEGEILBEVGGDLEEDDHHMEFCRVCKDGGEL CDTCPSSYHHKCLMPPLPEIPNGEWLCPRCTCPALKGKVQKI. WKWGQPSPTFVPRPDADPMTPSPRPLBGRPERQFFVKWGG YWHCSWYSELOLEHC\QWMFNYQRKDMDMBPSGPGFGFV KWGQPSPTFVPRPPDADPMTPSPRPLBGRPERQFFVKWGG YWHCSWYSELOLEHC\QWMFNYQRKDMDMBPSGPGGGDE S\RRKKNKDPKFAEMEERFYRYGIKPEW\MMIHRILNHSVDK HVHYLIKWRDLPYDQASWSEDVEIQDYDLFKQSYWNHRELM EBGRPGKKLKKVLKLKLERPFTYDTPYTVKYRGPEYLDAT TLHPYQMBGLMWLRFSWAQGTDTILADENGLGKTVQTAVFLY YKEGHSKGPFLVSAPLSTIIN\WERFEMWADDMYV\VTYVG DSRAIIRENEPS\FEDNAIRGGKKASRMKKEASVKFHYLLIS LITIDMAILGSIDWACTIINDAHRLKNNQSKFFRVINGYSLQ LLLTTPLQNNLEELFHLLMFTBFHNLEGFLEEPADLKK QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNH LFPVAMEAPRMPMGMYDGSALTRASGKLLLLQKHLKNKKCCNH LFPVAMEAPRMPMGMYDGSALTRASGKLLLLQKHLKNKKCCNH LFPVAMEAPRMPMGMYDGSALTRASGKLLLLQKHLKNLKCCNH RNAPGAQQFCFLLSTRAGGIGINLATADTVIIYDDWNPHND AFSRAHRIGGNKKVMIYRFVTRASVEERITGGITGNMRGEAI FNAPGAQQFCFLLSTRAGGIGINLATADTVIIYDDWNPHND AFSRAHRIGGNKKVMIYRFVTRASVEERITGGGITGNMRGEAI FNAPGAQQFCFLLSTRAGGIGINLATADTVIIYDDWNPHND AFSRAHRIGGNKKVMIYRFVTRASVEERITGGGTNKGC SSVIHYDDKAIERLDRNQDETELQCMMPSYLSSFKVAQY REEBMGEEEVEREIIKQESVDPDYWEKLLRHHYEQQQEDL NLGKKKRIKRQVNYNDGSGEDRWQDDGDSDGSVSVASBEG DDERSEAPRRPSKGLRNDKORKPLPPLLARWGGNIEVLGFN QRKAFLNAIMMYGMPPQDAFTTOWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPRGGLSRQHVLTRIGWMSLIRK EFEHNORWSMPELAEVERKKMSQPGSPSPRTPTPSTPGTGT NTPAPVPPAEDGIIKIERNSLKEERSIEGEKVKSTAPBTAIE QAPAPASBEBEKVVVPPPEGEKVEKABVKERGEBMETEPMFEPB (A AADVEKVEEKSAIDLTPIVVPDKEEKKEEEKKEVMLQNGBT DLNDEKGKKNIKQRFMFNIADGGFTELHSLWOMBERAATVIK YSIWHRRHDYWLLAGIINHGYARNQOIQNDPRYAILINBEPRG PSMALMTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVILK EELLSDMKADVTRLPATTARIPPVAVLLQMSERNILSRLANK EPTPQQVAQQQ DNDFILRTVHREPPVTAEPTRLLAENEDVVVVDKPSSIPVF SMALMTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVILK EELLSDMKADVTRLPATTARIPPVAVLLQMSERNILSRLANK EPTPQQVAQQQ DNDFILRNTVHREPPVTAEPTRLLAENEDVVVVDKPSSIPVF GRFRNNTVIFILGKEHQLKELHPLLRDLTSGVLMFAKTAA ERIHBQVRDROLEKEYVCRVEGEPPTEVTCKEPILVVSYK CRUPPRGPCETTYFORLSYNGGVWRCPPLTGATTHQIRVUH	1	İ	ĺ	
QWEAKEDNSGEBILBEVGGDLEEDDHHMBFCRVCKDGGEL CDTCPSSYHIHCLNPPLBEIPNGEWLCPRCTCPALKGKVQKI WKWQQPPSPTVPRPPDADPNTPSPKPLEGRPERGFVKWQG YWHCSWVSBLQLEIHC\QVMFRNYQKKNDMEPPSGDFGGE S\RKKKNKDPKPAEMEERFYRYGIKPEWNMIHRILINISVUK HVHYLIKWRDLPYDQASWSSEDVEIQDYDLFKQSYWNHRELM EGGRPGKKLKKVKLRKLERPPETPTUPTVKYERQPEYLDAT TLHPYQMSGLMWLRFSWAQOTTDILADENGLGKYTOTAVFLY YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVG DSRAIIRENEPS\FEDNAIRGGKKASRWKEASVKFHVLLTS LITIDMAILGSIDMACIIVDEAHRILKNNQSKFFRVLNGYSLQ LLLTGTPLQNNLEELFHLLMFLTPERFFHNLGGFLEFADIAK QIKKLHDMLG\PHALRRLKADVFKNMPSKTELIV\RVELSPM KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVYMDLKKCCHH LEPVAAMSAPKMPNGMYDGSALTRASGKLLLLOKMLKNLKG RVLIFSQMTKNLDLLEDFLEHGYKYREIDGGITGNMRQEAI FNAPGAQQFCFLLSTRAGGIGINLATADTVIIYDSDMWPHND AFSRAHRIGONKKVMIYRFVTRASVEERTTQVAKKKMUTHL RPGLGSKTGSMSKQELDDILKFGTBELFKDEATDGGDNKGE SVIHYDDKAIERLLDRNQDETEDTELQCMNEYLSSFKVAQY REEEMGEEEEVERBIIKQESVOPDVWERLLRHHYEQQGBL MLGKGKRIRKQVNYNDGSGEDRWQDDQSDNQSDSVASEEG SVENHYDDKAIERLLDRNQDETEDTELQCMNEYLSFKVAQY REEEMGEEEEVERBIIKQESVOPDVWERLLRHHYEQQGBL MLGKGKRIRKQVNYNDGSGEDREWQDDQSDNGSDYSVASEEG OFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGRIEVLGFN QRKAFLNAIMRYGMPPQDATTTGWLVRDLRGKSEKEFKAYVS MPHLCEPGADGAFTADGVVPRGLISRQHVLTRIGVMSLIRKK EFEHNVGWSMPELAEUERNKKMSQPGSPSPFTPPSTPGDT NTPAPVPPAEDGIIKEPSLLEESLIEGEKEVKSTAPETAIE QAPAPASDERVVVEPPEGEEKVEKAEVKERTERFMETEPKG AADVEKVEEKSAIDLTPIVVEDKEBKKESEEKKEVMLONGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVIK TSIMRRRIDYWLLAGIINTYARWQDIQNDRYAILNSPFKG NRGNIEIKKNKFLARRFKLLEQALVIEGLRAAYINNSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKUK, EBLLSDMCADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ DDDFLRTTYHRHEPPVTAEPIRLLAENEDUVVVDKPSSIPVF GRFRHNTVIFILIGKEHQLKELFLARAAYLMNSEDP PSMALNTRFAEVECLAESHQHLEKERMANKMANAVLHKUK, BELLSDMCADVTRLPATIARIPPVARLEGRARAYLKMSEDP PSMALNTRFAEVECLAESHQHLEKERMANKMANAVLHKUK, BELLSDMCADVTRLPATIARIPPVARLEGRARTVIKSEDP PSMALNTRFAEVECLAESHQHLEKERMANKMANAVLHKUK, GRUPFGKPCETVFORLSYNGSVWCREPLTGATTHQIRVUL GRUPFGKPCETVFORLSYNGSVWCREPLTGATTHQIRVUL GRUPFGKPCETVFORLSYNGSVWCREPLTGATTHQIRVUL	l			
CDTCPSSYHIECLNPPLPBTPMCEMLCPRCTCPALKCKVOKT. WKWGQPPSPTPVPRPDADAPNTPS PKPLEGRPERQFVKWQG YWHCSWVSELQLELHC\QVMFRNYQRKIDMDEPPSGDFGGGE S\RKKKIKDFKPAEMEERFYRYGIKPEN\MMTHRILMHSVDK HVHYLIKWRDLPYDQASMESEUGOYDLFKQSYWMRELMI EEGRPGKKLKKVKLRKLERPPETPTVDPTVKYERQPEYLDAT TILHPYQMEGLMWLAFSWAQGTDTILADEMGLGKTVQTAVFLY YKEGHSKSPFLVSAPLSTIIN KREFEMWAPDMYV\TYYG DSRAIIRENBFS\FEDNAIRGGKKASRMKKEASVKFHVLITS LITIDMAILGSIDWACLIVDEARRLKNNQSKPFRVLNGYSLQ LLLTTPPLQNNLEELFFILLMFLTPERFHNLEGFLEEFPADIAK QIKKLHDMLG\PHALRRLKADVFKNMPSKTBLIV\RVELSFM KKYYK\YILHSKFLKALN\ARGGROYSLLNVMDLKKCCHH LEFVAAMEAPRMPNGMYDGSALIRASGKLLLLQKMLKKLKEG RVLIFSQMTKMLDLLEDFLEHEGYKYERTDGGITGNMRQEAI FNAPGAQQFCFLLSTRAGGGINLATADTVIITDSDMWPHMD AFSRAHRIGQNKKWMIYRFVTRASVEERITQVAKKKMMLTHL RRGLGSKTGSNSKQELDDILKFGTBEIFDCATOGGGINKG SSVIHYDDKAIERLDRNQDETDDTELQCMMSYLSSFKVAQY REEMGEEEEVEREIIKQESVDPDVWEKLLEHHYEQQEDL NLGKGKIRKQNVYNDGSQEDRDWQDDQSDNQSDYSVASEEG SSVIHYDDKAIERLDRNQDETDDTELQCMMSYLSSFKVAQY REEMGEEEEVEREIIKQESVDPDVWEKLLEHHYEQQEDL NLGKGKIRKQNVYNDGSQEDRDWQDDQSDNQSDYSVASEEG OPDERSEAPRRPSKGLRNDKRFLPFLARRGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTOMLVRDLRGKSEKEFKAYVS MMHLCEPGADGAETTADGVYREJRGNVLTIRGUMSLITKK EFFHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIIKIERNSLKEEESIEGKEVKSTAPETAIE QAPAPASDEKVVEPEGEEKVEKABVEKEREPHETEPRG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLONGET DLNDEKGKNIKQRFMFNIADGGFTELHSLWQNEERAATVIK YSIMFRRIDVYNLLGGIINHGYARWODIQNDPXYAILNSEPKG NRGNFLEIKNKFLARRFKLLEQALVIEGCLRRAAVINNSEDP PSMALNTRFAEVECLAESHQALKESNAGNKPANAVLHKVLK EELLSDMKADVTRLPATTARIPPVAVELQMSERNILSRLANK EPTPQQVAQQQ DNDFLRNTYHREPPVTAEPIRLLAENEDVVVVDKESSIPVF GRFRNNTVIFILIGKEHQLKELHPLHRLDRLTSGVLMFAKTAA EPTPQQVAQQQ DNDFLRNTYHREPPVTAEPIRLLAENEDVVVVDKPSSIPVF GRFRNNTVIFILIGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHBGVRDROLEKEYVCRVEGEPPTEVTCKEPILVVSYK CRUPPRGFYCETVFOKLSYNGVRCPPLTGATTHQIRVUL	1	•	[
WKWGQPSPTPVPRPPDADPNTSPKDLEGRPERGFFVKWGG YMHCSWVSELQLELHC\QVMFRNYQRINDMEPPSGDFGDES S\RKRKINDPYFAEMEERFYRYGIKPEW\MNIHILIMISVDK HVHYLIKWRDLPYDQASWESEDVEIQDYDLFKQSYMWHRELM EEGRPGKKLKKVKLRKLERPPETPTVDPTVKYERQPEYLDAT TLHPYQMEGLWHLRSWAGGTDTILADEMGLGKTVQTAVFLY YKEGHSKGFFLVSAPLSTIIN\WEREFEMWAPDMYV\TYYGG DSRAIIRENEFS\FEDNAIRGKKASRMKKEASVKFHVLLTS LITIOMATLGSIDWACLIVDEAHRLKNNQSKFFRVLMGYSLQ LLLLTGTPLQNNLEELFHLLNFLTPERFHINLEGFLEEFADIAK QIKKLHDMLG\HMLRRLKADVKHMPBYSTELIV\RVELSFM KKYYK\YILHSKFLKALN\ARGGGQVSLLNVVMDLKKCCNH LFPVAAMEAPRMPNOMYDGSALIRASGKLLLLQKMLKNLKGE RVLIFSQMTKMLDLLEGFLEHBGYKFERLDGITGNMRQEAI FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHND AFSRAHRIGQNKKVMIYRFVTRASVEREITYDVAKKKMLTHL RPGLGSKTGSMSKQELDDILKRGTEELFKDEATDGGGDNKBG SSVIHYDDKAIERLLDRNQDETEDTELQGMMEYLSSFKVAQY REEEMGEEEEVEREIIKQEESVDPDYWEKLLRHYPEQQGEDL NLGKGKRIKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEG DFDERSEAPRRPSRKGLRNDKNKPLDPLLARWGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRK EFEHNVGRWSMPELAEVERNKKMGPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIENSKMSGOGSPSPKTPTPSTPGTD NTPAPVPPAEDGIKIENSKMSGOGSPSPKTPTPSTPGTD NTPAPVPPAEDGIKLEENSKMSGOGSPSPKTPTPSTPGTD NTPAPVPPAEDGIKIENSKMSGOGSPSPKTPTPSTPGTD NTPAPVPPAEDGIKIENSKMSGOFSPSTELHSLMGNERAATVYK YETWHRHDYWLLAGIINHGYRAWQDIQNDRYAILNEEP AADVEKVEEKSAIDLTPIVVENKEEKKEEEKKESVMLONGET UNDEKQKKNIKQRFMFNIADGGFTELHSLMQNBERAATVYK YETWHRHDYWLLAGIINHGYARWQDIQNDRYAILNEEP PSMALNTRPAEDVECLAESIQHLSKESMAGNKPANVLIKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILGRLANR EPTPQQVAQQQ DNDFLENTVHRHEPPVTAEPIRLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEQLKKELHPLHRLDRLTSGVLMFAKTAA EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILGRLANR EPTPQQVAQQQ DNDFLENTVHRHEPPVTAEPIRLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEQLKELHPLHRLDRLTSGVLMFAKTAA ERIHBCVRDRQLEKEVVCRVBGEFPTEFSTCKEETLUVSYKV CRUPPGKFVEGTFFVFOLSVRGGSSVVCCRPLTGRTHQTRVML CRUPPGKFVEGTFFVFOLSVRGGSSVVCCRPLTGRTHQTRVM	ļ			
YWHCSWVSELQLELHC\QVMFRNYQKRDMDEPPSGDFGGDE S\RRKNNDPKPAEMERFYRYGIKPEW\MMIHRILHSYDK HYHYLIKWRDLPYDQASWESEDVEIQDYDLFKQSYMNHRELM EEGRPGKKLKKVKLRKLERPPETPTVDFVYKYERQPEYLDAT TLHYYQMGGLMWLRFSMAQGTDTILADEMGIGKTVQTAVFLY YKEGHSKGFFLVSAPLSTIIN\WEREFFMADDMYV\VTYG DSRAIIRENEPS\FEDNAIRGGKKASRMKKEASVKFHVLLTS LITIDMAILGSIDWACLIVDEAHRLKNQSKFFRVLNGYSLQ QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM KKYYK\YILHSKFRALM\ARGGGNQVSLLNVVMDLKKCCNH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKKLKGE RVLIFSQMTKMLDLLEDFLBHEGYKYERIDGGITGNMRQEAI FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHND APSRAHRIQONKKVMIYRFVTRASVEERITQVAKKKMUTHL RPGLGSKTGSMSKQELDDILKFGTBEJFKDEATDGGGNNKGE SSVIHYDDKAIERLLDRNQDETEDTELQCMNEYLSFKVAQY REEMGEEEEVEREIIKQESVDPDYWEKLLKHHYEQQGELL NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDMQSDYSVASEG DFDRRSEAPRRPSKGLRNDKOKPLPPLLARVGGNIEVLGFM QRKAFINAIMMYGMPPODAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPRSGLSROHVLTRIGWMSLIRKK EFEHNWGRWSMPELAEUEENKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEESISGEKEVKSTAPSTAIE QAPAPASEDEKVVVEPPEGEEKVEKEEEKKEVMLQNGGT LDLNDEKQKKNIKQRFMFNIADGGFTELHSLMQNEERAATVTK YEIWHRRHDYWLLAGIINGGYARWQDIONDERYAAIUNSEDP MNGNFLEIKNKLARFFKLLEQALVIEEQLRRAAYLNMSEDP SMALNTRFREDEVELLAESQHLSKESMAGNKFANAVLIKVLK EELLSDMKADVTRLPATTARIPPVAVRLQMSERNILKSLANG EPTPQQVAQQQ DNDFLRNTVHRHEPPVTAEPIRLLEGELRAGNSANAVLIKVLK EELLSDMKADVTRLPATTARIPPVAVRLQMSERNILSRLANG EPTPQQVAQQQ DNDFLRNTVHRHEPPVTAEPIRLLEGELLTGGLMFAKTAA ERIHBCVVRDROLEKEYVCRVBGEFFTENTCKEPILVVSKVC CRVDPRGKPCETTFORLSVNGQSSVVCRCPPLTGRTHQIRVMI	1			
S\RRKNKDPKPAEMEERFYRYGIKPEW\MIHRILMHSVDK HVHYLIKWRDLPYDQASWESEDVEIQPYDLFKGSYWNHRELM EEGRFGKKLKVKLRKLIKLERPPETPTVDPTVKYERQPEYLDAT THHPYQMEGLNWLRFSWAQGTDTILADEMGLGKTVQTAVFLYY YKEGISKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVG DSRAIIREMEFS\FEDNAIRGGKKASRMKKEASVKFHVLLTS LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQ LLLTGTPLQNNLESLFHLLNFLTPERFHNLEGFLEEFADIAK QIKKHDMLG\PHMLERLKADVFKNMPSKTELTV\RVELSFM KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCHH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEG RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNNRQEAI FNAPGAQQFCFLLSTRRGGLGINLATADTVIIYDSDNNPHND AFSRAHRIGQNKKVMIYRPVTRASVEERITQVAKKKMLTHL RGCLGSKTGSMSKQELDDILKFGTBELFKDEATDGGGDNKEG SSVIHYDDKAIERLDRNQDETBTELQGNNEYLSFKVAQY REEBMGEEBEVEREIIKQESVDPDYWEKLLRHHYEQQGDL NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNSDYSVASEEG DFDERSEAPRPSRKGLRNDKDKPPFLLARVGGNIEVLGFN QRKAFLNAHMYSMPPDLARVGRONEVLIRHKYEQQGDL NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNSDYSVASEEG DFDERSEAPRPSRKGLRNDKDKPPFLLARVGGNIEVLGFN WRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFEHVNGRWSMPBLAEVERNKKNQPGSPSPKTPTPSTPGGT NTPAPVPPAPADGIKIERISKLEESISKGEKSVKSTPAPTAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEKKEEKEKNVLQNGGT DLINDEKOKKNIKGRFMNIADGGFTBLHSLMONEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEQLERRAAYLMNSEDP PSMALNTRFAEVECLAEROHLSKESNAGNRANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANG EPTPQQVAQQQ DNDFLENTVIRHBEPVTAEPITLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKENNAGNRANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANG EPTPQQVAQQQ DNDFLENTVIRHBEPVTAEPITLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELYNAGNSENNILSRLANG EPTPQQVAQQQ DNDFLENTVIRHBEPVTAEPITLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELYNAGSSVVRCRPLTGRTHQIRVVL CRYDPRGKPCETVFORLSYNAGSSSVRCRPLTGRTHQIRVVL CRYDPRGKPCETVFORLSYNAGSSSVRCRPLTGRTHQIRVVL			1	
HVHYLIKMRDLPYDQASWESEDVELQDYDLFKQSYMHRELM EEGRPGKKLKKVKLRKLERPPETFTOPTVKYERQPEYLDAT TLHPYQMEGLNWLRFSWAQGTDTILADEMGLGKTVQTAVFLY YKEGHSKGPFLVSAPLSTIIN\WERFFEMMAPDMYV\VTYUG DSRAIIRENEFS\FEDNAIRGGKKASMKKEASWKFVLLTIL LITIDMAILGSIDWACLIVDEAHRLKNINQSKFFRVLMGYSLQ LLLTGTPLQNNLEELFHLLNFLTPERFHNLEGFLEEFADIAK QIKKLHDMLG\PHMLRRLKADVFKMPSKTELLV\RVELSFM KKYYK\YLIHSKFLKALN\ARGGKNQVSLINVVMDLKKCCHH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEG RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNNRQEAI FNAPGAQOFCFLLSTRAGIGNILATADTVIITVDSMNPHND APSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHL RGGLGSKTGSMSKQELDDILKFGTBELFKDEATDGGDNKKG SSVIHYDDKAIERLLDNDDETDTELGCMNEYLSSFKVAQY REEEMGEEEVEREIIKQEESVDPDYWEKLLRHYYEQQQEDL NLGKGKRIRKQVMYNNOSQEDROWDDQSDNGDYSVASEEG DFDERSEAPRPSRKGLRNDKDFLPFLLARVGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADGABTFADGVPREGLSRGHVLTRIGVMSLIRKK EFFHVNGRWMPBLAEVERKKMSQPGS PSKYTPTPSTPGDT NTPAVVPPAEDGIKIEENSLKEEESIEGKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKABVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEBEKEKEEESKERVMLQNGET DLNDERQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVIK YEIWHRRHDYWLLAGIINHGYARNODIONDFRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEQLRAAYLNMSEDD PSMALNTRFAEVSCLAESHQHLSKESNAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ DNDFLENTVHRHEPPVTAEPIRLLÄENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA EENHBQVRDRQLKEGYVCRVEGEPTTEEVTCKEPILVVSYKV CRVDPRGKPCEKEYVCRVEGEPTTEEVTCKEPILVVSYKV	ł			
EEGRPGKKLKKVKLIKLERPPETPTVDPTVKYERQPEYLDAT TIHPYQMEGLINHLRFSWAQGTDTI LADEMGLGKTVQTAVFLY YKEGHSKGPFLVSAPLSIT IN\VEREFEWAAPDMYV\YTYG DSRAIIRENEFS\FEDNAIRGKKASRMKKEASVKFHVLLTS LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQ LLLTGTPLQNNLEELFHLLHFLTPERFHNLEGFLEEFADIAK QIKKHDMLG\PHMLERLKADVFKNMPSKTELIV\RVELSFM KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNH LFPVAAMEAPKMPNGMYDGSALIRASGKLILLQKMLKNLKEG RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGITGNNRQEAI FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDNNPHND APSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHL RPCIGSKTGSMSKQELDDILKFGTBELFKDEATDGGGDNKBG SSVIHYDDKAIERLLDRNQDETEDTELQCMNEYLSSFKVAQY REEBMGEEEEVEREIIKQESSVDPDVWEKLLRHHYEQQQEDL NIGKGRIRKQNMYNDGSQEDRDWODDOSDNGSPSYVASEG DFDERSEAPRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFN QRAFLNAIMRYGMPPCDAFTTGWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFEHNURGNSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPABCGIKIEENSLKEEBSIEGEKVEKSTAPBTAIE QAPAPASEDEKVVVEPPEGEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVIK YSIWHRRHDYWLLAGIINHGYARMQDIQNDPRYAILWEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEGLGRAAYLMNSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK BEILLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DINDFLRTVHRHBPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRRFNTVIFILGKEHQLKELHPLLBRLDRLTSGVLMFAKTAA ERIHBQVRNCQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRYDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVMI	l .			1 .
TLHPYQMEGLNWLRFSWAQGTDTILADEMGLGKTVQTAVFLY YKEGHSKGFFLVSAPLSTIIN/WEREFEWWAPDMYV\VTVG DSRAIIRENEFS\PEDMAIRGKKASARMKEASAVKFWILLTS LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQ LLLTGTPLQNNLEELFHLLNFTLFREFFHNLEGFLEEFADIAK QIKKLHDMLG\PHMLRRLKADVFKMWPSKTELLV,RVELSFW KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNH LFFVAMMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEG RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNMRQEAI FRAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHND AFSRAHRIGONKKWHYPFVTRASVEERITOVAKKKMMLTHL RPGLGSKTGSMSKQELDDILKFGTBELFKDEATDGGGDNKEG SSVIHYDDKAIERLLDRNQDETEDTELQCMNSYLSFKVAQY REEMGEEEVEREIIKQESVDFDYWEKLLRHHYEQQBDL NLGKGKIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEG DFDERSEAPRRPSRKGLRNDKDKPLPFLLARVGGNIEVLGFW QRKAFLNAIMRYGMPPQDAFTTOWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFFHNNGRWSMPELAEVENKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEERVEKKEEKEKKEMVLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILMEPFKG NRGNFIEIKNKFLARFKLLEQALVIEEQLARRAYLMMSEDP PSMALMTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLARN EPTPQQVAQQQ DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFFTEEVTCKEPILVVSKV CRUDRGKPCETVFORGLEKEYVCRVEGEFFTEEVTCKEPILVVSKV	1	1		
YKEGHSKGPFLVSAPLSTIIN WEREFEMMAPDMYV\VTYUG DSRAIIRENEFS\FEDMAIRGGKKASRMKKEASVKFHVLLTS LITIDMAILGSIDMACLIVDEAHRLKNNQSKFFRVLNGYSLQ LLLTGTPLQNNLEELFHLLNFLTPER FHNLEGFLEEFADIAK QIKKLHDMLG\PHNLRRLKADVFKMMPSKTELIV\RVELSFM KKYYK\YILHSKFIKALN\ARGGGNQVSLLNVWMDLKKCCNH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEG RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGTGNNRQEAI FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHND APSRAHRIGONKKVMIYRFVTRASVEERITQVAKKKMMLTHL RPGLGSKTGSMSKQELDDILKFGTBELFKDEATDGGGDNKEG SSVIHYDDKAIERLLDRNQDETEDTELQCMNSYLSFFKVAQY REEEMGEEEEVEREIIKQEESVDPDYWEKLLRHHYEQQQBDL NLGKGKRIRQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEG DFDERSEAPRRPSKKGLENDKNKPLPPLLARVGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFEHVNGRWSMPELAEVERNKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEGSIEGEKVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVVERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKEREPMTEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKEREPMTEPKG PKAADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVMLQNGET DLMDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVIK YEIWHRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARFKILLEQALVIECQLRRAAYLNMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRPRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKKTAA EPTPQQVAQQQ DNDFLRNTVHRHEPPVTAEPFREVLAENEDVVVVDKPSSIPVH GRPRHNTVIFILGKEHQLKELFPLHRLDRLTSGVLMFAKKTAA ERIHEGVRDRQLEKEYVCRVEBEEFFTEEVTCKEPILVVSKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHOIRVUK			1	
DSRAIIRENEFS\FEDNAIRGKKASRMKKEASVKFHVLLTS LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQ LLLTGTPLQNNLEELFHLLNFLTPERFHNLEGFLEEFADIAK QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNH LFPVAAMEAPFMPNOMYDGSALIRASGKLLLLQKMLKNLKEG RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGMNRQEAI FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHND APSRAHRIGONKKVMIYRFVTRASVEERITQVAKKKMMLTHL RPGLGSKTGSMSKQELDDILKFGTBELFKDEATDGGGDNKEG SSVIHYDDKAIERLLDRNQDETEDTELQCMMSYLSSFKVAQY REEEMGEEEEVEREIIKQEESVDPDYWEKLLRHHYEQQQEDL NLGKGKRIRKQVNYNDGSQEDDWQDDQSDNQSDYSVASEEG DFDERSEAPRRPSRKGLRNCKNFLPPPLLARVGGNIEVLGFN QRRAFLMAIMRYGMPPQDAFTTQMLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFFHVNGRWSMPELLAEVERKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEESIEGKEKVSTAPETAIE QAPAPASEDEKVVVPPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVMLQNGBT DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIONDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLMMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVUK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPPTQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRPRHNTVIFILGKEHQLKBLHPLHRLDRLTSGVLMFAKTAA EPPTQQVAQQQ DNDFLRNTVHRHEPPVTAEPIRLLAENEDVFTCSEPILVVSYKV CRVDPRGKPCETVFORLSYMGQSSVVRCRPLTGRTHQIRVEI		i	1	
LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQ LLLTGTPLQNNLEELFHLLINFLTPERFFIRLEGFLEEFADIAK QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNH LFPVAAMEAPRMPNGMYDGSALIRASGKLLLLQKMLKKNLKEG RVLIFSQMTKNLDLLEDFLEHEGYKYERIDGGITGNNRQEAI FNAPGAQOFCFLISTRAGGLGINLATADTVIIYDSDWNPHND APSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHL RPGLGSKTGSMSKQELDDILKFGTEELFKDEATDGGDNKEG SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYLSSFKVAQY REEEMGEEEEVEREIIKQESVDPDYWEKLLEHHYEQQGDL NLGKGKRIRKQVNYNDGSQEDRWQDDQSDNQSDYSVASEG DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFN QRAFLMAIMRYGMPPQDAFTTQMLVRDLRGKSEKEFKAYVS MRHLCEFGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFFHVNGRWSMPELAEVEBNKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWONEERAATVIK YEIWHRRHDYWLLAGIINHGYARWODIONDPRAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIERCARAAYLMMSLEP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATTARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRRPHNTVIFILGKEHQLKBLHPLHRLDRLTSGVLMFAKTAA EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRRPHNTVIFILGKEHQLKBLHPLHRLDRLTSGVLMFAKTAA ERHEQVVDRQLKEVVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVH	1 .		1	YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVGDK
LLLTGTPLQNNLEELFHLLNFLTPERFHNLEGFLEEFADIAK QIKKHHMUIG\PHMLERIKADVFKNMPSKTELIV\RVELSPM KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVMDLKKCCNH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEG RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNMRQEAI FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHND AFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHL RPCLGSKTGSMSKQELDDILKRGTBELFKDEATDGGGDNKEG SSVIHYDDKAIERLLDRNQDETEDTELQGMBYLSSFKVAQY REEEMGEEEEVEREIIKQESVDPDVWEKLLRHHYEQQGBDL NLGKGKRIRKQVNYNDGSDEDRDWQDDQSDDYSVASEEG DFDERSEAPRRPSRKGLRNDKNKPLPPLLARVGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEFGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFFHVNGRWSMPELAEVEBNKKMSQPGSPSPKTPTPSTPGIT NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGET DLNDEKQKKNIKQFMFNIADGGFTBLHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDF PSMALNTFAEVECLAESHQHLSKESMAGNRPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKLARA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKLARA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKLARA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKLARA	1		1	DSRAIIRENEFS\FEDNAIRGGKKASRMKKEASVKFHVLLTSYE
QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM KKYYK\YILHSKFIKALN\ARGGRQVSULINVVMDLKKCCNH LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEG RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNMRGEAI FRAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHND AFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHL RPGLGSKTGSMSKQELDDILKFGTBELFKDEATDGGGDNKEG SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYLSSFKVAQV REEEMGEEEEVERBIIKQESVDPDYWEKLLRHHYEQQGEDL NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEG DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVUTRIGYMSLIRKK EFEHVNGRWSMPELAEVEBNKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVKETEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVMLQNGET DLMDEKQKKNIKQRFMFNIADGGTTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTBEVTCKEPILVVSKV CRVDPRGKPCETVFORLSYMGQSSVWRCRPLTGRTHQIRVHI			· ·	LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQHK
KKYYK\YILHSKFIKALN\ARGGGNQVSILINVVMDLKKCCNH LFVAAMEAPKMPNGMYDGSALIRASGKLILLQKMIKRIKEG RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNMRQEAI FNAPGAQQFCFLLSTRAGGIGINLATADTVIIYDSDWNPHND AFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHL RPGIGSKTGSMSKQELDDILKFGTBELFKDEATDGGGDNKEG SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYSISFKVAQV REEEMGEEEEVERBIIKQESVDPDYWEKLLRHHYEQQQEDL NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEG DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEKFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGWMSLIRKK EFFHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEFRMETEFRG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGTTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTBEVTCKEPILVVSKV CRVDPRGKPCETVFORLSYMGQSSVWCRPLTGRTHQIRVHI	1	1	1	LLLTGTPLQNNLEELFHLLNFLTPERFHNLEGFLEEFADIAKED
LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEG RVLIFSQMTKMLDLLEDFLBHEGYKYERIDGGITGNMRQEAI FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHND AFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHL RPGLGSKTGSMSKQELDDILKRGTBELFKDEATDGGGDNKEG SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYLSSFKVAQY REEEMGEEEEVEREIIKQEESVDPDYWEKLLRHHYEQQGEDL NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSASEEG DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFN QRKAFLNALMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTEGDT NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWODIONDPRYAILNEEPFKG NRGMFLEIKNKFLARFFKLLEQALVIEEQLRRAAYLNMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ ONDFLRNTVHRHEPPVTAEPIRLLAENEDVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA EPTPQQVAQQQ DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL	1		2	QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM\Q
RYLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNMRQEAI FNAPGAQQFCPLLSTRAGGLGINLATADTVIIYDSDWNPHND AFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMITHL RPGLGSKTGSMSKQELDDILKFGTBELFKDEATDGGGDNKEG SSVIHYDDKAIERLLDRNQDETEDTELQGMNSYLSSFKVAQY REEEMGEEEEVEREIIKQEESVDPDYWEKLLRHHYEQQQEDL NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEG DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIKKK EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTEGDT NTTAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARFKLLEQALVIEQLRRAAYLNMSEDP PSMALNTFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYMGQSSVVRCRPLTGRTHQIRVHL		ł	1	KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNHPY
FRAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHND AFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHL RPGLGSKTGSMSKQELDDILKFGTBELFKDEATDGGDNKEG SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYLSSFKVAQY REEBMGEEEVEREIIKQESVDPDYWEKLLRHHYEQQQBDL NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEG DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADCASTFADCVPREGLSRQHVLTRIGVMSLIKKK EFEHVNGRWSMPELAEVERNKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEESKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNBPSCH PSMALNTRFAEVECLAESIQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILGRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFFHNTVIFILGKEHQLKELHPLLARLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYMGQSSVVRCRPLTGRTHQIRVHL	1		1	LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEGGH
FRAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHND AFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHL RPGLGSKTGSMSKQELDDILKFGTBELFKDEATDGGDNKEG SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYLSSFKVAQY REEBMGEEEVEREIIKQESVDPDYWEKLLRHHYEQQQBDL NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEG DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADCASTFADCVPREGLSRQHVLTRIGVMSLIKKK EFEHVNGRWSMPELAEVERNKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEESKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNBPSCH PSMALNTRFAEVECLAESIQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILGRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFFHNTVIFILGKEHQLKELHPLLARLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYMGQSSVVRCRPLTGRTHQIRVHL	1			RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNMRQEAIDR
AFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHL RPGLGSKTGSMSKQELDDILKRGTBELFKDEATDGGGDNKEG SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYLSSFKVAQY REEBMGEEEEVEREIIKQBESVDPDYWEKLLRHHYEQQQEDL NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEGG DFDERSEAPRRBSKGLRNDKDKPLPPLLARVGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEGSIEGEKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEESKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPPKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ ONDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVPORLSYNGQSSVVRCRPLTGRTHQIRVHL	1	l		
RPGLGSKTGSMSKQELDDILKFGTBELFKDEATDGGGDNKEG SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYLSSFKVAQY REEEMGEEEVEREIIKQESVDPDYWEKLLRHHYEQQGDL NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEG DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVHLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFFAKTA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVPPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL			1	AFSRAHRIGONKKVMIYRFVTRASVEERITQVAKKKMMLTHLVV
SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYLSSFKVAQY REEBMGEEEVEREIIKQEESVDPDYWEKLLRHHYEQQQEDL NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEG DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGRIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFEHVNGRWSMPELAEVEBNKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTBEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL				
REEEMGEEEEVEREIIKQEESVDPDYWEKLLRHHYEQQQEDL NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEG DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVVEPPEGEEKVEKAEVKERTEBPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEESKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ ONDFLRTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEFILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL		1	1	
NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEG DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFEHVNGRWSMPELAEVEBNKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIBENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVVEPPEGEEKVEKAEVKERTEBPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL	1			
DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFN QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFEHVNGRWSMPELAEVEBNKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIBENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVVEPPEGEEKVEKAEVKERTEBPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL			Ī	
QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVS MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRAAYLNMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL			1	
MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKK EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTBLHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDF PSMALNTFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKBLHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTBEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL			1	
EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDT NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQMEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLMMSEDF PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL	İ		1	
NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIE QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLMMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL		1	1	
QAPAPAS EDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKG AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVMLQNGBT DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLMMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ ONDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKSPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL			1	
AADVEKVEEKSAIDLTPIVVEDKEEKKEEEKKEVMLQNGET DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLMMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ ONDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL				
DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTK YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLMMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ ONDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKBLHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKBPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL				
YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKBLHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKBFILVVSYKV CRVDPRGKPCETTFORLSYNGQSSVVRCRPLTGRTHQIRVHL	1		1	AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGETPK
YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKG NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKBLHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKBFILVVSYKV CRVDPRGKPCETTFORLSYNGQSSVVRCRPLTGRTHQIRVHL				DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTKKT
NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDP PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL	1	1		YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKGEM
PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLK EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL		1		NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH
EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANR EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL		Ī		PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL
EPTPQQVAQQQ 6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL				
6006 1 965 DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVH GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL				
GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAA ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL	6000	 	0.65	
ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKV CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL	6006	1	302	
CRVDPRGKPCETVFORLSYNGQSSVVRCRPLTGRTHQIRVHL	1			GKEKUMIATETUGKEHÜPVERKERKUNKUNKUNGANIMEKKINAAS
[CRVDPRGKPCETVFQRDSYNGQSSVVRCRPDTGRTHQTRVHL	1			EKIHEGAKDKOPEKEIACKAEGELEIEFAICVELIDAASIKAGA
- ALLE TO BE A STATE OF THE PARTY OF THE PAR	1			CKVDPRGKPCETVFQRLSYNGQSSVVRCRPLTGKTHQIRVHLQF
LGHPILNDPIYNSVAWGPSRGRGGYIPKTNEELLRDLVAEHQ	L		J <u></u>	LGHPILNDPIYNSVAWGPSRGRGGYIPKTNEELLRDLVAEHQAK

Seq	SEQ	Predicted	Predicted end	Amino acid gagment acceptable
No:	_			(A=A)anine. C=Cveteine. D=Accounts Acid 2
cocresponding cofresponding cofresponding cofirst amino acid amino acid sequence sequence sequence codon, peosible nucleotide clear, x=100, peosible nucleot		,		Glutamic Acid. Fabbanylalanina Cadlusia
Leleucine Membhionine, NaApparagine, bofirst maino acid residue of amino acid residue of amino acid sequence seq		_		H=Histidine T=Teoleugine V=Tunine
to first anino acid residue of amino acid residue of amino acid anino acid sequence				L=Leucine, M=Methionine N-Assaragine
amino acid residue of amino acid sequence and code, proposible nucleotide deletion, apposible nucleotide deletion, apposible nucleotide insertion) GSLDVLDLCEGOLISEGITESTARSSELGEDULEELAAAA\GRME EVAKAAAGEAHTAGEAHTAGEAHTAGEAHTAGEAHTAGEAHTAGEAHTAGEAHTAGEAHTAGEAHTAGEAHTAGEAHTAGAAAAAGEAHTAGAAAAGEAHTAGAAAAGEAHTAGAAAAGEAHTAGAAAAGEAHTAGAAAAGEAHTAGAAAAGEAHTAGAAAAGEAHTAGAAAAGEAHTAGAAAAGEAHTAGAAAAGEAHTAGAAAGEAHTAGAAAAGEAHTAGAAAAGEAHTAGAAAGEAHTAGAAAAGEAHTAGAAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGEAHTAGAAAGAAAAAAGAAAAAAAAAA	İ			P=Proline, O=Glutamine, R=Arginine
residue of amino acid sequence Sequence		amino acid		S=Serine, T=Threonine, V=Valine.
amino acid sequence Codon, /-possible nuclectide deletion, -possible nuclectide insertion QSLDVLDLCEGOLSPGLTDSTAFSSELGKDDLSELGARAA\QKNE EVARAAPGCLUTIALABEGKAVETUVORQAGAT SLARRCDVPTCFIL GVERNARD	i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence Sequence		amino acid		Codon, /=possible nucleotide deletion
GSLOVIDLICEGOLSPGLITSTAFSSLGKDULERHANAN/ORDE BVARAPGCBUTTALABESKAVETUND() KOT\TCRVPAGATG SLAPRCOUPTCPTL BLGGVEVYPTORTOTITENEMOPRECSINGHKOGENGRUPE GPTPDSSEGNIS/LSSLSHINNLSHLTTSSSPRISPERSTELLK BEDLPPKAVSLGTVOINNVOTOCTOODPHOSINLASSCLEYVAS SPDERALVEARARIGIVFIGNSERTHEVKTLGKLERYKLIMILIE PSDRRRMSVIVOASPGEKLLPARAGESSILPKCIGGIKGTEI HVDEPFALKGLETLCLAYRKFYTSKEYBEIDER! FERRYTALOORUR ERLAAVPGFIENDLHGATAVBERLDGKWESTELAKINGIKV WULTGOKHETAVSVSLSCGHPHRYMMILELINGKSDSGCASGUR GLARRTEDHVIGHCUVPOTISSLABERIELEMENVCRICKAN LCCRMAPLGKAKVIRLIKISPERPTTLAVGGDARDVSHIGEAHV GUGIGMGGGRGARANSVALREHELEMENVCRICKAN LCCRMAPLGKAKVIRLIKISPERPTTLAVGGDARDVSHIGEAHV GUGIGMGGGRGARANSVALREHELEMENVERVCRICKAN LCCRMAPLGKAKVIRLIKISPERPTTLAVGGDARDVSHIGEAHV TUTVTVKAALETIFFATSVLLIGKTSILLONGGMFGHTFGTLVFTVM VITVTVKAALETIFFATSVLLIGKTSILLONGGMFGHTFGTLVFTVM VITVTVKAALETIFFATSVLLIGKTSILLONGGMFGHTFGTLVFTVM VITVTVKAALETIFFATSVLLIGKTSILLONGGMFGHTFGTLVFTVM VITVTVKAALETIFFATSVLLIGKTSILLONGGMFGHTFGTLVFTVM GROSPPHISKAGATSVARAFALLMVVTCLEIDIKKVTDHIL HTSTEKAQLITETNAGIKCLDSMCGPFGGARACNSYGMBLERVI GROSPPHSTANGTKICHDAGATAVPFFGGARACNSYGMBLERVI HTSTEKAQLITETNAGIKCLDSMCGFFGGARACNSYGMBLERVI GROSPPHSTYRKNIFSTATHENVALLDSIGLEVCKSHLE DFOGFEPDDFYLKNITTENDVALDEPSARRFRRCFAPEHRGPAR ASRSGETTFGLFVANNISSLEFARNKNINGLFKAGADSVEGVATVCK KCTYRDDLYSLIVKHIYRSHFQHVAAPYIAKAGEKSLGGAVPLOG SAABESSICKGCLPHESVEALUGHVISTORMONTYCTVANDKKLGTH HTNVVVPRSKFLMLLAFRGDKKSMGLPFLIGSLASGNVVRSLD SAABESSICKGCLFVHESVEALUGHVISTORMONTYCHADH HTNVVVPRSKFLMLLAFRGDKKSMGLPFLIGSLASGNVVRSLD SQCWXMSLSTRENNINSTORMMSSINGANSVALOSSORSPAAA ATGEPPGATTSTOKKKICTICHLEPSRNVYSKUPERERKRAEVV AVANYTHKINITSTORMMSSINGAGASSULOGSSKYDAA ATGEPPGATTSTOKKKICTICHLEPSRNVYSKUPERERKRAEVV AVANYTHKINITSTANGTSTANGTHAGNSTILLANGTCCHYCKTON GORTMAPSKLOKKICTICHLCGYTSMTATTILHAUHCGCGYCRS TFNUVKKRAJAMPRWHIDERMGFKTDSTLISPULLGGGSHTNIH LLVTTHINGADARSKSTOKKKICTICHLEPSPKSTCHKKRECOVSKYON GORTMAPSKLOKKICTICHLCGYTSMTATTILHAUHCGGRGFGANKHA ATGESCALASSKARAKARVATMOGREGENGKROSTICHLEPSRNDHER VLKUTEREBSKAGASSKATARAKANTMOGREGENGKNASSTOKAGNSKOM ENDELVLVAVACSSHIFTHAMATORGGELGARKARSKETKOTY Q	İ	sequence	1 -	\=possible nucleotide insertion)
SUAPRAPORIUTIALASEKAVETUVINO\ARQT\TLCRUPAGATG SLAPPROUPTCTUT SAPERCOUPTCTUT BEIGGVEYVFTOKTGTTLTENEMQFREGSIRGKYGEINGRLUPE GPTPDSSEGNISTLSSISJININISHTTSSSPRTSEPRETELIK BEIDLFPRAVSICHTVGINNVOTDCTGODPHOSINLAPSGLEYVAS SPERKALVEAARSIGHTYGINSTEWEYVICKKEREYKLLHILB FDSDRRMSVIVQAPSGEKLIFJAKGASSSILKKCIGGEIEKTEI HUDEFALKGLERTLGIATRYETTSKEYEDIKETFERATALORNE EKLAAVEGFIEKOLLILGATAVEDRLODKVRETTEALRINGIKU WULTGOKHETAVSVESLGCHHETRINILLELINGKSISGSCAPOLR GLARRITEBHVIGHGLVVOGTSISJALBEHERLIMSVCHCKSAV LCRMAPLOKAVITLIKISPRENTILLAVOGAMONYSHOLDANV GLARRITEBHVIGHGLVVOGTSISJALBEHERLIMSVCHCKSAV LCRMAPLOKAVITLIKISPRENTILLAVOGAMONYSHOLDANV GIGIMKGERGAARNSDVALAREKELIMSVCHCKSAV LCRMAPLOKAVITLIKISPRENTILLAVOGAMONYSHOLDANV GIGIMKGERGAARNSDVALAREKELIMSVCHCKSAV LCRMAPLOKAVITLIKISPRENTILLAVOGAMONYSHOLDANV GIGIMKGERGAARNSDVALAREKELIMSSUCHCHVITLAVICAT UVYFFYRANCEITDGLIVGTUTAVOGAMONYSHOLDANV GIGHTLINGVANDAVENTULLIKISPRENTILLAVOGAMONYSHOLTUPTUM VITTTVANALETHFAVTHIHLIVTAGSILFFYBLGYTGGLIMPF LSOMMYEVETOLLSSSAWFALLINUTVICLIGILIKVANDERLI HPTSTEKAQLITETNAGIKCLOSMCCPEGERACASVERMLERVI GREYPHILSRSMASADPFYTNOBSILTSTAMMISTER ASPSGEIMFOLDAVAVITCHLORLIKVAVITLISTMISSTO GREYPHILSRSMASADPFYTNOBSILLIKATUSTAMISTER DFKOFEPNDEYLINTTHEDVOLADPSAREKECPIPEHAG PAR ASPSGEIMFOLDAVITUSGLKRAKETVAKLLDGIDIGLVCKEHLE DFKOFEPNDEYLLINTTHEDVOLADPSAREKECPIPEHAG PAR ASPSGEIMFOLDAVITUSGLKRAKETVAKLLDGIDIGLVCKEHLE DFKOFEPNDEYLLINTTHEDVOLADPSAREKECPIPEHAG PAR ASPSGEIMFOLDAVITUSGLKRAKETVAKLLDGIDIGLVCKEHLE DFKOFEPNDYLLINTTHEDVOLADPSARADSVALAGANDVOLAVITUSGLKARATAVATORICARVA KKYTEPPLYLINTENALSSENGEN PARVAKLARAVITUSGLKARATAVATORICARVA ASPSJALGARANASILSSOLLAS PARVAKLARAVITUSGLKARATAVATORICARVA GRANDAVILOSANASILSSOLLAS PRICESCON VALGENAVITUSGLAVA GRANDAVILOSANASILSSOLLAS PRICESCON VALGENAVITUSGLAVA ANANYIMKLINTTEKCLYTRINIPTORICARDAVITUSGLAVATAVA ANANYIMKLINTTEKCLYTRINIPTORICARVATAVA GRANDAVILOSANASILSSOLLAS PROTESTAVATAVATAVATAVATAVATAVATAVATAVATAVATAV		· · · · · · · · · · · · · · · · · · ·		OSLDVLDLCEGDLSPGLTDSTAPSSELGKDDLSELAAAA\OKMR
SLAPRECUPTCPTL				BVAEAAPOELDTIALASEKAVETDVMNO\ROT\TLCRVPAGATG
GPTPDSSECHISTUSSELEITANLEHITTSSSPRISPENETELIIK BIDLPPRAVBLOTTVOINNYQTDCTOGDWGSMAPSQLETYLIK BIDLPPRAVBLOTTVOINNYQTDCTOGDWGSMAPSQLETYLIK BIDLPPRAVBLOTTVOINNYQTDCTOGDWGSMAPSQLETYLIK BIDLPPRAVBLOTTVOINNYQTDCTOGDWGSMAPSQLETYLIK BIDLPPRAVBLOTTVOINNYQTDCTOGDWGSMAPSQLETYLIK BIDLPPRAVBLOTTVOINNYQTDCTOGDWGSMAPSQLETYLIK BIDLPPRAVBLOTTVOINNYQTDCTOGDWGSMAPSQLETYLIK BIDLPPRAVBLOTTVOINNYQTECOGNUSSELEPRACHOGNE EKLAAVPOTERCHOTTVOINNYQTECOGNUSSELEPRACHOGNE GEARATCHANTAURIL STEPPERTURBURGBANGGARV GUGARRITERDIVIGHGLVVDOTSLESLAREHEKLEPMSVCRUCSSN LCCRMAPLOKANVIRLIKISPERTTANDGORMONGGARV GIGINGEGROAARNSDYATARPKELSKLEVHGHTYTIK NICTT SLPTILTYSLEQUIVDENVLOINNYGTIKAPTVIRLIKIVNYCHELDIK KVOVENHIL VQYPPKRAVCETTOFGLYGYTCHSQQTITSDYNTHYTIKVYNCHELDIK KVOVENHIL USSKAPITPSSVALLIGKUTSCHSQQTITSDYNTHYTIKVYNCHELDIK KVOVENHIL HITTSTEKAQLTETNAGIKCLDSMCCPPSEGBACASVGRMLERVI GRCSPTHISERSBASDPTYTNOSILLIKAVTGETLIK KVOVENHIL HITTSTEKAQLTETNAGIKCLDSMCCPPSEGBACASVGRMLERVI GRCSPTHISERSBASDPTYTNOSILLIKAVTGARTIK KVOVENHIL HITTSTEKAQLTETNAGIKCLDSMCCPPSEGBACASVGRMLERVI GRCSPTHISERSBASDPTYTNOSILLIKAVTGARTIK KVOVENHIL HITTSTEKAQLTETNAGIKCLDSMCCPPSEGBACASVGRMLERVI GRCSPTHISERSBASDPTYTNOSILLINGVATERPOKACHEN ASRNSOENTHGLUSSSGANFATILMYCTCHTORKYLETH IKITHADNASAPSSLSTFORNKINDOLRPRQADSVEQAVYLED FSSKFSAYKSHERVUNSEDPERRITLLINGVATTAPDEKKLETH IKITHADNASAPSSLSTFORNKINDOLRPRQADSVEQAVYLED SNABESSIHCKRCLPHRAYSHIVBERFRITLLINGVATTAPDEKKLETH IKITHADNASAPSSLSTGVANAPYTAKOGSSINGVANGLE SQAVARIASIERKNINSTGVANAPYTAKAGGSSINGVANGLE SQAVARIASIERKNINSTGVANAPYTAKAGGSSINGVANGLE GOGNARIASIERKNINSTGVANAPYTAKAGGSSINGVANGLE GOGNARIASIERKNINSTGVANAPYTAKAGGSSINGVANGLE SQAVARIASIERKNINSTGVANAPYTAKAGGSSINGVANGLE GOGNARIASIERKNINGVANGLEPROTTOKANVANSLE SQAVARIASIERKNINGVANGLEPROTTOKANVANSLE ANAPYTHAVANGVANGLEPROTTOKANAPYTAKOGSSINGVANGLE GOGNARSSINGVANGLEPROTTOKANGSSINGVANGLE GOGNARSSINGVANGLEPROTTOKANGSSINGVANGLE GOGNARSSINGVANGLEPROTTOKANGSSINGVANGLEPROTTOKANG GOGNARSSINGVANGLEPROTTOKANGCOSSINGSHIH LLVITTINGDAPASSVATHONDORPROTTORMONSTANAVRIDED SGOGSDABSSKAPAAKAGTANGGTRAGGTTINGVANGCOSSINGH ULKVITURDAVGSSRAP			1	
GPTPDSSEGNLSYLSSLSHLANNLSHLTTSSFRTSPENETELIK EHDLPFRAVBLOTTOGIORDEMOSLISTAS SPDERALVERABARIGIVEIGNSEETMEUNTLIKKLERYKLLIKE EFSDERRINSYLVORAPSGEKLIPAKABASSIJEKETKEI HUDEFALKACLETILCIAYEKFISKEYEEIDKEIFERATALOGU EKAAVEPIEKACLETILCIAYEKFISKEYEEIDKEIFERATALOGU CLARRATIEDHVIORIGUVDDTGISLALREHEKERTEALEMAGIIV WULTGDKHETAVSVSIS.GGIFHRITWILLELINGKSDSCA.DGI CLARRITEDHVIORIGUVDDTGISLALREHEKERWOCHRICSAV LCCRMAPLOKAVURLIKISPEKEPITLAVODANDVSNICGARIA GIGIMGEBERGAANNSDYA IAREKISKLIPVERISHAVERISHAV GIGIMGEBERGAANNSDYA IAREKISKLIPVERISHAVERISHAV UVYFFYKNUCFITPOPLVOPYCLESGOTLYDSVYLITAVNILSIKTPLYAFT ILGESHAFIFFEGSYLLIGKOTSLLGNOGMEGNMETEOTLYPTWM VITTVYVANLSTEHTWEN INILIAYESILISTEPLYFT ILGESHAFIFFEGSYLLIGKOTSLLGNOGMEGNMETEOTLYPTWM VITTVYVANLSTEHTWEN INILIAYESILISTEPLYFT ILGESHAFIFFEGSYLLIGKOTSLLGNOGMEGNMETEOTLYPTWM VITTVYVANLSTEHTWEN INILIAYESILISTEPLYFT ILGESHAFIFFERANGIKCILSKOFTENGSILITASTMOSTS. GROSPIHISRSMSASDPPTYNDRSILITASTMOSTS. GROSPIHISRSMSASDPPTYNDRSILITASTMOSTS. GROSPIHISRSMSASDPPTYNDRSILITASTMOSTS. ASRRSGETHWIGLEVENDISHLINGVOCHADEKELINGAVERIEF PESKIFFSAYKSHEVNISGESFRARKRERFRERKERPEPHAGPAR ASRRSGETHFOLDVANLISSLERKARKTVEKLISSIGLEVCKEHLE DFROFEDDFF LINTTWENDGLMDESLITENDDVRTKPPCCXSAC FESKIFFSAYKSHENTAVISEDPERITLLINDVYCHADEKLICHT IKTEHAPNASAPSSILSTFKDKINKNDGLEPRQADSTEGAVYVELG SNABEBSSIHCKRCLFPRKSYTENDAVRTUEDHERIGTGVOTVAMI HINVYPRSKELHLAPRODUKKMIJENDARPTIANGEKILGENVARSLO SNABEBSSIHCKRCLFPRKSYTENDAVRTSTEDHERIGTGVOTVAMI HINVYPRSKELHLAPRODUKKMIJENDARPTIANGEKILGSKONVARSLO GOSNERJGIGGRAPVETONOSULPSAGNSVARSLOSSKONSO APARYSLOSANASSISSCOLKSPSISGSCASRVLOGSSSKPASICSSKONS APARYSLOSANASSISSCOLKSPSISGSCASRVLOGSSSKAPAL ANANYIMKINNFTSKCLYCHRYLTOTLINBMI.HIGLSCOVEKS SQCAVERLISTIFKKKILTIKCHCGVYTSNTMTASTITHLUKGROVKKYR ANANYIMKINNFTSKCLYCHRYLTOTLINBMI.HIGLSCOVEKS SQCADAFKKONSTOLKKILCTICHTETPOTLYNDENSPINDENSPIND LLVTTNIRDAPASSVATHAVNINGSPSIAPKKKKCHTORGOSSKYROSY TREBERKLASSLINW,WK, SDIALSKFFINKKKCHTORGOSSKYROSY TUHVVEKKLITKCHCGVYTSNTMTASTITHLURGRVCKKYROV TUHVVEKKLITKCHCLORYTSNTMSYSTIKHORDEN SGOSEDARSKPAAKKATURQDBROJASPA*TOTSGTRAARGSTW LLVATVIDRAGSSKAP	6007	3	2351	HELGQVEYVFTDKTGTLTENEMOFRECSINGMKYOEINGRLVPR
BEDLEPKAVSLACHTOQINNVQTDCTGGGGPMQSNLARSQLEYLLHILE FISDRRRMSVIVQAPSGEKLLPAKGARSSILPKCIGGIEKTYLLHILE FISDRRRMSVIVQAPSGEKLLPAKGARSSILPKCIGGIEKTYLLHILE FISDRRRMSVIVQAPSGEKLLPAKGARSSILPKCIGGIEKTYLLHILE FISDRRRMSVIVQAPSGEKLLPAKGARSSILPKCIGGIEKTYLLHILE EKLAAVPGIEKDLILLGATAVEDBLQDKVRFTTEALHANGIKV WULTCOKHERTVSVISLGGIPHETWNITLEILNGGEKVY WULTCOKHERTVSVISLGGIPHETWNITLEILNGGEKVY WULTCOKHERTVSVISLGGIPHETWNITLEILNGGEKVY UCKARALIGKAKVILRIVISISPETTLANDGANDYORGANV GCARRITEDHVIQKGLVVDGTSLSLAREHEKLPMSVCRICGAV LCCRMAPLOKAKVILRIVISISPETTLANDGANDYORGANV GGIMGEGROAARNSDYALARFKFLSKLLFVHGHFYVIRLATL VQYFPYSHOVET TYPGELYQFYCLESQGTJUDSVYLILIK\RICHIT LOYSTPYSHOVET TYPGELYQFYCLESQGTJUDSVYLILIK\RICHIT LIGSBAFIFFGSVLLIGKOTSLIGNGGMRSHWTEGTLIFTYCT SLPILTYSLLEQUVDPHVIQNKYBSILPTVSHTURIKLSIKTELWT LIGSBAFIFFGSVLLIGKOTSLIGNGGMRSHWTEGTLIFTYCT SLPILTYSLLEQUVDPHVIQNKYBSILPTVSHTURIKLSIKTELWT LIGSBAFIFFGSVLLIGKOTSLIGNGGMRSHWTEGTLIFTYCT SLPILTYSLLEQUVDPHVIQNGSLIGKORGHRSHWTEGTLIFTYCT LIGSBAFFSAFIFFGLEVNINGICKTHORSILPTVSHTERVIT LIGSBAFFSAFIFFTHMSILTAMSILLFANGILLPTVSHTERVIT LIGSBAFFSAFIFFTHMSILLFANGILLPTVSSLIGKTHORSILTSTONSTON GROOTSTANGILLPTVSHTURMSILLFANGILLPTVSCAPEHAGPAR ASRSGETHFGLEVNINGISLRKAKTVKKILSDIGLEVCKEHE DEKOFPHNEYLINTTMSUMGHDSSILTRANGTVFFCCSACP FSSKFFSAKSHFRNVHSEDFSRRILLLNCPYCTFRADEKKILEST LIKTHAPNASAPSSLSSTFKENNINGILKPKOCATSPENAYCH KCTYRDPLYEILVRIHIVRHIPQHVAAPYTAKAGEKSLINGSVYCK KCTYRDPLYEILVRIHIVRHIPQHVAAPYTAKAGEKSLINGSVYCK KCTYRDPLYEILVRIHIVRHPQHKAMOVILLPGVATAMIG SNARESSSHICKELPPHS VS SARISSVALOKSVEGGVSV QSMRIGLIGGNAPVSIPQDSGSVKOLLPSGMRSVALOKSVEGGVSV QSMRIGLIGGNAPVSIPQDSGSVKOLLPSGMRSVALOKSVEGGVSV QSMRIGLIGGNAPVSIPQDSGSVKOLLPSGMRSVALOKSVEGGVSV QSMRIGLIGGNAPVSIPQDSGSVKOLLPSGMRSVALOKSVEGGVSV AAANYTMINITATSPEKLLYCHTILGGSSVKNAS AARGEPTSSLTSCHLANGTVANGSVEGGNASVALOKSVEGGVSV AAANYTMINITATSPEKLLYCHTILGGSGVKNASVALOKSVEGGVSVAAA AATGEPRANTSCHLANGVANGVEGGRAFATOTGGGSTRANGSVALOKSVEGGVS ANGENGESSILGAGGGVANGHAPSTANGTANGSVALOKSVEGGSPSC LLVILGUNITATSAARAGAVSSLAGAARSPAFTOTGGGSTVANGSVALOKSVEGGSPSC ACHTICATATATATATATATATATATATATATATATATATATA				GPTPDSSEGNLSYLSSLSHLNNLSHLTTSSSFRTSPENETELTK
SPDERALVERARATIGIVE IGNSEETMEUTTIGKLERYKLIGHERY FISDRERMSVIVORAPSGEKLIP AKRABSSIJEKGEISKETEI HUDEFALKGLETTLCIAYEKETSEKEYEE IDKRIFFERATALOGUE EKLAAVEPEI EKLAAVEPEI EKULTLCIAYEKETSEKEYEE IDKRIFFERATALOGUE GLARRITEEHVIGHLUVDOTSEIGLALREHERELTBLERMGITV WULTODKHETAVSVSIS.GGIFFRETWILLELINGKSDSCAFOLER GLARRITEEHVIGHLUVDOTSEISLALREHERELTBLERMGITVE WULTODKHETAVSVSIS.GGIFFRETWINLELINGKSDSCAFOLER GLARRITEEHVIGHLUVDOTSEISLALREHERELTBLERMGITVE WULTOVALTURGUNGUN VORTUSALAREHERELTBLERMGITVE UCTHALLOKAVURLIKISPERETTLAVODOANDVSNIOSAHV GIGIMGEBEGGAANSDYA IRREKLEKLIPVERVISLISTELLAVOT SIAPILIYSLIS.GUNDPEVLOLREN SILVENTURGISTELLAVOT HILGESHAFIFFEGSYLLIGKOTSLLGNGGMEGNETPOTLIVENT UTTYVANALETHENPUTINILIVENSI LIPETYPETYLELING VYTYVANALETHENPUTINILIVENSI LIPETYPETYLEN TIL HUTSTEKAGLUETHINGALKOLDBENCEPPEGEACASVORMIERVI GGCSPTHISERMBASDPFYTNORSILLISTNOSSTC GGSPTHISERMBASDPFYTNORSILLISTNOSSTC GGCSPTHISERMBASDPFYTNORSILLISTNOSSTC GGCSPTHISERMBASDPFYTNORSILLISTNOSSTC ASRRSGETBERUPVINGASILRERRERRERRERRERRERRERRERRERRERRERRERRER	1	1	[EHDLFFKAVSLCHTVQINNVOTDCTGDGPWOSNLAPSOLEYYAS
FSDRRRMSVIVQAPSCEKLLFAKGRASSILPKCTGCEIKTKI HNDEFALKGLIKLIAYRFISKEYEDIKK FEARTALQORVE EKIAAVPOPIEKOLILIGATAVEDRIQOKVEPTERLEMAGIKV WULTOCHETAVSVISLGCHHPITMMILELIKOSBECKAGUE, GLARRITEDHVIQHGUVUOGIGLALBEHEKLFMEVCRICSAV LCCRMAPLGKARVIRILKI SJERPKITLAVGONDVENICBANV GIGIMGKEGRQAARNSDVAIRARKFISKLLFVIGHEYYIRIATL VQYFYKNUCTITOPLAYOFULFSQOTLINDVENICBANV GIGIMGKEGRQAARNSDVAIRARKFISKLLFVIGHEYYIRIATL VQYFYKNUCTITOPLAYOFULFSQOTLINDVENICHILVING SUPLIVSILLBGHUDPHVLQNKPPLYRDISKNILLSIKTFIVM LIGSHAFITFFSYLLIGKDTSLINDCOMPROMPTGTUTTYM VITVTVKMALETHSWWINHLVIWGSILTYSVSLIPVYUHTYM LIGSHAFITFFSYLLIGKDTSLINDCOMPROMPTGTUTTYM VITVTVKMALETHSWWINHLVIWGSILTYSVSLIPVYSLLYCGILLBPF LASOMWFFPJQLISSGSAWFAILMVVTCLFIDIIKVPDHIL HPTSTERQLIFTNAGIKCLDSMCCPPSGBEACASVCRMLERVI GROSPTHISRNBASDPFYTMDRSILTISTMDSSTC GROSPTHISRNBASDPFYTMDRSILTISTMDSSTC FSAKFSAKSHFRNINGSGRAPPSFARRERGPAPEHAGPAR ASRSGSTMFGLEVNNLGSLKRARKTVKKLISDIGLSYCKEHLE DPKGPENDFYLKNITTWBUNGLUDPSLTKKNDDVFYKFPGCSACP FSSKFSAKSHFRNINGSGLKAPVEPSARRERGPAPEHAGPAR ASRSGSTMFGLEVNNLGSLKRARKTVKKLISDIGLSYCKEHLE DPKGPENDFYLKNITTWBUNGLUDPSLTKKNDDSVDYFKVFCCSACP FSSKFSAKSHFRNINGSGUNGUDPSLTKANGDVFYKFCCSACP FSSKFSAKSHFRNINGSGUNGUDPSLTKANGDVFYKFCCSACP FSSKFSAKSHFRNINGSGUNGUNGUTFKOFCCSACP FSSKFSAKSHFRNINGSGUNGUNGUTFKOFCCSACP FSSKFSAKSHFRNINGSGUNGUSPSLANGVARGLE GOSMRIGLIGGRAPVSI POQSGSVKQLLDSGINGSVGGSKPQALA ARBESSILKKRCLPMYRSFSALVOHVILBGTGVOYTAMIG HTNVUVPRSKELMILAPKPONKSSMLOPERGSVGGSSERDA ARAGPPONTSSTOKWICTICNLEPERVVSVHPEKEHKREVP ANAMYIMKLHRFTSKCLCKNTYLDTDTLLAMNGVSSVFDAAA ATGSPPONTSSTOKWICTICNLEPERVVSVHPEKEHKREVP ANAMYIMKLHRFTSKCLCKNTYLDTDTLLAMNGVSSVFDAAA ATGSPPONTSSTOKWICTICNLEPERVVSVHPEKEHKREVP ANAMYIMKLHRFTSKCLCKNTYLDTDTLLAMNGSSKPDAA ATGSPPONTSSTOKWICTICNLEPERVVSVHPEKEHKREVP ANAMYIMKLHRFTSKCLCKNTYLDTDTLLAMNGSSKPDAA ATGSPONTSSTOKWICTICNLEPERVVSVHPEKEHKREVP ANAMYIMKLHRFTSKCLCKNTYLDTDTLAMNGSSKPDAKKRODSSSP SPREARFERSTOKARSTTOSHERERGUNGSSKPTAKKRODSSKPTAKKRODSSKPTAKKRODSSKPTAKKRODSSKPTAKKRODSSKPTAKKRODSSKPTAKKRODSSKPTAKKRODSSKPTAKKRODSSKPTAKKRODSSKPTAKKRODSSKPTAKRODSSKPTAKKRODSSKPTAKKRODSSKPTAKRODSSKPTAKRODSSKPTAKRODSS				SPDEKALVEAAARIGIVFIGNSEETMEVKTLGKLERYKLLHILE
HUDEFALKGLETICLIAYREFTSKEYEELDIKRI FERRYTLAJORNE EKLAAVOPT IEKOLILIGATVADERLODKUSPTIERLEMAGIEV WULTOOKHETAVSVSLS-CCHFHETMULLELINGKSDEKAGLER QLARRITEDHUVOIGUVUDGISLALBEHEKLFMEVOERICSAV LCCRMAPLOKAKVIRLIKISPEKETLAVGORANUSMICBAHV GIGIMGERGROARNSDYALREFTSKLEFHGEFTYIRLATL VOYFFYRNVCFITPOPLYOFYCLFSQOTLYDSVYILTIY\NICPT SEPLILYSLLEGHVDPHVLQNKPTLYRDISKNELLSKEFTLWT ILGESHRAFIFFGSYLLIGKUTSLLANGGWINFUTFUTNIVNI USTYTVEMALETHEWINHLUTMGSIIFYEVESLYFYGGILMPF LLSCOMMFYPYJCLLSSGSAMPAILMEWYTCHIKVPDHALI HPTSTEKAQLITETNAGIKCLDSMCCFPBGRAACASVGRMLERVI GROSPHISTBERGALITETNAGIKCLDSMCCFPBGRAACASVGRMLERVI GROSPHISTBERGALITETNAGIKCLDSMCCFPBGRAACASVGRMLERVI GROSPHISTBERGALITETNAGIKCLDSMCCFPBGRAACASVGRMLERVI GROSPHISTBERGALITETNAGIKCLDSMCCFPBGRAACASVGRMLERVI GROSPHISTBERGALITETNAGIKCLDSMCCFPBGRAACASVGRMLERVI GROSPHISTBERGALITETNAGIKCLDSMCCFPBGRAACASVGRMLERVI GROSPHISTBERGALITETNAGIKCLDSMCCFPBGRAACASVGRMLERVI GROSPHISTBERGALITETNAGIKCLDSMCCFPBGRAACASVGRMLERVI GROSPHISTBERGALITETNAGIKCLDSMCCTCACPBGRAACASVGRMLERVI GROSPHISTBERGALITETNAGIKCLDSMCCTCACPBGRAACASVGRMLERVI GROSPHISTBERGALITETNAGIKCLDSMCCTCACPBGRAACASVGRMLERVI GROSPHISTBERGALITETNAGIKCLDSMCCTCACPBGRAACASVGRMLERVI GROSPHISTBERGALITETNAGIKCLDSMCCTCACPBGRAACASVGRA		1		
EKLANVEGIEKOLLIGATAVEDRICODKVERTERLEMAGIKV WULTGEMERTAVSUSLSCHERPERMILLELIGKSBECAROLE GLARRITEDHVIQHGUVUDGTSLSLALREHEKLPHEVERRICSAV LCCRMAPLOKAVIRILKIS PSERRITLANDGANDVSHIQSANV GIGIMGEGRQAARNSDYALAREKFLSKLLFVHGHFYYRIATAT UQYFPYRNVCITTPGLTQFYCLFSQGTLYDSVYLTLY,VHICTY SLPILIYSLLRGHVDHVIQHKFTLYRDISKRILLSIKTFLWT ILIGSRAFIFFFGSYLLIGKTSLLSKRIKTSLKSIKTPLWT UTVTVVROALETHRWTWINHLYTWGS ITFYSSFYCGILWPF LASOMWFFFJQLLSSGSAWFAILMVVTCLFADIIKVDBHL HTSTEKAQLTETNAGIKCHOSMCOPFDEGAGKORMERFOT GROSPHISROWASDPFYTMDRSILTISTMOSSTC 6008 4554 1089 AVERRAGAREGGRALFAGATAVPPSARRERGCAPEDHAGBAR ASRSOGTHFGLPVNNLGSLKARKVKILISDIGLSYCKEHIE DEKQFENDFYLKNTTWBUOLUMPSLITKNQDWSTYCKCHIE DEKQFENDFYLKNTTWBUOLUMPSLITKNQDWSTYCKCHIE DEKQFENDFYLKNTTWBUOLUMPSLITKNQDWSTYCKCHIE DEKQFENDFYLKNTTWBUOLUMPSLITKNQDWSTYCKCHIE GSSPHISROWASDPSKROLDERGRAFACH KITHAPNASAPSSISTFKOKNKNDGLKEKQADSVEGAVYCK KCTYRDLYEITVKHIYTRHEHQVAAPYIAKGSLINGAVPLG SNABBESSIHCKRCLBWKSYSEALUQHVIEDHERIGYOVANIG HTNVVPRSKEITVKHIYTRHEHQVAAPYIAKGSLINGAVPLG SNABBESSIHCKRCLBWKSYSEALUQHVIEDHERIGYOVANIG HTNVVPRSKEITVKHIYTRHEHPVARPYIKAPGSLAGNVKSLLF SQQWWRLSIEKHMLAPREQDYKSMGLPSKIGGEGGRS QAPANYSLOSANASSLSSGGLKSPSLOSOASRVLQDSSSKRAA ANGPPROMYSSTOKWKICTI CHIELPROVYSCIGEGGRS APANYSLOSANASSLSSGGLKSPSLOSOASRVLQDSSSKRAA ANGPPROMYSTOKWKICTI CHIELPROVYSCHEKKHEKERUOIO TVHEVEKKLITYKCHIYCHUTSHMTASTITLHCGUSKTYM LLVTTYNLRDAPASSVAYHAQNNPPVPPKPQFVQERADIFVKS SPQAAPYYKKUNGKTLCFLCFSILKGFISDAAHHLRERHOVIO TVHEVEKKLITYKCHICLGVYTNAMTASTITLHCKGUSKTYM GQDKTRAPSRINGSPSLAPVKRTYPGMSPFLKKKKLDDDSDS SFFEREPEEPVLALDPKGH, PEDDSYBARRSTKCKCURGCKYKPOVL LGFROMELINKVRIEMFPSKCLJEFNIDENGSKYTHATTYT KQDPYP TRREISKLAASJAWVWKJSDIASHFSNKRKKCVROCKKYKPOVL LGFROMELINKVRIEMFPSKCLJEFNIDENGSKYTHAMTSTYT KQDPYP TRREISKLAASJAWVWKJSDIASHFSNKRKKCVROCKKYKPOVL LGFROMELINKVRIEMFPSKCLJEFNIDENGSKYTHAMTSTYT KQDPYP TRREISKLAASJAWVWKJSDIASHFSNKRKKCVROCKKYKPOVL LGFROMELINKVRIEMFPSKCLJEFNIDENGSKYTHAMTSTYT KQDPYP TRREISKLAASJAWVWKJSDIASHFSNKRKKCVROCKKYKROVL GRAVAGGAGCTESTVARGGRGCTHANDGAGNVWGLING NGKRGCEESSTLOPGVYTOKGRGKMCKWKHONSYKGHVSNDSVTGG RAVAGGAGGESTVTTAGGGCLGKAKRAVFTNO		·		
WULTOCHETAVSYSIS_GCHFHETMAILELINGKEDSER_AGE_AGE_AR GLARRITEDHIOGRUVUPGISLALMEREHEM_PEVCRNCSAV LCCRMAPLOKAKVIRLIKISPENETILAVGGANDVSHIDEAHV GIGINGKEGRGAANSDANIAR PREFISKLIK-PEVCRNCSAV LCCRMAPLOKAKVIRLIKISPENETILAVGGANDVSHIDEAHV GIGINGKEGRGAANSDANIAR PREFISKLIK-PEVGGHYYNIRLATL VOYFPYKNVCFITPOELYOPYCLESGOTLYDSVYLTLAV\MICTET SLP LLYSILBOHDDPHYLONKPTLYRDISKNRLLSIKTPLYWIT ILGPSHAPIFFFGSYLLIGKDTSLANGGMENWITETILYFTW VITTYTWAMALETHBWYMINHLUTWGSIIFYSVESEPSOLIHEPY LCSONNYFPYLOLLSSGSAWAR ILMWVTCHSIIKKYDEHHI HPTSTEKRQLITETMAGIKCLDSMCCPFBGERACASVCRMLERVI GROSPHISERSHASDPYTHDRSILTLSTMUSSTC AGVERÄGARROFGRALPAGATAVPFPSARRRECPAPEHAGPAR ASPRSOKTHFQLEVNNLGSILKARKTVKKLISIGLISYCKEHLE DPKOFEPNDFYLINITYMEDVOLDDPJLKKNODYFKKPCCSACP FSSKPFSAVKSHFRNWHSEDPENRILLLCYPTADKYKLTEHT IKI HHAPNASAPSSISSTYKDKNKNNDGKPKQADBVSCAVYVCK KCTYMDPLUETURHTYMEDVOLDDPJLKKNODYFKKPCCSACP FSSKPFSAVKSHFRNWHSEDPENRILLLCYPTADKYCTLEHT IKI HHAPNASAPSSISSTYKDKNKNNDGKPKQADBVSCAVYVCK KCTYMDPLUETURHTYMEDVOLAPPILAGNKYGKTSUGGSSKYADA SAMBESSIHCKRCLPWPKSYBALVOHVIEDHERIGYOVTAMIG HNNVVPRSKLIVENFUNKTYDVAPPILAGNKYGKSVGGFSV GOMNINGLIGGRAPVSI PCOGGSVKYGLIPSKNRSVGLGSSKYADA ATGPPORNTSSTOKMKICTI CINSLEPENVYSWEFSENGAVELOG APARYSLOSANASSISSGUKKSPISSGOSARVLOGSSKYADA ATGPPORTSSTOKKKICTI CINSLEPENVYSWEFSENKAREVP AVNAYIMKIHMPTSKCLIVCHYLYPDTILLAHNIGLSCPYCRS TPNIVEKMAAHMRNVHIDEBMGFKTDSTLEFDLTIQGSHTNIH LLUTTYNIRDAPESVAHADABSVAHADNIPPVPPKPCOKENCOGRADIPVKS SROAAVYYKKOVOKTICTICLCSILKSDISDLAHHLERRIVOTO TVHPVEKKLITYKCHICLGVYTSMTASTITIHGISCCPYCRS SROAAVYYKKUHEMDPDAGCLEPHDENGSCOKEADIPVKS SROAAVYYKKUHEMDPDAGCLEPHDENGSCOKEADIPVKS SROAAVYYKKUHEMDPDAGCLEPHDENGSCOKEADIPVKS SROAAVYYKKUHEMDPDAGCLEPHDENGSCOKEANSTONGCOK GOKTAMASBIRDAVKHEMDPAGCLEPHDENGSCOKEANSTONGCOK GOKTAMASBIRDAVKHEMDPAGCLEPHDENGSCOKEYSTONGC GOKTAMASBIRDAVKHEMDPAGCLEPHDENGSCOKEYSTONGC GOKTAMASBIRDAVKHEMDPAGGGENOKTONGCOKEYSONGONG GOKTAMASBIRDAVKHEMDPAGGGENOKTHONGCOKEYSONGONG GOKTAMASBORDELSHOTOLENGGSTONGSTICHOLPFRAMASONY AVITEDAR HOSLAGVKLEDDAGGGGCOKENGSTONGSTONGONY HULKVULVEVALUTHURGSCHOKANGSTONGST	1			
LCCRMAPLOKAKVIRLIKISPERPITLAVODGANDSMICZHAW GIGIMIGKERQAARNSDYATARPKELSLIKIPWIGHTYIRIATL VQYFYKNUCFITPOFLYQPYCLESGOTLDSVYLLIX/NICCT SLPILIYSLLGONDFUPLAVONKPITLYNDISKRILLSIKTFLYMT ILGFSHAFIFFFGSYLLIGKDTSLLGRGMFONMTFGTLVFTVM VITTYTVRABLETHEWTWINHLVTMGSIIFFFFFSFGGILMPF LOSONMYPYTQLLISSGSAMFAILMAVTCLFLDIIKKVPDEHL HPTSTEKAGLTETHAGIKCLDSMCCFFEGBACASVORMLERVI GRCSPTHISRSWASDPFTNDRSILTLISHMDSSTC 6008 4554 1089 AGVRRAGARRGGGRALFAGATAVPFSARRERCPAPEHAGPAR ASRPSOSTHOPLOPNNINGSLIKRARTVALLDGLEYCKEHIE DFKOFEPNDFYLKHTYMEDUGLMDBSITKNODYRKPFCCSACP FSSKFFSAYKSHFRNVHSZDFBAILLDCYCTFRADKTLETH IKIFHAPNASAPSSSLSTFKDRINNDGLKKRAGNSVEGAVYYCK KCTYRDPLVEIVRHIVRHFCHWARYIAKGESELGAVPLG SNARESSIHCKCLPMPKSYPALVQUYLEDHERIGYQVYTAMIG HINVUVPRSKPLMLIAPKPODKKSMGLPPRIGSLASGNVN GSLP SQWWINLSIPKPPLMATGVANMSSVELANYGVSKGVSVS QSNRIGLGGNAPSISGOLKSPSLSGSDVLGOSSSKPADA ATGPPPGNTSSTGKWKICTICNELFPENVYSVHPEKEHKAEKVP AVANYIMKIHNFTSKCLYCNRYLEPDTLLINHMLHGISCPYCRS TFNUZEKMAAMERNIVHIDEMGPKIDSTSFPDLTLQGGGNTNIH LLVTTYNLEDAPASSVAYHAQNINPPVPPKGVQEKADIPVKS SPQAAVPYKLOCHSILKGFGLSGVSCO GGGKTNAPSRINGSPSLGCFSIKGSPGLAPHLKKRKLDDDSDS SPFEKKPEBPVVLAUDPKGH\PEDDSYBAKKSCLYCHDEKYKPGVL GGGKTNAPSRINGSPSLGCFSIKGSPFLKKYRCDDENS SPFEKKPEBPVVLAUDPKGH\PEDDSYBAKKSCLYKPGVL LGFNMKELNKVKHEMDFDAEGLFFINHERCORVRDSKYKPGVL LGFNMKELNKVKHEMDFDAEGLFFINHERCORVRDSKYKPGVL LGFNMKELNKVKHEMDFDAEGLFFINHERCORVRDSKYKPGVL LGFNMKELNKVKHEMDFDAEGLFFINHERCORVRDSKYKPGVL LGFNMKELNKVKHEMDFDAEGLFFINHERCORVRDSKYKPGVL LGFNMKELNKVKHEMDFDAEGLFFINHERCORVRDSKYKPGVL LGFNMKELNKVKHEMDFDAEGLFFINHERCORVRDSKYKPGVFINKD SSQSEDARSSRPAAKKARMGORDEGLKARNSKYGKVEGFFINKD SSQSEDARSSRPARKARMGORDEGLKARNSKYGKVEGFFINKD SSQSEDARSSRPAAKKARMGORDEGLKARNSKYGKVEGFFINKD GOGNKASSENDERLSHOPLUKKRINGGCEGG-VEDSVTGG RAVAGGAGSGSSTOPTPVGGGCEGLAGSVARSVFTONGGVEGGFFINGD NCHIHVDAVC*SSHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLKOKEVOASVCRGFFSVOATAPAOFMAHSSTGKVEGFFINKS NCHIHVDAVC*SSHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLKOKEVOASVCRGFFSVOATAPAOFMAHSSTGKVEGFFINKS AVTRGSAVQREGFFSVOATAPAOFMAHSTIHOLGFPENWA AVTRGSAVQREPGSTTTGGTFTANGGAGGPTHUFULFHEN AVTRGSAVGREFINSHTTINGTTLIQLIFFUNHAGLHEL	1			WVLTGDKHETAVSVSLSCGHFHRTMNILELINQKSDSECAEQLR
GIGIMGKEGRQARNSDYATARPKFLSKLLFYHGFYTYRLATL VQYFYYKNUCFTTPOFLYDYCLFSQQTUDSVYLTLY/NICFT SLPILIYSLLECHUDPHYLQNKPTLYRDISKRRLLSIKTFLYTT ILGFSHAFIFFGSYLLIGKDTSLLGWGCMFGTUFFTVFTU VTTYTVEMALETHEWTW INHLYTWSS IFFFFFSFYGGILWPF LOSQMWFFVFIQLLSSGSAWFAILMVYTCLFLDI IKKYPDHLI HTSTETRAGULTETNAGIKKLDSMCCPFEGARCASVGRMLERY GRGSPTHISRSWSASDPFYTNDRSILTLSTMDSSTC GRSSPTHISRSWSASDPFYTNDRSILTLSTMDSSTC ASPRSQETMFQLPVNNLGSLRKARKTVKKILSDIGLEYCKEHIE DFKQFEENDFYLKKTYTHEUVGLUNDSLTKNQDYSTKFPCGSACP FSSKFFSAKYSKKSHFRNVISSBPENRILLNCYYCTPNADKKTLETH IKIFHAPNASAPSSSLSTFKDRNKNDGLKPKQADSVEQNYYCK KCTYRDLVELVRHIVTRHFQFWAAPYLGKSGKSLINGVPLG SNARESSIHCKRCLFPPKSYBALVORVIEDHERIGVOVTANIG HTNVVVPRSKPLMLIAFRCDKKSMGLPSGLSAGNVLGSSKKAAA ATGSPPGNTSSTQKKKICTICNELFPENVYSWHFEKHAEKVP AVANYIMKHNFTSKCLYCHKYLTPTLAHFGHAAPYLHGLGCYCRS TFNOVERMAAHMRWHIDEMGPKTDSTLSFDLTLQGGSKKAAA ATGSPPGNTSSTQKKKICTICNELFPENVYSWHFEKHKAEKVP AVANYIMKHNFTSKCLYCHKYLTPTLAHFGHAAPYLGGSHTNHK LLUTTYNLBDABSSVAHAQNNPPVP BEVQKGGSKVGKOGSHAAA ATGSPPGNTSSTQKKKICTICNELFPENVYSWHFEKHKAEKVP AVANYIMKHNFTSKCLYCHKYLTPTLAHFGHACHYO TVHPVEKKLTYKCHHCLGYYTSIMTASTITHLHURGGGKTQM GQDKTMAFSRLNOSPSLAFVKRTTEGMEPFLLKKRKLDDDSDSP SFFEKPEEPPVLALDPKGH\EDDSYBARKSSLTKYFT\KQPYP TRRSIEKLAASLWV\MK\DIASHFANTASTITHLHURGGGKTQM LGFMMKELMKVKHEMDPDAEGLFENHDEKDSKVARSKTADKKLM LGKEDDSSBOFFNLEESBNSGSPPDVEERSHTJONFDAE ULKVIPPDASSSEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDUVVEKUGGASPSEGGGVOSPFENTGEMKFOTNSDB SSGSEDARSSKPAAKKAATMGGORGCLKKWSSGKVEGFHSKM QSOKKNASENDERLSNPQIEMGORGCLGKWNSSGKVEGFHSKM QSOKKNASENDERLSNPQIEMGORGCLGKWNSSGKVEFFHSKM QSOKKNASENDERLSNPQIEMGORGCLGKWNSSGKVEFFHSKM QSOKKNASENDERLSNPQIEMGNTIDSBDGGGPTMNTTGVAEF MGSLLGGVKLSSQQA CHIJOHAVARQSSKSABPQASAFFTTGTGGFTFKAARGGSW EAYTLGHUMMMFPIQRPPLJMKGRRIMGGKCEG-VSDSVTGG RAVAGGASGARTVFTRAGGGCCLGKSVARSVTTROGCOWGLL NGKRGCCESGVIFFGTVIGTIGSCTFKARAGGSW EAYTLGHUMMFPIQRPPLJMKGRIMGGKCEG-VSDSVTGG RAVAGGAGSGRTVFTRAGGGCCLGKSVARSVTTROGCOWGL VKKEVGASPARASKLATURG SIGNSGFTLOPLGCRPTTSVSL FULAPDAGGGGGFTANTAGGCCFTKVARSFCKORTHSVB OKCHHIVVAROSSISAAPARAFENSTIIS VARPGWOHM VLUKKEVGASPARAGGKCCHAKSVBARSVFTROGCOWGL LNGKRGCCESGV		i		QLARRITEDHVIQHGLVVDGTSLSLALREHEKLFMEVCRNCSAV
VQYFYKNVCFITPOFLYGYCLESQOTLXDSVYLIX\NICET SLPILIYSLEGHUDPEHYLONKPTYLYBIDISKRELISTKTELWT ILGFSHAFIFFGSYLLIGKDGSLLGNOGMFORMFTGTLUFTVM VITYTVMALETHFWINHLUTWGSIIFYYSSLFYGGILWF LOSOMMFPVFJCLSSSAWFAILMVYTCLEIDIIKKVFDEHL HPTSTEKAGLTETNAGIKCLDSMCCFFEGEAACASVORMLERVI GROSPTHISRSMASDFFTYNDRSILTLISTMDSSTC 6003 4554 1089 AGVRRAGARRGFGRALFAGATAVPFSARRRRCFAFEHIGFBAR ASRYSGETMFGLPVNNLSGILRKARKTVKLEIGIESYCKEHIE DFKOFENNDFYLKNITTMEDUGLMDDSLTKNQDVFTKSPCCSACP FSSKFFSAVKSHRFNVLSBDFENRILLNCPYCTFNADKKTLETH IKIFHAPNASAPSSLSTFKOKNNNDGLKPKGADSVEQAVYTCK KCTYRDPLYEIVRGHIYRBHFQHVAAPYIAKGGKSKLGAVPLG SNARESSICKCLFMFKSYBALVQUYLGKERGAVPVGGYSV GGSRRLGLGGNAPVSIFOGOSGVKOLLPSGNASGNV\RSLP SQQWNRLSIFFKPHLANTSKYBALVQUYLGYSKRYAQA ATGPPONTSSTQIKKTCTICMELPPENVYSVHPEKEHKAEKVP APAYSLGSANASSLSSGULKSPELSGOSILGSGORSQ APAYSLGSANASSLSSGULKSPELSGOSILGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSQ APAYSLGSANASSLSSGULKSPELSGORILGGSGORSY AVANYIMKIHNFTSKCLYCNTYLDTDTLLINMLITIGCPYCRS TYNUZKRMAHMRHVITTELEPPHYNTSFDLTILQGSHTNIH LLVTTYNLEADAPASSVAYHAQNINPPVPPKPGVKQEKADEKVRS SPQAAVPYKKVOGKTLCCJCFSILKGIPSPULTGGGGRTAD TVHPVERKLITYKLETTLAMMASD SPROAPVYKKVOGKTLCCJCFSILKGIPSPULTGGGGKTAD GGDKTNAPSRNAOSPELAPKRTYCMPTYLCPYPY TRREIBKLAASIAV\MX\DIASHFANATTILLHUHCCGGGKTON GGDKTNAPSRNAOSPERLOSSSTETHILBETHLMMINSDS SPFEKPEEPPVLAALDPKH\PVWFUCHGFBRASP VLKVIPPONASSSRAARKATAMGORBEQLKWRSSTGKVEFFYSKN QSGNKAASSNDERLSHPQGGECLGAKSVRASYFTGNGPOWGLI NGKRGCCESSSYLFGINTYGGGGECLGAKSVRASYFTGNGPOWGLI NGKRGCCESSSYLFGINTYGGIOGERPTTVSC RAVAGSQARTVTTAGGGGCLGAKSVRASYFTGNGPOWGLI NGKRGCCESSSYLFGINTYGGIOGERPTS		ļ		LCCRMAPLQKAKVIRLIKISPEKPITLAVGDGANDVSMIQEAHV
SSPILITSLEGENUPHYLORDISKNRLLSIKTFLYWT ILGSHSHAFIPFFGSTLLIGKNTSLLGGKNENDRFORTUFTUM VITYTVKMALETHFWTW.INHLUTWGS.IIPYFVFSLPYGGILWPP LGSQNMYFVPIQLLSSGSAWFAIILMVVTCHEDIIKKVFDRHL HPTSTERQCUTETNNGIKCLDSMCCPPEGEAACASVGRNEERVI GRCSPTHISRSWSABDPFYTNDRSILTLSTBDSSTC AVVRRAGARRGPGRALPAGATAVPPSGEAACASVGRNEERVI GRCSPTHISRSWSABDPFYTNDRSILTLSTBDSSTC ASPRSGETMFGUPVNNLGSLKKARKTVKKILSDIGLEYCKERIE DPKOPERDPYLKNTTWEDVOLDDBJKTMQDVETKPFCCSACP FSSKFFSAYKSHFRNVHSEDFENRILLNCPYCTFNADKKTLETH IKIFHAPNASAPSSSLSTFKONKNDGLKPKQADSVEQAVYYCK KCTYRDPLYKSIVKHU YREHRGVIVADKOPKETKAPVYCK SNARESSSHCKRCLFWPKSYSALVQHVIEDHERIGYQVTANIG HTNVVVPRSKPLMLLTAPPQDKKKMGPFIGGLASGNVLG SNARESSSHCKRCLFWPKSYSALVQHVIEDHERIGYQVTANIG HTNVVVPRSKPLMLLAPPQDKKSMGPFIGGLASGNVRSLP SQQWNRLSIPKPNLNSTGVUMMSSVHLQQNNYGVSVCQGYSV QGSMRLGLGGNAPVSIPQOGSOVKQLIBMGNRSTGLGSEQRSQ APARYSLQSANASSLSSQLKSPSLSQSQASRVLGQSSKPAAA ATGPPFONTSSTÇKKKLCTICDSLFPENVYSVHFEREHKAEKVP AVANYIMKHNTTSKCVCYNCYLPTILMMLHGLGSCPYCR TFNOVERMAHMRWHIDEEMGFKTDSTISFDLTLQQGSHTNIH LLVTTYMLRDAPABSSVATHAQNNPPVROPKOVGKADLPVKS SPQAVPYKCDUGKTLCPLCFSILKGPISDALAHHLRREHQVIQ TVHPVEKKLTYKCHICGVYTSNMTASTITHLWHCRGVKTQN GQDKTNAPSRLNQSPSLAPVKRTYRGMFPFLLKKKLDDDSDS SFFEEKPEBPVULALDRIGH\EDDSYBARKSFLTKYFT\KQPYP TRRSIEKLASLKVVK\SSLASHFSVEKCVPDCEKYKRGVUL LGFMMKELMKVKHENDPDASGLFENNDEKDSRVNASKTADKLIN LGKEDDSSDSFENLESENSGSSPFVEVEKKSVDNPEER VLKVIPPDASSSBFEKLDQKSDGSKVETIHLTSBPTKLHMNASDS EVDQDDVVEKKDGASPSESSGPSGQVOSPFEVERFISHDNPEER VLKVIPPDASSSBFKLNGVSTIDSEDGGFINMTDGVAEP MHGSLAGVKLSSQQA EXTLGQHWMFPIQRPLVMKGRRIMCGKCEKG*VSDSVTGG RAYAGSQASQRTVFTAGGGECLGAKSVRASVTGNFGKNSK QSGKNASSNDBRLSNPQIERKGNSTIDSEDGGFINMTDGVAEP MGSLAGVALSSQQA EAYTLGHQHWMFPIQRPLVMKGRRIMCGKCEKG*VSDSVTGG RAYAGSQASQRTVFTAGGGECLGAKSVRASVTINSPGVWGL GRAYGSGAVGRGFSSTLFGTTVYSL FVLAPODGGVPFVGGGLVTVLGLUVPDSTRIFTVHTQLFLEH I*KLGALDVAYARGGRGFGGFTTHTVSL FVLAPODGGVPFVGGGLVTVLGLUVPDSTRIFTVHTQLFLEH I*KLGALDVAYARGGRGFGGTTHTOSLHT VLKGRGCCGGRSVAGGGRVAGGGVGGGGTUSHDSCHOR AVTRGSAVQRRPSTTISSHTVPTXQGELIDWWAGADGVVQNG DFFVVGLAGIFHLIDDPLRQIELISFQRRV*GGCGVCKPDSOPVP	1			
III.GFSHAFIFFFGSYLLIGKNITHGATISTTUFTUW VITTYVKMALETHEFMYMINHUTUGS II.FYFFGEFGGILHPP LGSQNMYFVFIQLLSSGSAWFAIILMVVTCLFLDIIKKVFDRHL HPTSTERQQLTETNAGIKCLDSMCCFPEGBAACASVGRMLERVI GROSPTHISSMSABDFYVTNDSSILTLISTMDSSTC AGVARAGARRGPGRALPAGATAVPPFSARRRRECPAEBIAGPAR ASRSGSTMFOLPVNINGSILKARRYKLISDIGEJEVCKERIE DFKQFEPNDFYLLNTTWEDVGLMDPSLTKNQDYRTKPFCCSACD FSSKFFSAYKSHFRNVHSEDFBRRILLNCPYCTFADKKTLETHI IKIFHAPNASAPSSSLSTFKDKNKNDGLKPRQADSVEQAVYCK KCTYRDPLYEIVKHI VRRHIGHVAAPYIAKAGRSLNAAVFLG SNARBESSIHCKRCLPPHKSYEALVOREHBERGYOVTAMIG HTNVVVPRSKPLMLIAPRPQDKKSMGLPPRIGSLAGENV\RSLD SQQMVNRLSIPKPNLNSTGVMMSSVHLQQNNYGVKSVOQGYSV GQSRRLOLGGNAPVSIPQGOSVKQLLPSGNSRSYGLSGCRSQ APARYSLQSANASSLSSQQLSPSLSQSQASRULGGSSSKPAAA ATGPPPONTSSTQKKKLTITINELPHCHQGVSKYDVQYSV GQSRRLOLGGNAPVSIPQGOSVKQLLPSGNSRSYGLGSEGRSQ APARYSLQSANASSLSSQQLXFSILGQSSSKPAAA ATGPPPONTSSTQKKKLTITINELPHCHQGSSKPAAA ATGPPONTSSTQKKKLTITINELPHCHQGSSKPAAA ATGPPONTSSTQKKKLTITINELPHCHQGSSKPAAA ATGPPONTSSTQKKKLTITINELPHCHQGSGSVKPAAA FRINDEKKLTYKCHLCEVTSSMTASTDFLLLQGSHTNIH LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQFKVQSKADIPVKS SPQAAVPYKCOUGKTLCPLCFSILKGPISDFLKKKRLDDDSDSS FFFEKEREBEPVVLALDFURGH \LDBURGKTSTDFLLLQGSGTNA GQDKTNAPSRLNQGSSLAPVKRTYEGMEPPLLKKRKLDDDSDSS SFFEKEREBEPVVLALDFURGH \LDBURGKTSTDFLLLAGGSTQKT GQDKTNAPSRLNVGSSLAPVKRTYEGMEPPLLKKRKLDDDSDSS FFFEKEREBEPVVLALDFURGH \LDBURGKTSTTTHLWHCRGGVGKTN GQDKTNAPSRLNVGSSLAPVKRTYEGMEPPLLKKRKLDDDSDSS SFFEKEREBEPVVLALDFURGH \LDBURGKTSTTTHLWHCRGGVGKTN LGKENGSCVBLSVQG SSQBABSSKPABAKKKATMQGDRGLKWKNSSYGKVGFFHSKD OQSWKNASENDERLSNDGILBGNSTTIDSBGBGFDTNTCMKFOTTSDB SSQSEDARSSKPAAKKKATMQGDRGLKWKNSSYGKVGFFHSKD OQSWKNASENDERLSNDGILBGNSTTTDSBGTPKAABCGGWW EAVTLGHQHWMMPFIQRPPLJWKGRRIMCGKCKKGVSDSVTGG RAVAGPQASVRCRFFSTAGGGECLGAKSVASAFYFTGNOGTTHALDFLHH VLKGALDAFHLLTLYTCSSFNVAYGFGGFTHSDB SGAVAGPQASVRCRFFSSVTDAAGFMARSPPGLGGEPTTTTSVSL FVLAPODGGVPFVGGGLVTVLGLVVPOSTRHFVHTQLFLHH I*KLGALDVAFHLLTLYCSSFNVAYG*GKNGGTTHALDFLHH I*KLGALDVAFHLLTLYCCSSFNVAYG*GKNGGTTHALDFLHH I*KLGALDVAFHLTLYTLYCSSFNVAYG*GKNGGTTHALDFLHH I*KLGALDVAFHLTLYTLYCSSFNVAYG*GKNGGTTHALDFLHH I*KLGALDVAFHLTLYTCSSFNVAYG*G	1			VQYFFYKNVCFITPQFLYQFYCLFSQQTLYDSVYLTLY\NICFT
VITTYTVKNALETHFNTWINHLUTVGSIITFYFYFLFYGGILMPF LSQNMYPVFUIGLISSGAWPAILLMYCTLPLIIKKVPDEHL HPTSTEKRQLTETNIGIKCLDSMCCFPEGEAACASVGRMLERVI GRCSPTHISRSWASADFFYTVIDRSILTISTMDSSTC AOVERAGARRGEGRALFAGATAVPFTYDRSILTISTMDSSTC ASPRSQETMFQLPVNNLGSLKARKTVKKILSDIGLEYCKEHIE DFKQFEFNDFYLKNTTMEDVGLUDDSJGLEYCKEHIE DFKQFEFNDFYLKNTTMEDVGLUDDSJGLEYCKEHIE DFKQFEFNDFYLKNTTMEDVGLUDDSJGLEYCKEHIE DFKQFEFNDFYLKNTTMEDVGLUDDSJGLEYCKEHIE FSSKFFSAYKSHFRWYHSEDFERNILLNCPYCTFYNADKKTLETH IKIFHADNASAPSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK KCTYRDPLYEIVRKHITREHFQIVAAPYTAKAGEKSLNGAVPLG SNARESSIHCKRCLFWPKSYSALVQHYLEDHERIGYQVTANIG HTNVVVPRSKPLMLLAPPQDKKSMGHPGIGSLAGSNV/SELP SQQWNRLSIPKPNLNSTGVNMMSSVHLQQNNYKSVGQGYSV GQSNRLGLGGNAPVSIPQOSGVKQHQDSNYKSVGQGYSV APARYSLQSANASSLSGQLKSPSLSQSQASRULQGSSKPAAA ATGPPPGNTSSTQKWKICTTICNELFPENVYSVHPEKEHKABKVP AVANYIMKHHNFTSKCLYCRNYLPTUTLLNHMLHGLSCPYCRS TFNIVERMAAHMRWHIDEEMGFKTDSTLSFDLTLQQSHTNIH LLUXTYNHLRDAPASSVAYHAQNNPPVFKPQPKVGKKAPLPVK SPQAAVPYKKDUGKTLCPLCFSILKGPISDALAHHLRREHQVIQ GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKKKLDDDSDSP SFFEKPEEPVULALDPKGN\EDDSYBARKSFITYKFT\KQFYF TRRSIEKLLASSLWV\W\SSILASHFRKKCVRDCEKKKPGVL LGFMMKELNKVKHENDPDASGLFENHDEKDSTVANSKTADKKLM LGKEDDSSSDSFENLEESENGSGSPPDPVFEWBFKISNNPEBH VLKVIPEDASSSEEKLDQKSDGSKYETHHTEEPTRLHHNASDS EVDQDDVVENKOGAJPSESGGGGGGQVFDEPNTMTDGVABE SQSSDARSSKPAAKKATMQGDRGLKWKNSYGKVEFFNSKD QSGWRASENDBRLSNPQIEWGNSTIDSBDGEGPINMTDGVABE SQSSDARSSKPAAKKATMQGDRGLKWKNSYGKVEFFNSKD QSGWRASENDBRLSNPQIEWGNSTIDSBDGEGPINMTDGVABE AVANGEQASQRTVFTAGGGGCLGLGKSVRASVTSOFTRANSCOM CHILVLGVLVAVAQASSKAAGAQASAF*TGTGSTFKAARGGGWW EAVTLCHQHIMMPFIQRPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRTVFTTAGGGCCLGLGKSVRASVTSOFTRYSSI WCSLLAVLVAVAQSSSRAAGAQASAF*TGTGSTFKAARGGGWW AVTRGSAVQRSVRGGFSSVTPAQFRANFGLGGEFTTTVSLSI FVLAPODGGGVPFVGGGLVTVLGLVVPDSTRHFYVHTQLFLEWIN AVTRGSAVQRRSTITISSIHVDTKIQGELIDWWAGADGVQWG DFFVVGLAGIFHLIDDPLRQIELISFQRRV*EQCOVKPDSQPVP REPURGLEGGGFTATGCSKRUKEDCLOVKDSSPRIF	1			
LESOMMFEVFIGLLSGSAMFAIILMUVTCLPLDIIKKVFDRHL HTSTEKROLTETINGIKCLDSMCCFPGEBARACASVGRMLERVI GRCSPTHISRSWSASDPFYTNDRSILTLSTMDSSTC GRCSPTHISRSWSASDPFYTNDRSILTLSTMDSSTC AGVRRAGARRGFGRALFAGATAVPPFSARRRRCPAPEHAGPAR ASPRSOSTMFGLPVNILGSLRRARTVKKILSDIGLEVCKEHIE DFKGFENDFYLKNTTWEDVGLWDPSLTKNODVRTKPFCCSACP FSSKFFSAYKSHFRWHSEDPERILLKDCPYCTPNADKKTLETH IKIFHAPNASAPSSSLSTFKDKNKNDGLKRKQADSVEQNVYCK KCTYRDPLYBTVKKHIYRRHFYCHWAAPYIKAGEKSLMGAVPLG SNARESSIHCKRCLPMFKSYEALVQNVIEDHERIGYQVTAMIG HTNVVVPRSKPLMLIAPKPOPKKSMGLPFRIGSLASGNV\RSLP GQWMRISIPRENLSTGVNMWSVLQQNNYGVKSVQGYSVY GQSMRLGLGGNAPVSIPQQSQSVKQLLPSGNGRSYGLGSSGRSQ APARYSLQSANASSLSSGGLKSPSLSQGASRVLQQSSSKPAAA ATGFPFDONTSSTGKWKICTICNELFPENVYSVHFRKEHKABKVP AVANYIMKIHNFTSKCLYCNRYLPFDTLLAHMLIHGLSCPYCRS TFNOVEMAAHMRIWHIDEMGPKDSTLSFDLTQQGSHTNIH LLVTTYALRDAPASSVAYHAQNNPPVPPKVQKKADIPVKS SPQAVPYKKDVGKTLCPLCFSILKGPISDALAHHLIRRRHQVIQ GQDKTNAPSRLNQSPSLAPVKTTYEQMEPFLLKKRKLDDDSDS SFFEKREPEPVVLALDPKGH\EDDFASTARRSFLTKTYF\KQPYP TRREIEKLAASLWVWK\SQIASHFSNKRKKCVDCCEKYKBGUL LGFMMKELNKVHEMDFDAEGLFENHDEKDGSVNASKTADKKLN LGKEDDSSDSFENLEESSNESSFPPPVFEVEPKISNDNEEK VLKVIFEDASSESEKLDQKEDGSXYETIHLTEPTKLMHNASDS EVDQDDVVEWKDGASPSSGFGSQVSDFFENTGEMRFGTMSDS SSQSEDARSSKPAAKKATMGGDREQLKWMNSSYGKVSGFFKSK QQSWKNASENDERLSBNSGSFPPPVFEVEPKISNDNEEK VLKVIFEDASSESEKLDQKEDGSXYETIHLTEPTKLMHNASDS SSQSEDARSSKPAAKKATMGGDREQLKWMNSSYGKVSGFFKSK QQSWKNASENDERLSBNPQIEWQNSTFENTGEMFGTMSDS SSQSEDARSSKPAAKKATMGGDREQLKWMNSSYGKVSGFFKSK QQSWKNASENDERLSBNPQIEWQNSTFTRABEGSGTW EAVTLGHGHWNMFPIQRPPLWAGRRIMCGKCKG*VSDSVTGG RAVAGSSQSTUTVIVAGVGRGRTMCGKCKG*VSDSVTGG RAVAGSSQSGTPTGFSSVDTAPAGGGCCUKMSSYGRAPGTGGTTTSVSL FVLAPQOGGGVFVFGGGVVFUAGSPWAGSFTTTSVAPGSWQDHA VLKKEVQASVRCRGFESSVDTAPAGTSSPCTHTONGFOWGILL NGKRGCFESSYLFGFIVIGKIQSLEAKVPLPVNQGTGERASPG NCEHTVDAVC*SEHH*DHTLAAAPLENSTITS*VAPGSWQDHA VLKKEVQASVRCRGFESSVDTAPAGGGGCVAGKNGGTTHTFOHHTOLFLIEP I*KLGALDVAFHLITLTVCSSFFNVAGSPGGGGTTTSVSL FVLAPQOGGGVFVFGGGVVFUAGGRVAGKGRGTTHOLGPAFRO AVTRGSAVQRAPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHGIELSFQRX*BGGCGVVFNGGGPVP			,	
HPTSTEKAQLTETNAGIKCLDSMCCPPEGGEACASVGRNLERVI GRCSPTHISRBWSASDPFYTNORSILTLISTMDSTC AGVRRAGARRGPGRALPAGATAVPPFSARRRRCPAPEHAGPAR ASRPSQETMTQLPVNNLGSLRKARKTVKLLSIGLBYCKEHIE DFKOFEPNDFYLKNTWEDVGLMDFLTKNDDVRTKPFCCSACP FSSKFFSAYKSHFRNVHSEDFENRILLNCPYCTFNADKKTLETH IKI FHAPNASAPSSLSTFKDKNKNDDLKPKQADSVEQAVYYCK KCTYRDPLYBIVKHIYRHFYHVAAPYIAKAGEKSLMGAVPLG SNARESSIHCKRCLPMPKSTADLVQHVIEDHERIGYQVTAMIG HTNVVVPRSKPLMLIAPKPOKKSMGLPPRIGSLASGNV\RSLP SQQMVNLISIPKPNLMSTCVVMMSSVHLQONNYGVKSVCQGYSV GQSMRLGGRAPVSIPQOSGSVKQLLPSGNGRYGLLSSGRGQ APARYSLQSANASSLSSGQLKSPSLSGSQASRVLGQSSSKPAAA ATGPPPONTSTQKWKICTICNELPPENVYSVHFFKEHKARKVP AVANYINKHNNTFSKCLVYNNYLDTLINHMLINGLSCPYCRS TFNDVERMAAHMENVHIDEBMGPKTDSTLSFDLTLQQGSHTNIH LLVTTYNLRDAPAESVAYHAQNNPPVPPKGPKVGEKADIPVKS SPQAAVPYKCDVGKTLCPLCFSILKGFISDALAHHLRRRHOVIO TVHPVEKKLTYKCIHCLGVYTSNNTASTITHLVHCRGVGKTON GODKTNAPSRLNOSSPLAPVKRTVEQMEPPLLKKKLDDDSDS SFPEEKBEEPVLLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASIMV\WK\SDIASHFSNKKKCVRDCEKYKRGVL LGFNMKELNKVHEMDFDAECLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESSNESGSPFDVFUSPKISINDNEEBH VLKVIPEDASESEEKLDQKEDGSKYFTIHLTBEPYKENHDHEDS SSGSEDARSSKPAAKKATMGGDREQLKMKNSSYGKVEGFWSKD QSQKKNASENDERLSNPQIEMORISBERGGGVYNSDBEBH VLKVIPEDASESEEKLDQKEDGSKYFTIHLTBEPYKLHHNASDB EVDQDDVVEWKDGASPSESGPGSQVSDFEDNTCEMKPGTWSDE SSGSEDARSSKPAAKKATMGGDREQLKMKNSSYGKVEGFWSKD QSQKKNASENDERLSNPQIEMORISBERGGGFTKAEAGSGVW EATTLCHQHWMFPIQRPPLVMKGRRIMGCKCEKG*VSDSVTGG RAVAGSGASGRTVTTAGGGECLGKKSRASFYFTONGPWGLL NGKRGGCFESGVLFGFIVGKIOSLERKVPLPPNCCTGERSPC HLVLGVIVPVARQSSHSAGPAQSAF*TGTGSGTFKAAEGSGCW EATTLCHQHWMFPIQRSPFLVMKGRRIMGCKCKGC*VSDSVTGG RAVAGSGASGRTVTTAGGGECLGKYRASFYFTONGPWGLL NGKRGGCFESGVLFGFIVGKIOSLERKVPLPPNCCTGERSPC NCRIHIVDAVC*SEH+*DAFLAAAFLENSTIIS*VAPGSWODHA VLQKEVQASVCRGFESVDTAPAGGGECLGGEFTTTSVSL FVLAPQOGEGVFVFGGQLVTVLGLVVPQSIRRIFFVHHTOLFLIH II*KLGALDVAFHLITLTVLCSSFNYG*GKNGGTFLHQLFAEWN AVTRGSAVQRPSITISSHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHGIELSFGRRV*REGCGVKPDSGPVP	}			
GRGSPTHISRSWASDPYTNDRSILTLISTNDSTC AGVRRAGARRGPGRALPAGATAVPPPSARRRRRCPAPEHAGPAR ASRPSQETMPGLPVNNLGSLRKARKTVKKLLSDIGLEYCKEHLE DPKOPEPNDPYLKNTTWEDVGLWDPSLTKNDDVRTKPPCCSACP FSSKPFSAYKSHRWNHSEDPERLLLDCPYCTPMADKKTLETH IKIPHAPNASAPSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK KCTYRDPLYBLTVKHLYRRHYCHWAAPYLKAKGEKSLMGAVPLG SNARBESSIHCKGLEPMRSYBEALUQNIVIEDHERIGYDVTAMIG HTNVVVPRSKPLMLLAPKPOPKKSMGLPPRIGSLASGNV\RSLP SQQMVNLSIPRENLASTGVNMMSSVHLQNNYGVKSVGQGYSV GQSMRLGLGGNAPVSIPQOSOVKQLLPSGNRGKSYGLGSERRAA ATGPPPGONTSSTGVKKICTICNELPPENVVSWIPFEKEHKABKVP AVANYIMKIHNFTSKCLYCNRYLPPTDTLLHHMLHGLSCPYCRS TFNDVEKMAAHMRNVHIDEBMGPKTDSTLSPILTQQSSIKPAA ATGPPGONTSSTGVKKICTICNELPPENVVSWIPFEKEHKABKVP AVANYIKKIHNFTSKCLYCNRYLPPTDTLLHHMLHGLSCPYCRS TFNDVEKKMAAHMRNVHIDEBMGPKTDSTLSPILTQQSSHTNIH LLVTTYNLRDAPAESVAHAQNNPVPPKPGPKVGBKADIPVKS SPQAAVPYKKDVGKTLCFLCFSILKGFISDALHHLRRRHQVIQ TVHPUBEKLTYKCHLCGYYTSMVTASTITLHLVHCRGVGKTQM GQDKTNAPSRLNQSPSLAPVKRTYEQMEPPLLKKKLDDDSDB SFFEEKBEBPVVLALDPKGH\EDDSYBARKFKKCVRDCGVGKTAD LGFMKBLINKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSPENLEESNEGSPFDPVFEVERKISNDNPEEH VLKVIFEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSSEGGSQVSOFPENTCEMKRGTKNSDE SQSGDARSKPRAKKATMGGREQLKWMSSYGKVGFPKSKO QSQNKNASENDERLSNPQIEWQNSTIDSBDGGFDTNMTDGVAEP MHGSLAGVKLUSSQQA 6009 4272 1534 CHGGGHTFPREINLSLGG*EPH*AR*QAVRSEEKSIC*GSPSC HLVLGVLVPARQSSHSAGPAQSAFR*TGTGGGTFKAAEQSGVW EAYTLGHQHWNMPPIQRPPLVMKGRRIMGKCEKG*VSDSVTGG RAVAGSQASGRTVVTTAGGGECLGAKSVRASVFTKOPGSWGLH NGKRGGCFBSGVLFGFIVIGKIOSLEAKVPLPVNGCTGBRRSPC NCRHITUDAVC*SEHR*H*PHILARDFSTIS*TAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLGGEFTTTSVSL FVLAPQDGEGVFFVEGGLVTVLGLUVPQSIRTFFVHHTQLFLHP II*KIGALDVAFHLILTLVCSSFTWAVGY*GKNGGTTHAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLGGEFTTTSVSL FVLAPQDGEGVFFVEGGLVTVLGLUVPQSIRTFFVHHTQLFLHP II*KIGALDVAFHLILTLVCSSFTWAVGY*GKNGGTTHAPGSWQDHA AVTRGSAVQRRSTTISSIHVDTKIQQELHDWWAGAGGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFGRRV*EQCQGVVFDOSGVPP	Ì			
ASPRSQETMFQLPVNNLGSLRKAKTVKKILSDIGLSYCKEHIE ASRPSQETMFQLPVNNLGSLRKAKTVKKILSDIGLSYCKEHIE DFKGFENDFYLKNTTWEDUGLWDPSLTKNQDYRTKPPCCSACP FSSKFFSAYKSHFRNVHSEDFENRILLNCPYCTFMADKKTLETH HEMPMSASPSSLSTFFKNKNDGLKPKQADSVGAVYYCK KCTYMDDJYELVRHIYRBHFQHVAAPYIAKAGEKSLNGAVPLG SNARBESSIHCKRCLPMPKSYBALVQHVIEDHERIGYQVTAMIG HTNVVVPRSKPLMLIAPKPQDKKSMGLPFRIGSLSGMV\RSLP SQQMVNRLSIPKENLINSTGVNMSSVHLQONYGVKSVGQCYSV GQSMRLGLIGGNAPVSIPQSOVKQLLDSGNGRSYGLGSGRSQ APARYSLQSANASSLSSQQLKSPSLSQSQASRVLQGSSSKPAAA ATGPFPGNTSTTKWKICTICNELFFENVYSWHFFKERKAKVVP AVANYIMKINNFTSKCLYCNRYLPTDTLLNHMLINGLSCPYCRS TFNDVEKMAAHMRNVHIDEBMGPKTDSTLSFDLTLQGSSHTNIH LLVTYLNLRDAPASVAYHAQNPPPPPPPPPPVPVGVGKADLPVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLBERHQVIQ TVHPVEKKLTYKCHLGLGYTSNMTASTITLHLVHCGGVGKTON GQDKTNAPSSLNGSPSLAPVKTPGMEPPLKKKKLDDDSDS SFFEKPEBEPVLALDPKGH\CHECKYFTYKGPYP TRREIEKLAASLWV\MK\SDIASHFSNKRKKCVRDCCKYKFGVL LGFMMKELNKVKHEMPFDAEGLFVENDEFPKLMHNASDS EVDQDDVVEKDGASPSLAPVSTROMSTDEBEDGFPKLMHNASDS EVDQDDVVEKDGASPSESGSPPDVFVEVERISNDMPERK VLKVIPDASESSERLDQKGDGSKYETIHLTEPPKLMHNASDS EVDQDDVVEKDGASPSESGDPGOQVSDPEDNTCEMKPGTWSDB SSQSEDARSSKPAAKKATMQGDRGLKKMSSYGKVEGFWSKU QSQMKNASENDERLSNPQIEMONSTIDSEDGEGPINNTDGVARP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLGHLTPPREINLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAPR*TGTGSGTPKAAEQSGW EAYTLGHQHMNMFPIQRPPLVMKGRLINGKCEGK*VSDSVTGG RAVAGSQASGRRYTVPTAGGGECLGAKSVRASVFTONOPGWIGLL NGKRGGCFESGYLFFIVIGKIQSLAVVPLPVMSQGTGBRASPG NCRIHIVDAVC*SEHH*DHFLAAAPLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFFSVDTAFAGFWAMSPPGLQGBFTTTSVSL FVLAPQDGGAVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHIP I KLGALDVAFIHLLILUCSSFNVAYG*GKRBCSRCHDLLFPRIMGLFHIN AVTRGSAVGRPSITISSIHVDTKIQQELHDVMAGAGDGVQWG DPFVGGLQVFVVEGGLVTVLGGLVFDCGKYPDSQQVFG PFLRVGGLQGAVFRGGGRKCWRDLLFFPRIMGLSHRT				HPTSTEKAQLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVI
ASRPSQETMFQLPVNNLGSLRKARKTVKKILSDIGLEYCKEHIE DFKQFENDFYLKNTTMEDVGLMDPSLTKNQDYRTKPFCCSACP FSKKFSAYKSHFNVMSEDFILLMCPYCTPKADKKTLETH IKIFHAPMASAPSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK KCTYRDPLYEIVRKHIYREHFQHVAAPFYLAKGEKSLMGAVPLG SNAREESSIHCKRCLPMPKSYEALVQHVLEDHERIGYQVTAMIG HTNVVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGRVV\RSLP SQQMYNLSIP EKPHLMSTGYMMSVHLQQNNYGVKSVQGGYSV GQSMRLGGGNAPVSIPQGSQSVKQLLPSGNGRSTGLSEGRSQ APARYSLQSANASSLSSGQLKSPSLSQSQASKULQGSSKPAAA ATGPPPGNTSSTYGKWKICTICHJPENVYSVHPSKEHKABKVP AVANYIMKINNFTSKCLYCNRYLPTDTLLNHMLIEGLCPYCRS TFNDVEKMAAHMRNVHIDEBMGPKTDSTLSFDLTLQGSHTNIH LLVTTYNLRDAPAESVAYHAQMPPVPPKPQFKVQBKADIFVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLBRRHQVIQ TVHPVEKKLTYKCHCLGVYTSMTSTTILHLVEGGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEPPLLKKRKLDDDSDS SFFEEKPEBPVLALDPKGH\EDDSYEAKSFLTKYFT\KQPYP TRREIEKLAASLAWV\WK\SDIASHFSSTKTKYET\KQPYP TRREIEKLAASLAWV\WK\SDIASHFSKKKCVRDCEKYKGVL LGFMMKELNKVKHEMPPDAEGLFENDEKGSRVNASKTADKKLN LGKEDDSSDSFENLEESNEGSPPDPVFEVEPKISNDNPEH VLKVIPEDASESEEKLDQKEDGSKYETTHLTEEPTKLMHNASDS EVDQDDVVEKKDGASPSESGFGSQOVSDFENTCEMKFGTWSDB SSQSEDARSSKPAAKKATMQGDRSQLKMKNSYSVGKVEGFWSKN QSQNKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA CHGLGHLTPFREINLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARGSSHSAGPAQSAPR*TOTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRINGKGEEKG*USDSVTGG RAVAGEQASQRRTVFTAGGGECLGKSVRASVFTNONGOFGRASC NCRITUDAVG*SEHH*DHFLAAPLENSTIIS*VAPGSWODHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLUVPGS IRHTFVHHOLFLFLUN AVTRGSAVGRRPSTTISSIHVDTKIQQELHDVMAGABGVVQKG DPFVVGLAGIFHLULDCVSESFNVAYG*GKNGCTLHQLFEAUN AVTRGSAVGRRPSTTISSIHVDTKIQQELHDVMAGABGVVQKG DPFVVGLAGIFHLULDCVSESFNVAYG*GKNGCKEKSHEDEFNENG DPFVVGLAGIFHLULDCVSESFNVAYG*GKNGCKEKSHEDEFNENG DPFVVGLAGIFHLULDCVSESFNVAYG*GKNGCKEGSCRUNGLEFNENG DPFVVGLAGIFHLULDCVSESFNVAYG*GKNGCKEGSLENGT PVLAPQDGEGVPFVEGQLVTVLGLUVPQS IRHTFVHHOLFLFLUN AVTRGSAVGRRPSTTISSIHVDTKIQQELHDVMVAGABGVVQKG DPFVVGLAGIFHLIDDPLEGGGRVAGGKKCWRDLLFPRKWGLSHRT	6000	4554		
DFKQFEPNDFYLKNTTMEDVGLMDPSLTKNQDVRTKPFCGSACP FSSKFFSAYKSHFRNVHSBDFENRILLNCPYCTFNADKKTLETH IKI FHAPNASAPSSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK KCTYRDPJYBIVRHIYRBHFQHVAAPY JAKAGEKSLMGAVPLG SNARBESSIHCKRCLFMPKS YEALVQHVIEDHERIGYQVTAMIG HTNVVVPRSKPLMLIAPKPQDKKSMGLPFRIGSLASGNV\RSLP SQQMVNRLSIFKENLMSTGVINMSSVHLQONYGVKSVGGYSV GQSMRLGIGGNAPVSIFQOSGVKQLLPSGNGRSYGLGSEGRSQ APARYSLQSANASSLSSGQLKSPSLSQQASRVLQGSSKPAAA ATGPPEONTSSTQKWKLCTICNELFPENVSVHFFKEHKABKVP AVANYIMKINHFTSKCLYCNTYTPTTLLNHMLINGLSCPYCRS TFNDVEKMAAHMRNVHIDEEMGPKTDSTLSFDLTLQQGSHTNIH LLVTTYNLRDAPAESVAYHAQNNPPVPPRPPRVQBKAQIFVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHIRRRHQVIQ TVHPVEKKLTYKCHCLGYYTSMTASTITLHLVECROVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEPPLLKKKLDDDSDSP SFFEEKPEPPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\NK\SDIASHFSNKKKCVRDCEKYKRGVL LGFMMKELNXVKHEMDFDAEGLFFNDEKDSKVANASKTADKKLN LGKEDDSSSDSFENLEESBLSGSSPDDVFEVERKISNDNPEEK VLKVTPEDASESSEKLDQKSDGSKVSTHLTTEEPTKLMHNASDS EVDQDDVVEKVGGASPSESGFOSQQVSPFENNTCEMKPGTWSDB SSQSEDARSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKIN QSQKKNASENDERLSNPQIEWONSTIDSEDGEQFINNTDGVAEP MIGSLAVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVVVARQSSHSAGPAQSAF**TGTGGFTPKAAEGSGVW ANGRGGFESGYTLFGFIVIGKIQSLECKS*VASVTTGNQPGVMGLL NGKRGGCFESGYTLFFIVIGKIQSLECKS*VASVTTGNQPGVMGLL NGKRGGCFESGYTLFFIVIGKIQSLECKS*VASVTTGNQPGVMGLL NGKRGGCFESGYTLFFIVIGKIQSLECKS*VASVTTGNQPGVMGLL NGKRGGCFESGYTLFFIVIGKIQSLECKS*VASVTTGNQPGVMGLL NGKRGGCFESGYTLFFIVIGKIQSLECKS*VASVTTGNQPGVMGLL NGKRGGCFESGYTLFFIVIGKIQSLECKS*VASVTTGNQPGVMGLL NGKRGGCFESGYTLFFIVIGKIQSLECKS*VASVTTGNQPGVMGLL NGKRGGCFESGYTLFFIVIGKIQSLECKS*VASVTTGNQPGVMGLL NGKRGGCFESGYTLFFIVIGKIQSLECKS*VASVTTGNQPGVMGLL NGKRGGCFESGYTLFFIVIGKIQSLECKS*VASVTTGNQPGVMGLL NGKRGGCFTSSTVAYG*GKRGGTTLHQLFAENN AVTRGSAVGRRPSITISSIHVDTKIQQELHDVMVAGADGVQMG DPFVGLAGIFHLLDTDPLGGGRRVAGGGKCKWDLLFPRKWGLSHRT FVLAPQGGGRYFVGGGRKYAGGGKCKWDLLFPRKWGLSHRT	8008	4554	1089	
FSSKFFSAYKSHFRNUHSEDFENRILLNCPYCTFNADKKTLETH IKIFHAPNASAPSSLSTFKDKNKNDGLKPKQADSVEQAVYCK KCTYRDPLYETVRKHIYREHFQHVAAPYIAKAGEKSLMGAVPLG SNARBESSIHCKRCLFMPKSYEALVQHVIEDHERIGYQVTAMIG HTMVVVPRSKPMLIAPKPQDKKSMGLPPRIGSLASGNVRSLD SQQMVNRLSIPKPNLNSTGYMMMSSVHLQQNNYGVKSVCGGYSV GQSMHLGLGGNAPVSIPQOSQSVKQLIPSGNGRSGLGSEQRSQ APARYSLQSANASSLSSGQLKSPSLQSQSAGRVLQGSSSKPAAA ATGPPPGHTSSTQKWKICTICNELFPENVYSVHPEKEHKAEKVP AVANYIMKINHFTSKCLYCNRYLPPTDTLLNHMLHGLSCPYCRS TFNNDVEKMAAHMRNWHIDEBMGPKTDTLISFDLTLQQGSHTNIH LLVTTYNLRDAPASSVAYHAQNNPPVPPKPQDKVQBKADLPVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ TVHPVEKKLTYKCHCLGVYTSNMTASTITHHLVHCRGVGKTON GQDKTNAPSRLNQSPSLAPVKRTVEQMEFPLLKKRKLDDDSDSS SFFEKPEEPVVLALDPKGH LBDSYBARKSFLTKYFT KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFMMKELNKVKHEMDPDAEGLFENHDEKDSRVMASKTADKKLN GENDASSDSFENLEESSESSESPTDVFFVEWFKISNNDFERK VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGFPDVSDFFENTCEMKFGTWSDS SSQSEDARSSKPAAKKATMGGDREQLKWKNSSYGKVEGFWSKN QSOMKNASENDERLSNPQIEWONSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGFAQSAFR*GTGSGTFRAAEGSGWW EAYTLGHGHNMMPPIQRPPLJWKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGECLGAKSVRASVFTGNQFGVMGLL NGKRGGCFBSGYLFGFIVICKIOSLEKVPLPVNGGTGRRASPG NCRIHUDAUC*SSHH*OHILAAPLENSTIIS*AVAGFSNQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLGGETTHTOLFLHP I*KLGALDVAFCHHLTLTVCSSFNVAYG*GRMGGTTHHOLFAENU AVTRGSAVQRPSITISSIHVDTKIQQELHDVMVAGADGVVQMG DPFVVGLAGIFHLIDDPLAQELFSQRRV*EQCQGVKPDSQPVP RPLRVGLLQGGPLVRGGGRRVAEQCGGVKPDSQPVP RPLRVGLLQGGPLTTGSGLFRAFCLSHTT				
IKI FHAPNASAPS SSLSTFKDKNNNDGLKPKQADSVEQAVYYCK KCTYRDPLYEIVRKHI YREHFQHVAAPYIAKAGEKSLNGAVPLG SNARESS IHCKRCLFPMKSYEALVQHVI EDHERIGYQVTAMIG HTNVVVPRSKPIMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP SQQMVARLSI PKPNLNSTGVNMMSVHLQQNNYGVKSVGQSYSV GQSMRIGIGGNAPVSI PQOSOSVKQLLPSGNSTYGLGSEQRSQ APARYSLQSANASSLSSGQLKSPSLSOSQASRVLGQSSSKPAAA ATGPPPGMTSSTQKWK ICTI CNELFPENVYSVHPEKEHKABKVP AVANYIMKIHNFTSKCLYCNRYLPTDTLLNIMLHGLSCPYCRS TFNDVEKMAAHMRNVHIDEBMGPKTDSTLSFDLTLQQGSHTNIH LLVTYNLRDAPABSVAHAQNNPPVPPKPQPKYQEKADIPVKS SPQAAVPYKKDVGKTLCPLCFS ILKGPISDALAHHLRERHQVIQ TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLYHCKGVGKTQN GODKTNAPSRLNQSPSLAPVKRTVEQMEFPLLKKRKLDDSDSP SFFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIBKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFMMKELINKVKHBMDPDABCJFENHDEKOSVNASKTADKKLN LGKEDDSSSDSFENLEESSNESGSPFDPVPEVEPKISNDNPEBH VLKVIPBDASSEEKLDQKEDGSKYETIHLTBEPTKLMHHASDS EVDQDDVVEWKDGASPSESGFSQQVSDFENNTCEMKPGTWSDE SQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQNKNASENDERILSNPQIEWQNSTIDSBDGGFDDMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFREINLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAF**TGTGSTFRAACGSGWW EAYTLGHQHHNMFPIQRPPLYMKGRRIMGCKCKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNPGTWGGLI NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGGTGRRASPG NCRIHIVDAVC*SEHH*DHFLAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPFGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHHLTLVCSFNVAYG*GRNGGTTLHQLFAEVN AVTRGSAVQRFPSITISSIHVDTKIQQELHDVMVAGADGVVQMG DPFVVGLAGIFHLIDDPLHQIELFSPRRV*EQCQGVKPDSQVVF RPLRVGLLQUGPLVRGGGRRVAECKGCHSPLSKT				
KCTYRDPLYEIVRKHIYRRHFOHVARPYIAKAGEKSLINGAVPLG SNARBESSIHCKRCLFMPKSYBALVQHVIEDHERIGYQVTAMIG HTNVVVPRSKPLMLIAPRPQDKKSMGLPPRIGSLASGNV\RSLP SQQMVNRLSIPRPNLMSTGVINMSSVELQQNNYGVKSVCQGYSV GQSMRLGGRAPVSIPQQSQSVKQLLPSGNGRSYGLGSEQRSQ APARYSLQSANASSLSSGQLKSPSLSQSQASRVLGQSSSKPAAA ATGPPPGNTSTQKWKICTICNELFPENVYSVHFEKEHKABKVP AVANYIMKIHNFTSKCLYCNRYLPTDTLLINHLIHGLSCPYCRS TFNDVEKWAAAHMRWHIDEBMGFKTDSTLSFDLTLQGSSHTNIA LLVTTYNLRDAPASEVAYHAQNNPPVPPKPQPKVQEKADIPVKS SPQAVPYKKVDVGKTLCPLCFSILKEFISDALHHLRERHQVIQ TVHPVEKKLTYKCIHCLGYTSINMTASTITLHLVHCGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEPPLLKKRKLDDDSDSP SFFEEKPEEPVVLALDPKGH\TSDEVARSKTTKYFT\KQPYP TRREIEKLAASLNV\WK\SDIASHFSNKRKCVRDCEKYKPGVL LGFMKKLINKVKHENDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSDSFENLEESSNESGSPDPVFEVEPKISNDNPEEH VLKVIPEDBASSSERLLDQKEDGSKYETIHTEPTKLMHASDS EVDQDDVVEWKDGASPSESGPGQQVSDFEDNTCEMKPGTWSDB SSQSEDARSSKPAAKKKATMQCDREQLKWKNSYGKVEGFWSKD QSQKNASSENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNISLQG*EFH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGWMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVURCRGFESVDTAPAGGMALBSPTITSSVL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTHQLFAEVN AVTRGSAVQRRPSTIISSIHVDTKIQQELHDVMVAGADGVVØG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPDVRGGGRRVAGRGKRCWRDLLFFWRMGLSHRT	i			
SMARESSIHCKRCLFMPKSYEALVOHVIEDHERIGYQVTAMIG HTNVVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP SQQMVNRLSIPKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP SQQMVNRLSIPKPLMSTGVNMMSSVHLQQNNYGVKSVGGYSV GQSMRLGLGGNAPVSIPQOGQSVKQLLPSGNGRYGLGSEQRSQ APARYSLQSANASSLSSGQLKSPSLSQSQASRVLGQSSSKPAAA ATGPPPGNTSSTQKWKICTICMELPFDNVSVHFEKEHKAEKVP AVANYIMKIHNFTSKCLYCNRYLPTDTLLNHMLHGLSCPYCRS TFNDVEKMAAHMRMVHIDEEMGPKTDSTLSFDLTLQQGSHTNIH LLLVTTYNLRDAPAESVAVHAQNNPPVPPPKPQFKVQEKADIPVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERRIQVIQ TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEPPLLKKRKLDDDSDSP SFFEEKPEEPVVLALDPKGH\EDSVEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDLASHFSNKRKKCVRDCEKYKPGVL LGFMMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSDSFENLEESSNESGSPDPVPEVEPKISNDNPEEK VLKVIPEDASESEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGPGSQVOSDFEDNTCEMKPGTWSDS SQSEDARSSKPAAKKATMQGDREQLKWMNSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWGNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNISLGG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHMMMFPIQRPPLVMKGRRIMGGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGWMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGBRASPG NCRIHIUDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGWAHSPPGLGGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*6KNGGTTHQLFFAEVN AVTRGSAVQRRPSTTISSIHVDTKIQQELHDVMVAGADGVVØG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQVKPDSQVVP RPLRVGLLQVDPLVRGGGRRVAGRGKRCWRDLLFFWRMGLSHRT				
HTNVVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLE SQQMVNRLSIPKPNLMSTGVNMMSSVHLQQNNYGVKSVGQGYSV GQSMKLGGNAPVSIPQOSQSVKQLLPSGNRGSYGLGSEQRSQ APARYSLQSANASSLSGQLKSPSLSQSQASRVLGQSSSKPAAA ATGPPPGNTSSTQKWKICTICNELFPERVYSVHFBKEHKABKVP AVANYIMKIHNFTSKCLYCRRYLPPTDTLINHM, IHGLSCPYCRS TFNDVEKMAHMRNVHIDEBMGPKTDSTLSFDLTLQQGSHTNIH LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQFKVQBKADIPVKS SPQAAVPYKKDVGKTLCPGFILKGPISDATHLHRERROVIQ TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTTEQMEPPLLKKKKLDDDSDSP SFFEKPEPVVLALDPKGH\EDDSYEARKSFLTXYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKKKCVRDCEKYKPGVL LGFMKKELNKVKHEMPFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESENESGSPFDPVFEVEPKISNDNPEEH VLKVIPEDASESEEKLDQKEDGSKYETHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGGSQQVSDFEDNTCEMKPGTWSDB SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQKKNASENDERLENPQIEWQNSTIDSEDGEGFDNMTTGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTFKAAEQSGVW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTCNQPGVWGLL NGKRGGCFESGYLTEFGIVTGKIGSLERAVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQCEPTTTSVSL FVLAPQDGEGVPFVSGGVTVLGLVVPQSIRHTFVHTQLFFLPH I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDWWAGADGVVQMG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKKCWRDLLFPWRMGLSHRT			•	
SQQMVRRLSIPKPNLNSTGVMMMSSVHLQQNNYGVKSVCGGYSV GQSMRIGLGGNAPVSIPQQQGVKQLLPSGNGRSYGLGSEQRSQ APARYSLQSANASSLSSGQLKSPSLSQSQASRULGQSSSKPAAA ATGPPPGNTSSTQKWKICTICNELFPENVYSVHFEKEHKAEKVP AVANYIMKHHNFTSKCLYCNRYLPPTDTLINMLIHGLSCPYCRS TFNDVEKMAHMRNUN HDEEMGPKTDSTLSFDLTLQQGSHTNIH LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQFKVQEKADIPVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ TVHPVEKKLTYKCHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTVEQMEFPLLKKRKLDDDSDSP SFFEEKPEEPVULALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYRGVL LGFMNKELNKVKHEMDFDARGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESSNESGSPFDPVFEVEPKISNDNPEEH VLKVIPEDASSEEKLDQKEDGSKYETIHLTEEPTKLHHNASDS EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDB SSQSEDARSSKPAAKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFFRELNISLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHCHWNNFPIQRPLLVMKGRRIMCGKCKC*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIGSLEAKVPLPVNQQTGERASPG NCRIHIVDAVC*SEH*DFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVESQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQMG DPFVVGLAGIFHLLDDPLIQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKKCWRDLLFPWRWGLSHRT	1			WENTAMPSCHIMI INDEPENDENT PROPERTY NOT B
GQSMRIGLGGNAFYSIPQQSQSVKQLLPSGNSRSYGLGSEQRSQ APARYSLQSANASSLSSQQLKSPSLSQSQASRVLQQSSKPAAA ATGPPPGNTSSTQKWKICTICNELFPENVYSVHFEKEHKAEKVP AVANXIMKIHNFTSKCLYCNRYLPTDTLLNHMLIHGLSCPYCRS TFNDVEKMAAHMRNVHIDEEMGPKTDSTLSFDLTLQQGSHTNIH LLVTTYNLRDAPABSVAYHAQNNPPVPPKPQFKQFKADIPVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ TVHPVEKKLTYKCIHCLGVYTSNMTASTITHHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP SFFEEKPEEPVVLALDPKGH\EDDSVEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKKKCVRDCEKYKPGVL LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESNBSGSPTDPVFEVEFKISNDNPEEH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGPSQQVOSDFENTCEMKPGTWSDB SSQSEDARSSKPAAKKRATMQGDREQLKWKNSSYGKVESFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFREINLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGIFVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFFSSVDITAFAGFWAHASPFGLQGEPTTTSVSL FVLAPQDGGGVFFVEGGLVTVLGLVPQSIRHTFVHHTQLFLIPP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRSITISSIHYDTKTQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPNWWGLSHRT	1 .			COOMINEL STEVENT METCLEMAGGIER CONTROLLER CHIEF
APARYSLQSANASSLSSQLKSPSLSQSQASRULGQSSSKPAAA ATGPPPGNTSSTQKWKICTICNELFPENVYSVHPEKEHKABKVP AVANNIMKHNFTSKCLYCNRYLPTDTLINIMLINGLSCFYCRS TFNDVEKMAAHMRNVHIDEBMGPKTDSTLSFDLTLQQGSHTNIH LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQFKVQEKADIPVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ TVHPVEKKLTYKCHCLGVYTSMTASTITHLUVLCGGGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP SFFEKPEPBLYALADPRGH\BDDSYLBARKSFLTKYFT\KQPYP TRREIEKLAASLWVWK\SDIASHFSNKRKKCVPDCEKYKPGVL LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESSNEGSSPFDPVFEVERKISNDNPEEH VLKVIPEDASESEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGGSQQVSDFEDNTCEMKPGTWSDB SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSBDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMGCKCKGYSDSVTGG RAVAGEQASQRTVTTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGPWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGGLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKTQQELHDVWWAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRV*EQCGVKPDSQPVP RPLRVGLLQVGPLVVGGGGRRVAGRGKCKCWDLLFFWRWGLSHRT	1			COSMBIGICENTA DAS I DOOGO CITYO I DECAMBERAT CORORDO
ATGPPFGNTSTQKWKICTICNELPPENVYSVHPEKEHKABKVP AVANYIMKIHNFTSKCLYCNRYLPTDTLLMHMLIHGLSCPYCRS TFNDVEKMAAHMRWHIDEEMGPKTDSTLSFDLTLQQGSHTNIH LLVTTYNLRDAPAESVAYHAQNNPPVPPRVQPKVQEKADIPVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEPPLKKRKLDDDSDSP SFFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFERLEESENESGSPFDPVFEVERFKISNDNPEEH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKFGTWSDB SSQSEDARSSKPAAKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA CHGLQHLTFFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHAGPAQSAF*TGTGSGTFKAAEQSGYW EAYTLGHCHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGRQPGVWGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGBRASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWODHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQVKVPSQPPV RPLRVGLLQVGPLVRGGGRRVAGGGKRCWRDLLFFWRWGLSHRT	i		,	APARYSI OSANASSI SSCOT, KSDSI COCOACDUT COCCCUDA A A
AVANYIMKINFTSKCLYCRRYLPTDTLLNHMLIHGLSCPYCRS TFNDVEKMAAHMRNWHIDEBMGPKTDSTLSFDLTLQGSHTNIH LLVTTYNLRDAPABSVAYHAQNNPPVPPKPQPKVQEKADIPVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ TVHPVEKKLTYKCHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRLDDDSDSP SFFEEKPEBPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFNNKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESSNESGSPFDVFEVEPKISNDNPEEH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGPGQQVSDFEDNTCEMKPGTWSDB SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEGFDNMTDGVAEP MHGSLAGVKLSSQQA CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPOSIRITFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRPBITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGGGKKCWRDLLFFWRWGLSHRT	1 : 1			
TFNDVEKMAAHMRMVHIDEEMGPKTDSTLSFDLTLQQGSHTNIH LLVTTYNLRDAPAESVAYHAQMNPPVEPKPQFKVQEKADIPVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP SFFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFNNKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESSNESGSPFDPVFEVEPKISNDNPEEH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDB SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGGTGBRRSPG NCRIHIVDAVC*SEHH*DHFLAAAPLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQEEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLITLVCSSFNVAYG*GRNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKCCWBDLLFFWRWGLSHRT	1 1			
LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQPKVQEKADIPVKS SPQAAVPYKKDVGKTLCPLCF5ILKGFISDALAHHLBERHQVIQ TVHPVEKKLTYKCILGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP SFFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFNNKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESNESGSPFDPVFEVEPKISNDNPEEH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGPGSQQVSDFEDTCTEMKPGTNSDE SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNISLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVWGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFFVGLAGIFHLLDDPLEGIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKCWRDLLFPWRWGLSHRT				
SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ TVHPVEKKLTYKCIHCLGVYTSINMTASTITIHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDS SFFEERPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFNNKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESSNESGSPFDPVFEVEPKISNDNFEEH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASSESGGPGSQQVSDFEDNTCEMKPGTWSDB SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSBDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVULGVLVPVARQSSHSAGPAQSAFR*TGTGSGTFKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGWGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGGTGBRASPG NCRHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*KRNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCGGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	1 . 1			
TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTMAPSRLNQSPSLAPVKRTYEQMEFPLLKKKKLDDDSDSP SFFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVMASKTAPKKLN LGKEDDSSSDSFENLEESNESGSPFDPVFEVEPKISNDNPEEH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKGASPSESGPGSQQVSDFEDNTCEMKPGTWSDE SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVILVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGRRASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFFVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHOVIO
GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP SFFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYRGVL LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPEEH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGPSQQVSDFEDNTCEMKPGTWSDB SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGBRASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFFVGLAGIFFLIDDPLHQIELSFQRRV*EQCQKYPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	.			
SFFEEKPEEPVULALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPEEH VLKVIPBDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDB SSQSEDARSSKPAAKKKATMQGDREQLKWKNS\$YGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSBDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA CHGLQHLTPFREINLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				GQDKTNAPSRLNQSPSLAPVKRTYEOMEFPLLKKRKLDDDSDSP
TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSDS FENLEEESNESGSPFDPVFEVEPKISNDNPEEH VLKVI PEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDB SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVCRGFFSSVDTAPAGFWAHSPPGLQEEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				SFFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP
LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESNESGSPFDPVFEVEPKISNDNPEEH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDB SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL
LGKEDDSSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPEEH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDB SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSBDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN
EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDE SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFREINLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				LGKEDDSSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPEEH
SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS
QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGBRASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT		ļ		EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDE
MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGBRASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	1 1	1		
CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT]		
HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGGGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				
EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	ן פטטפ ן	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC
RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				
NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				
NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				
VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT		1	İ	
FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				NCKIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA
I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT		J		
AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT				
DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT			ļ	
RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT		İ	ĺ	
		Į	ļ	
KDDLKGGDRGHVVVIVLCRLGSLVGGLGTDELLWFGGR*LIIIG		1		
• •	<u>-</u>			RUDDRGGDRGHVVVIVDCRLGSLVGGLGTDELLWFGGR*LIIIG

			The second containing of the property of
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
!	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence	4-4	\=possible nucleotide insertion)
	Jequence		I**RGRLSGEWGCGLGRGELFQVSIGIGVSIVHIGQGDHEVLGG
1			AGLVERGALHATGQGVEALVQQLLDVGPAGALGLCDGAALFQGP
]			GRVGQLPAEGLQVCITLVAQWRMHDGRELGGAEWPWQALHGAAI
		1	CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQRRWRG*TR
ļ			
ļ		[R*NGLTIHCFN*LI*GAVCCRLVILRWCGLLEVHGVYGT*IHCL
			GSFPGRLWP*PFISQERPNGHCQWEFRLAVPSWKCRWSRWRVRG
	1		TWRYGNPLLNLL*GAWLGGAACGGQQGGPLSTWQACTGPGQAAF
			LPPFQGACRPRTQRCRTWVCPIAWRQLLAYTRD
6010	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
"""	_		AGISONAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD
ł		1	PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA
1		1	TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL
1		1	VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
1		1	IPAOISSEGSOAOEPILVSAKPMLESSSYLIRTARSLAINPKDP
1		1	
1		1	PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
		1	IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP
1			IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM
			TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK
1	ì	1	EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG
ĺ			TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD
1	1		YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\
1	1		ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI
	1		TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA
	İ		KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA
ŀ	1		
1	1		SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM
	1	1	YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ
+	1		ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE
i			DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC
ł		İ	TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA
i		ļ	EAMKGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRAK
1	†	Ì	PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
	1		VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA
		1	SEEKLISSAKOVAASTAOLLVACKVKADQDSEAMRRLQAAGNAV
1			KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
] ·	
			LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6011	446	1835	LLQPAMRKSPGLSDCLWAWILLLSTLTGRSYGQPSLQDELKDNT
1		-	TVFTRILDRLLDGYDNRLRPGLGERVTEVKTDIFVTSFGPVSDH
1			DMEYTIDVFFRQSWKDERLKFKGPMTVLRLNNLMASKIWTPDTF
1		1 .	FHNGKKSVAHNMTMPNKLLRITEDGTLLYTMRLTVR\AECPMAF
1			GRDFPM\D\AHACPLKFGSYAYTRAEVVYEWTREPARSVVVAED
1		1	GSRLNQYDLLGQTVDSGIVQSSTGEYVVMTTHFHLKRKIGYFVI
1		1	QTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSIS
			ARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGYA
1		1	
		1	WDGKSVVPEKPKKVKDPLIKKNNTYAPTATSYTPNLARGDPGLA
ł	1		TIAKSATIEPKEVKPETKPPEPKKTFNSVSKIDRLSRIAFPLLF
	1		GIFNLVYWATYLNREPQLKAPTPHQ
6012	351	5013	PAELFQSFAIWHKELYDWRLGPWNQCQPVISKSLEKPLECIKGE
	1	1	EGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQACLIPCQQD
-			CIVSEFSAWSECSKTCGSGLQHRTRHVVAPPQFGGSGCPNLTEF
			QVCQSSPCEAEELRYSLHVGPWSTCSMPHSRQVRQARRRGKNKE
1			REKDRSKGVKDPEARELIKKKRNRNRQNRQENKYWDIQIGYQTR
			WENDERGAME TANKER WANTER TANKER WANTER TO THE TANKER WANTER TO THE TANKER WANTER TANKER WANTER THE TAN
1	1		EVMCINKTGKAADLSFCQQEKLPMTFQSCVITKECQVSEWSEWS
	1		PCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFEEKEPCLS
-			QGDGVVPCATYGWRTTEWTECRVDPLLSQQDKRRGNQTALCGGG
1	1		IQTREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNTT
1			OLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRIT
1	1		NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK
	ĺ		BCGPGTQVQEVVCINSDGEEVDRQLCRDAIFPIPVACDAPCPKD
			CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP
- {			CVLSTWSTWSSCSMTCSGRTTEGRQTRARSTDATAGEEGGTRCF
1			NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW
1	-		NGEASCSVGMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ı	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	Debeddine, Memethionine, Neasparagine,
		· ·	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
j -	1		PCKKDCIVTPYSDWTSCPS\SCKEGDSSIRKQSRHRVIIQLPAN
1			GGRDCTDPLYEEKACEAPQACQSYRW\KTHKW\HRCQ\LVP\WS
			VQQDSP\GAQEGCGPGRQARAITCRKQDGGQAGIHECLQYAGPV
1			PALTQACQIPCQDDCQLTSWSKFSSCNGDCGAVRTRKRTLVGKS
	1		KKKEKCKNSHLYPLIETQYCPCDKYNAQPVGNWSDCILPEGKVE
Ì			VLLGMKVQGDIKECGQGYRYQAMACYDQNGRLVETSRCNSHGYI
			EEACIIPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYN
1			GGRPCPKLDHVNQAQVYEVVPCHSDCNQYLWVTEPWSICKVTFV
	1		NMRENCGEGVQTRKVRCMQNTADGPSEHVEDYLCDPEEMPLGSR
1	1		VCKLPCPEDCVISEWGPWTQCVLPCNQSSFRQRSADPIRQPADE
	i		GRSCPNAVEKEPCNLNKNCYHYDYNVTDWSTCQLSEKAVCGNGI
1 .	}		KTRMLDCVRSDGKSVDLKYCEALGLEKNWOMNTSCMVECPVNCO
	1		LSDWSPWSECSQTCGLTGKMIRRRTVTQPFQGDGRPCPSLMDQS
1	1	1	KPCPVKPCYRWQYGOWSPCOVOEAOCGEGTRTRNISCVVSDGSA
1	1	1	DDFSKVVDBEFCADIBLIIDGNKNMVLEESCSQPCPGDCYLKDW
1			SSWSLCQLTCVNGEDLGFGGIQVRSRPVIIQELENQHLCPEOML
1			ETKSCYDGOCYEYKWMASAWKGSSRTVWCORSDGINVTGGCLVM
1	1	ļ	SQPDADRSCNPPCSQPHSYCSETKTCHCEEGYTEVMSSNSTLEQ
ŀ	İ	ĺ	
			CTLIPVVVLPTMEDKRGDVKTSRAVHPTQPSSNPAGRGRTWFLQ
			PFGPDGRLKTWVYGVAAGAFVLLIFIVSMIYLACKKPKKPQRRQ
			NNRLKPLTLAYDGDADM
6013	1161	710	GAFIAGVPVQPVLIRYPNSLDTTSWAWRGPGVLKVLWLTASQPC
			SIVDVEFLPVYHPSPEESRDPTLYANNVQRVMAQALGIPATECE
			FVGSLPVIVVGRLKVALEPQL/WGTGKSASEGWAVRWLCGRWGR
			ARPESNDQPGRVCQAATAL
6014	2857	613	EAVAGGMEKSRMNLPKGPDTLCFDKDEFMKEDFDVDHFVSDCRK
1	ŀ		RVQLEELRDDLELYYKLLKTAMVELINKDYADF\VNLSTNLVGM
İ			DKALNQLSVPLGQLREEVLSLRSSVSEGIRAVDERMSKQEDIRK
	· ·		KKMCVLRLIQVIRSVEKIEKILNSQSSKETSALEASSPLLTGQI
1	į		LERIATEFNQLQFHACQSK\GMPLLDKVRPRIAGITAMLQQSLE
	İ		GLLLEGLQTSDVDIIRHCLRTYATIDKTRDAEALVGQVLVKPYI
1 :	·		DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS
	İ		EKGNTVPGYDFLVNSVWPQIVQGLEEKLPSLFNPGNPDAFHEKY
		• .	TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI
			RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRRCWSD
			EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE
1	}		IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV
]		ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS
1		ė	ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS
			SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET
1			VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL
			QLALDVEYLGEQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ
			p
6015	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC
		223/	VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
			RITYWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
!			GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
1			
			HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
1			EGIEEEDQEEDKNIVVDDITEQKPBPQDDGKSTESDVKADGDSK
			GSEEVDSHCKKALSHKELYERARELLVSYEEEQFTVLEKFRYLP
	ļ		KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
1			FEQLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
			ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF
1			SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII
į l			F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVQEGSEASPIG
1			KSPYTLDSLYWSVKPASSSFGSEAKAQQQEEQGSVNDVKBEEKE
1			EKEVLPDQVEEEEENDDQEEEEEDEDDEDDEEEDRMEVGPFSTG
			QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
1 .			SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
, ,			\SCGVGS\GNCSNSSSSNFRGAFLLEARGSLH\GL\KTGLQLF
6016.	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC
	<u></u>		

Deginning nucleotide location locati	CEC	Drodistad	D	I had a said a second as the said
Mocation Corresponding	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
cortesponding to first amino acid amino acid residue of amino acid VRKSSLESABGUVVMLANGERARMOVTYLEPDDHKLGRYAIN RITURGENERAL REPORT PROPERTY OF THE PROPERT		, , ,		Glutamic Acid F-Phonylalanina C Clusina
Leleucine, M-Methionine, N-Asparagine, popular deside of amino acid residue of amino acid sequence divergence with the control of the control of amino acid sequence divergence divergence with the control of the control of amino acid sequence divergence di delle di delettori	1.0.		1	H-Histidina I-Isolausina V-Isolausina
to first amino acid residue of amino acid amino acid sequence ##Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, A=possible nucleotide deletion, A=possible nucleotide deletion, Vermsplessensulvarianter RTTWRSRSORSLPLAVASTADLERCKLDVTGCDGTDELKLLY GRALVEFWALERCARDERSARDVTVTFCPDDHKLGRYANA RTTWRSRSGORSLPLAVASTADLERCKLDVTGGTDELKLLY GRALVEFWALERCARDVTLERCKLDVTGGTDELKLLY HKROPHINDCRRGCTFVLDMLGXTTWGCGLENSLRETWELEER KGIEBEDGEBONIVTVDTTGCPERCHOGENSTEDVERCHERCH RKOPHINDCRRGCTFVLDMLGXTTWGCGLENSLRETWELEER KGIEBEDGEBONIVTVDTTGCPERCHOGENSTEDVERCHERCH RKOPHINDCRRGCTFVLDMLGXTTWGCGLENSLRGTWGCRETER GGEBVDSHCKKALSHKELTSRARELLVSYKERGFTVLEFFYLE RKOPHINDCRRGCTFVLDMLGXTTWGCGGESTSDVAKAGHER GGEBVDSHCKKALSHKELTSRARELLVSYKERGFTVLEFFYLE RKOPHINDCRRGCTFVLDMLGXTTWGCGGESTSDVAKAGHER REVLEDOVERSERNDDGLEDERGRWUPPFSTG GSSTAFRARLLAKGKAGCGERGSTFTLIGATVELLAVATKTGGARGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	ł			ILeugine M-Methionine N-Agramatine
amino acid residue of amino acid sequence Sequence WTTPYTOPION, YTYPOSIEN, X-UNIKNOWN, **Stop Codon, /=possible nucleotide deletion, _>possible nucleotide insertion) WKRKSSLPLSANGTVANUSSRARMOVTYTUPEDBHLDYAIN RITWASSSONELPLANGTATULINGKLUDTGHOTDELLLY GRALVAPVNLIESEKTKRAKVPLKCLAGGVATIFORITVOLKHEIN HKNMPHINDCRRGCYTVLDHOKTYTMCRELESSIKETWLENGER EGEEDOBEDNITVDDITTEGKPEPDDERSIKENSETWLENGER GSERVESSICKALSHESTYRARELLUSYREEGPTVLERFUNGTY ALLERNHESELPALOISGIRFTTILRHTVELIVANITKTGRNARFI FROLANGLESTERVENDULVLYRPFSGFPGDEGSSCNANGHESK SAGNERAREGWELPUNGSSGRESHOORDEDBESORMEVOPFSU ALLERNHESELPALOISGIRFTTILRHTVELIVANITKTGRNARFI FROLANGLESTERVENDULVRYPRSGFORPGLEGGSSVANNYEEGH SAFTLDGINGSVANSTERSSTORSKANGOGGSSVANNASSTORSKANGOGGSSVANGOGGSSVANNASSTORSKANGOGGSSVANNASSTORSKANGOGGSSVANNASSTORSKANGOGGSSVANNASSTORSKANGOGGSSVANNASSTORSKANGOGGSSVANNASSTORSKANGOGGSSVANNASSTORSKANGOGGSSVANNASSTORSKANGOGGSSVANNASSTORSKANGOGGSSVANNASSTORSKANGOGGSSVANNASSTORSKANGOGGSSTORSKANGOGGSSVANNASSTORSKANGOGGSSVANNASSTORSKANGOGGSSVANNASSTORSKANG	1			P-Proline O-Clutamine P-Arginine
residue of amino acid sequence whysiolanucleotide insertion) veksispiesahorvanksakmogvytpedbanksakmogvytpedbanksakmogvytpedbanksakmogvytpedbanksakmogvytpedbanksakmogvytpedbanksakmogvytpedbanksakmogvytpedbanksakmogvytpedbanksakmogvytpedbanksakmogvytpedbanksakmogvytpedbanksakmogvytpedbanksakmogvytpedbanksakmogvytpedbanksakmogvytpedbanksakmogvogvationalistickering sakmanksakmogvytpedbanksakmogvationalistickering sakmanksakmogvytpedbanksakmogvationalistickering sakmanksakmogvationalistickerin	-			
amino acid sequence Codon, /=possible nucleotide deletion Vegesible nucleotide insertion Vegesible nucleotide insertion Riversischen in the control of the c	Į.			
Sequence \possible mucleotide insertion		· ·		Codon /-possible nucleotide deletion
VEGIGSLPLSAMCI VVANISERSENDED VIVATURED CONTRIBUTED IN THINKERSSENDED LAUASTADLI LEKE LAUDVIGGLOTEDELLLY GRALVERVALLISERETEFANYPLECLAGEVNI PONT VOLRRELT HEMPHINDCREGOVY PLOUNDER VEGIGSER SENDEN AND AND AND AND AND AND AND AND AND AN			sequence	
RITTWISSISCRIEPLAVASTADLIRCKILDVTGGLTDERILLY GRALUFFUNILESERTFEYAVEYEKICAGEVINIPDMY VOLKREIT HKKMPHINDCRGCTFYLDMLGATTWCROLDSSIRETWELEEFE EGIEBEDGEBENNIVUDITTGCKPEPODDGKSTESDVALGDGK GSESUDSHCKKALSIKELVERRARELLVSYEREGOFTVLEKERTYLD KAIKANNIPSERVECVLABLKGVTCHENEAVLDAPLODGELVDT FROGAALGIEVEENVOLINDULVPKPPSGFROFTVLEKERTYLD ALLERRASELPLAIGISSIPPTYLERVENTULNTORUNGPRANGENDER ALGERMASELPLAIGISSIPPTYLERVENTULNTORUNGPRANGENDER SAGGWEARRGWELFYGGSALDWPRWEBGLGSPCMASPOLLRI PLAMGOGLODE KOBERLURICSITYOGGSINGLVORGSASPIG KSPYTLDSLYWSYKDASSSFGSRAKAQOGEGGSVNIVKEERKE REVLPOPQVEREERRANDGEREERBEDEDDERGRENBENDEPS SPETTAPARLIALOKRGALGGSAWQVSSEDVENDTPPLICHMEN SPETTAPARLIALOKRGALGGSAWQVSSEDVENDTPPLICHMEN SPETTAPARLIALOKRGALGGSAWQVSSEDVENDTPPLICHMEN SPETTAPARLIALOKRGALGGSAWQVSSEDVENDTPPLICHMEN SPETTAPARLIALOKRGALGGSAWQVSSEDVENDTPPLICHMEN SPETTAPARLIALOKRGALGGAWQVSSEDVENDTPPLICHMEN SPETTAPARLIALOKRGALGGAWQVSSEDVENDTPPLICHMEN SPETTAPARLIALOKRGALGGAWQVSSEDVENDTPPLICHMEN SPETTAPARLIALOKRGALGGAWQVSSEDVENDTPPLICHMEN SPETTARALIALOKRGALGGAWQVSSEDVENDTPPLICHMEN SPETTARALIALOKRGALGGAWQVSSEDVENDTPPLICHMEN SPETTARALIALOKRGALGGAWQVSSEDVENDTPPLICHMEN SPETTARALIALOKRGALGGAWQVSSEDVENDTPPLICHGMEN SPETTARALIALOKRGALGGAWQVSSEDVENDTPPLICHGMEN SPETTARALIALOKRGALGGAWQVSSEDVENDTPPLICHGMEN SPETTARALIALOKRGALGGAWGVSSEDVENDTPPLICHGMEN SPETTARALIALOKRGALGGAWGVSSEDVENDTPPLICHGMEN SPETTARALIALOKRGALGGAWGVSSEDVENDTPPLICHGMEN SPETTARALIALOKRGALGGAWGVSSEDVENDTPLICHGMEN SPETTARALIALOKRGALGGAWGVSSEDVENDTPLICHGMEN SPETTARALIALOKRGALGGAWGVSSEDVENDTPLICHGMEN SPETTARALIALOKRGALGGAWGVSSEDVENDTPLICHGMEN SPETTARALIALOKRGALGGAWGVSSEDVENDTPLICHGMEN SPETTALIALOKRGALGGAWGVSSEDVENDTPLICHGMEN SPETTALIALOKRGALGGAWGVSSEDVENDTPLICHGMEN SPETTALIALOKRGALGGAWGVSSEDVENDTPLICHGMEN SPETTALIALOKRGALGGAWGVSSEDVENDTPLICHGMEN SPETTALIALOKRGALGGAWGAWGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG		- Jodanno		
GMALVAFYNLISERKTEPAKVPLKCLAGEVNI PDN IVDLARREIL HKAMPHINDCRRGCYFULMINGKYTKGOLDENISERTENIELERF BGIEEEDGEBONITVVDDITEOKPEPODORKSTESDVRANCOSK GSEVENSHCKKARISKELYRRARRELINSYTEGETTELERFT E BGIEEEDGEBONITVVDDITEOKPEPODORKSTESDVRANCOSK GSEVENSHCKKARISKELYRRARRELINSYTEGETSDEVALOGEL KAIKANNIPSERVECVIJAELKOVTCONERAVLIJAFLODGELJUP FROLALGITYEERUKDINDVIVLEPSPSOPGOLLARIKHOOPTO ALLERMISELPALGISGIERTYLLRATVELIVANTKTORNARPE SAQMERREGWELPCASALDUR PREVIDELIVANTKTORNARPE ALLERMISELPALGISGIERTYLLRATVELIVANTKTORNARPE PARAMOGLODEN BOEKLURICSIYTOGSENSHVORGSEAPTIG KSPYTUDSLAYWSVENSSSTORSKAROQUEGOSYNDVKEEKKE RKEULPDQVEBEBERDDQEBBEBDEDDEDDERDRIKWSPSTOR GKSPYTARARALLAGOKROALGOSANOVSSEDVENDTFP\LORMARS RKEULPDQVEBEBERDDQEBBEBDEDDEDDERDRIKWSPSTOR GKSPYTARARALLAGOKROALGOSANOVSSEDVENDTFP\LORMARS RKEULPDQVEBEBERNDDQEBBEDDEDDERDRIKWSPSTOR GKSPYTARARALLAGOKROALGOSANOVSSEDVENDTFP\LORMARS RKEULPDQVEBEBERNDDQEBBEDDEDDERDRIKWSPSTOR GKSPYTARARALLAGOKROALGOSANOVSSEDVENDTFP\LORMARS RKEULPDQVEBEBERNDDQEBBEDDEDDERDRIKWSPSTENDTAG GKSPYTARALLAGOKROALGOSANOVSSEDVENDTFP\LORMARS RKEULPDQVEBEBERNDDQEBBEDDEDDERDRIKWSPSTENDTAG GKSPYTARALLAGOKROALGOSANOVSSEDVENDTFP\LORMARS RKEULPDQVEBEBERNDDQUERNSGATSVERPTIOLISMARKSILAL EKEBEBERSKYTISLIKTALRIKMENTITE DUGILSCILIFIKK RKEULPDQVERSEBERNSKYTISLIKTALRIKMENTITE PILODGLISCILIFIKK TINDYTSSESRIHTSLICICIKALINNSGARAVLAHASESINVIAO SLISTENITIKVANLEILIGAVVETIRGITHSTAMPENTITELINOKAGOPOSTELEN DELEFAKREPTIOLISMARSKARISTICICIKALINNSGARANALINOKAGOROSSEL DPRIHLIKTRY JEMAGLICKARINSTLORHLIPPOTAPHISTICICIKAGOKROBENTILIFIK HCLOMPYKRSONIVOYVHLLLORI IQQIVIONKGOPOSTELEN PRIHLIKRAGANITAGANOVARALDAGANITAGAN	İ			
HKMPHINDCRRCYTYUDIGOKTYMCRQLENSIRETWELEE BEIEBEDGEBUNTVODITIONSPROVERDOBMSKTSTWALDED GEBEUDSHCKKALSHKELLYSTRARELLYSTERGETYULKRYDJ KAIKANNINS FORVECVLARIKAGYTCHRERAVLAD FLOGGIJUPT FROLAALOI EYERNYDLADVLYPEPSGWOCHLIGLISGNPTO ALLERMAGGLODE BORKLILI GIS CITYLTURTVELT LYANGRAFP SAGOWBARRGWRLFNCSALDM PRIVESCLGS CRASSPOLITI PKAMGGGLODE BORKLILI GIS TYTYGGRBSLVONGGSBASPIG KSPYTLISLYMSVVRASSSGGBAKAGOGROGGSVADVASERER KSPYTLISLYMSVVRASSSGGBAKAGOGROGGSVADVASERER KSPYTLISLYMSVVRASSSGGBAKAGOGROGGSVADVASERER SEPTARANILLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO GESTPARNARLLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO GESTPARNARLLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO GESTPARNARLLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO GESTPARNARLLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO GESTPARNARLLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO GESTPARNARLLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO SEPTARNARLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO SEPTARANILLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO SEPTARANILLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO SEPTARANILLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO SEPTARANILLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO SEPTARANILLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO SEPTARANILLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO SEPTARANILLAGKRGALGGSAMOVSSBVRWOTPPLORPSTO SEPTARALGKRGAMGGPSTO SEPTACH TO CONTROLORPSTO NPALOTIMERALPHPUP THE DEVELOPMENT SEPTILLAGE SEPTARANILLAGKRGALGKANTAL				
BGIEREDQBEDKNITVDDITEOKRPEDDDIGSTENDIKADEGE GEBENDSHCKKALSIKELIYARREDGYTLEKFEPILD KAIKANNINSPRVECVLARIKGYTCENERAVLDAPLDDGEJLY PROLAALQIEVERVINDMULVUPPEPSGWOCHLRIGHSONPTO ALLERMIASLPALGISGIRFTYILDHTVELIVANTKTGRNARRP SAGWEARRGHPLENGASLIDHERWESGLGSPODLERI PALALERMIASLPALGISGIRFTYILDHTVELIVANTKTGRNARRP SAGWEARRGHPLENGASLIDHERWESGLGSPODLERI EPALAMOGLOBE BEBENDEDDEBBEDRHEVORDSEBER KEPULDDQUEBERRDDDEBBERRHEVORDSPODLARI PALAMOGLOBE BEBENDEDDBERDRHEVORDSPODLARI ERVILDDQUEBERRDDDEBBERRHEVORDSPOLGERI ERVILDDQUEBERRDDDEBBERRHEVORDSPOLGERI SEGVIS ORIGINASSINDREGGENISTE VICTORIANDHERPET VICTORIA SCOVOS ORIGINASSINDREGGENISTE VICTORIANDHEP VICTORIA SCOVOS ORIGINASSINDREGGENISTE VICTORIANDHEP VICTORIA SEGVIS ORIGINASSINDREGGENISTE VICTORIANDHEP VITTORIA SCOVOS ORIGINASSINDREGGENISTE VICTORIANDHEP VITTORIA SEGRESBERRAKTISSLKTALHKIPPHEVER DIDGISCILIMPET TRADITURE VICTORIANDHER VICTORIANDHER VICTORIANDHER VITTORIANDHE				
GSEEVUSHCKRALSHKELLJYSTERGETTYLEKTYL RAIKANNINSPRYEVULAELKGYTCERREAULDGELJUPT FROLAALOIEYEERNYULAUNULVPRPSGYMOPLLRGLISGNPTO ALLERMAGELDAIGTSTRITTLERTYLLTVATUTGNARPE SAGOWRARRGWRLENGSASLDWERWESGLASPCRASPOLLTR PKAMOGGLOBY BORGEKLAIGTSTYTYGGERSLAYGOGOBOGSTANDYGEBEE SAGOWRARRGWRLENGSASLDWERWESGLASPTO KSPYTLISSLYSTVAGASSASDWERWESGESPTO QSSPTABRARLLAQRRGALGGSAWQYSSEDVRAUPVEEBEE EKEVLPDQVEEBEBNDDQEBEBEDDDDDEDEBENTEWGPSTY QSSPTABRARLLAQRRGALGGSAWQYSSEDVRAUPTPYLCRFMP GOSPTABRARLLAQRRGALGGSAWQYSSEDVRAUPTPYLCRFMP SRPRTPABLMLBRYDTHVIPWTRVL BORGERSTYCK TOTICA SCUOSI QNGNSSSSSSNFRGATSHEPTYLDQLBYRGAWGA SRPRTPABLMLBRYDTHVIPWTRVL BORGERSTYCK TOTICA SCUOSI QNGNSSSSSSNFRGATSHEPTYLDQLBYRGAWGA SRPRTPABLMLBRYDTHVIPWTRVL BORGERSTYCK TOTICA SCUOSI QNGNSSSSSSNFRGATSHEPTYLDQLBYRGAWGA SRPRTPABLMLBRYDTHVIPWTRVL BURGHLEYGELYGLDL SRCHAUPTPH SELVENDER SELVEDLLBLTGHERRAFBLD ABKKNOIVCSKKKOOBENKGATSHPERYTDDLBYRGARDALD KREEDERSKYTISSLIGGITRALMNISGGRAVULAHSESISUVL SERVENDER SELVENDER SELVEDLBLTGHERRAFBLD ABKKNOIVCSKKKOOBENKGATSHPERYTDDLBYRGARDALD EKEBEBERSKYTISSLIGGITRALMNISGGRAVULAHSESISUVL SELVENDER SELVENDER SELVENDER SELVENDER SELVENDER SELVENDER THOMPTENSEN HILDITESSER SELVENDER SELVENDER SELVENDER SELVENDER THE SELVENDER S				
RAIKANNISPRVECULALIKSVTCENERAVICLICALISONPTO PROLAALCI EVERVINDNOLLIVEPPSOGWOLLICALISONPTO ALLIEMISELPALGI SGIRTYTILDRITUSI LYANYTICORANDI PROLAALCI EVERVINOSALIUM PRIVESCILOS PCNAS POLIERI PANAGOGLODE ROBELLIA CSI YTUGGERSI LYORGSEAS PIG KSPYTLOSI HYNVRASSI SGERAKAÇOUSGOSOSYMUVKESER REVLEDOVERSEERDODERDE ERENDEVEPPSTO OESSPTARNALLAQURGALAGISANOVSS SENVRMOT PP ALORNO SEPTARNALLAQURGALAGISANOVSS SENVRMOT PP ALORNO SEPTARNALLAQURGALAGISANOVSS SENVRMOT PP ALORNO SEPTARNALLAQURGALAGISANOVSS SENVRMOT PP ALORNO SEPTARNALLAQURGALAGISANOVSS SENVRMOT PP ALORNO SEPTARNALLAQURGALAGISANOVSS SENVRMOT PP ALORNO SEPTARNALLAQURGALAGISANOVSS SENVRMOT PP ALORNO SEPTARNALLAQURGALAGISANOVSS SENVRMOT PP ALORNO SEPTARNALLAQURGALAGISANOVSS SENVRMOT PP ALORNO SEPTARNALLAGURGALAGISANOVSS SENVRMOT PP ALORNO SEPTARNALLAGURGALAGISANOVSS SENVRMOT PP ALORNO SEPTARNALLAGURGA SENVRO SEPTARNALLAGURGA SENVRMOT SELVENTAL ALORNO SEPTARNALLAGURGA SENVRMOT SELVENTAL SELVENTAL SERSEBERS KTI SELVETAL SELVETAL SELVETAL SELVETAL SELVETAL TENDET SELVETAL SELVETAL SELVETAL SELVETAL SELVETAL TENDET SELVETAL SELVETAL SELVETAL SELVETAL SELVETAL TENDET SELVETAL SELVETAL SELVETAL SELVETAL SELVETAL TENDET SELVETAL SELVETAL SELVETAL SELVETAL SELVETAL TENDET SELVETAL SELVETAL SELVETAL SELVETAL SELVETAL TENDET SELVETAL SELVETAL SELVETAL SELVETAL SELVETAL TENDET SELVETAL SELVETAL SELVETAL SELVETAL SELVETAL TENDET SELVETAL SELVETAL SELVETAL SELVETAL SELVETAL SELVETAL TENDET SELVETAL				
FROLANLOI EYERNYLLMÜLLERVÜLL VANGALISONPTO ALLERMISELBALGISCHTYLLRAVISL LYNKTORNARP SAGOWRARRGWRLPIGSASILDW PRWYSSCIASPCRASPOLLTI P KYMROGGLODP KORKILLIG STYTYGGERSLYNGGSSASPIG KSPYTLDSLYWSVKPASSSGGRAKAGOORGGSVRIDVERBERE RKEVLPDQVEBEBENDDQEBEBEDDDEDDEDBERERRRWSVGPSTO QESPTABNARLLAQRRGALGGSAWQVSSEDVRHDTPP LAGRWR SRPRTPABLMLBWYDTHI PWTKPVLL BORLBYTCK LYDTGG SCOUSS (NGNSSUSSSSNFRGATSPICERRRSLING LA KYGGOLF SCOUSS) (NGNSSSSSSNFRGATSPICERRRSLING LA KYGGOLF SKOUSS) (NGNSSSSSSNFRGATSPICERRRSLING LA KYGGOLF SKOUSS) (NGNSSSSSSNFRGATSPICERRRSLING LA KYGGOLF SKOUSS) (NGNSSSSSSNFRGATSPICETCK) TOTAL REFERENCE SELVESTARTRYRESTEDDLING KREAMFALD ARKWOJT VGSKKKOOERKGATSPIETY LOCKRRAMFALD ARKWOJT VGSKKKOOERKGATSPIETY LOCKRRAMFALD ARKWOJT VGSKKKOOERKGATSPIETY LOCKRRAMFALD ARKWOJT VGSKKKOOERKGATSPIETY LOCKRRAMFALD ARKWOJT VGSKKKOOERKGATSPIETY LOCKRRAMFALD ARKWOJT VGSKKKOOERKGATSPIETY LOCKRRAMFALD ARKWOJT VGSKKKOOERKGATSPIETY LOCKRRAMFALD ARKWOJT VGSKKKOOERKATSPIETY LOCKRRAMFALD ARKWOJT VGSKKKOOERKATSPIETY LOCKRRAMFALD ARKWOJT VGSKKKOOERKATSPIETY LOCKRRAMFALD SERENIKTRY LA LILAUCH LOCKRAMFALD ARKWOJT VGSKKKOOERKATSPIETY LOCKRRAMFALD ARKWOJT VGSKKKOOERKATSPIETY LOCKRAMFALD ARKWOJT VGSKKKOOERKATSPIETY LOCKRAMFALD ARKWOJT VGSKKKOOERKATSPIETY LOCKRAMFALD ARKWOJT VGSKKKOOERKATSPIETY LOCKRAMFALD ARKWOJT VGSKKKOOERKATSPIETY LOCKRAMFALD ARKWOJT VGSKKKOOERKATSPIETY LOCKRAMFALD ARKWOJT VGSKKKOOERKATSPIETY LOCKRAMFALD ARKWOJT VGSKKKOOERKATSPIETY LOCKRAMFALD SERVENDE SERVENDE SELVENDE SELVENDE LILAUT LOCKRAMFALD ARKWOJT VGSKKKOOERKATSPIETY LOCKRAMFALD SELVENDE SELVENDE SELVENDE SELVENDE SELVENDE SELVENDE SELVENDE SELVENDE DETERLETEN LOCKRAMFALTY LOCKRAMFALD BELEFARKOOER SELVENDE SELVENDE SELVENDE SELVENDE SELVENDE DETERLETEN LOCKRAMFALTY LOCKRAMFALD BELEFAR LOCKRAMFALD BELEFAR LOCKRAMFALD BELEFAR LOCKRAMFALD BELEFAR LOCKRAMFALD BELEFAR LOCKRAMFALD BELEFAR LOCKRAMFALD BELEFAR LOCKRAMFALD BELEFAR LOCKRAMFALD BELEFAR LOCKRAMFALD BELEFAR LOCKRAMFALD BELEFAR LOCKRAMFALD BELEFAR LOCKRAMFALD BELEFAR LOCKRAMFALD BELEFAR LOCKRAMFALD BELEFAR LOCKRAMFALD				-
ALLERMISELPALGISCIRPTY LIRMITUEL LVANITATERIARRY SAGOWEARRISMELPACASION PROMESCICAS POLIAIT P \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	ļ			1
SAGWRARGWRLENCSASLDWPRMWESCLGSSCKARSDLIKIT P KAMCGGLODEN SORKLINT CSTYTYGGENOVOGGERS PTE R SPYTLDSLYMSVEPASS FGSRARAQOGEGGSVMDVKEBEKE EKEVLPPOVEBEBENDDOEBEESDEDDDIDDEBEDRWEOSPST QESPTABRARLLAQKRGALQGSAMQVSSEDVRDYTPF PLOFMY SRPRTPARLIMLENTDTHVIFWTRVILDERLEPSTCK YDTIGL SCOUGS (NOCSNISSSSWERGATLLEARGSH, MG, KYGLQL) 6017 203 3469 SHQBIEDNSAMAPEKRGGGISFIFCCFRNNDHPEITYRRNDS NPALQTMEPSLAPPPVBELDUMPSELVEDLDIDKHRRAMFALP ARKWQTYCSKKKODGENGATSWPEFYIDOLMSWAARKSLLAL EKEEBEBERSKT ESLKTLARKFWPRVTRE IDLSKILINTKK THOTETSBRIHTSLIGCIKALMNNSGGRAHVLAHGSBINVIAQ SLSTENIKTKVAVUREILGAVCLVPGGHKKVAUHTYKASSET THOTLINDLOKSTGRYRDEVSLKTLAMSPINAVLSGGAGVESL DFRLHLRYR PHILOIHPVMDKLKHENSTLDHLIDFFERLINE DELSPAKRREIVHIDTKSATTMSPINAVLQCAGVESL DFRLHLRYR PHILOIHPVMDKLKHENSTLDHLIDFFERLINE DELSPAKRREIVHIDTKSATTMSPINAVLQCAGVESL PRINTVRNLVINAVENEVKOWKOGARKMREINELQKKEKKERSTEPHSVIHA HCLOMPYKRSGMTVQTWILLDRII QUIVIQNOKGQDEPSTLENN FNINTVRNLVINAVENEVKOWKOGARKMREINELQKKEKKERSTEPHSVIHA HCLOMPYKRSGMTVQTWILLDRII QUIVIQNOKGQDEPSTLENN FNINTVRNLVINAVENEVKOWKOGARKMREINELQKKEKKESTEO DAKTQKREBMGTLINKKKKLEKSTTEHKOVKQOVADLTAQHE LSPRPPPLEPGGPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP				
P. V.CAMCGGLODE\GORKLIBITCSITYTGGGGNYDVKEEREK REYTLDSLYWSVPRASSPSGSRARQOGGSVANDVKEEREK EKEVLPDQVEEEEENDDQEEEEDEDDEDDEEEDRMEVGPPSTG QESPTAENARLLAQKRGALGGSAMQVSSEDVRNDTPP\LGMPRE SRPRTPAELMEENTDTHIJTRITVEVL\GORGESTACKITGGLE SRPRTPAELMEENTDTHIJTRITVEVL\GORGESTACKITGGLE SRPRTPAELMEENTDTHIJTRITVEVL\GORGESTACKITGGLE SRPRTPAELMEENTDTHIJTRITVEVL\GORGESTACKITGGLE SRPRTPAELMEENTDTHIJTRITVEVL\GORGESTACKITGGLE SRPRTPAELMEENTDTHIJTRITVEVL\GORGESTACKITGGLE SRPRTPAELMEENTTHIJTRITVEVL\GORGESTITTRICQLIF SRPRTPAELMEENTTHIJTRITVEVL\GORGESTITTRICQLIF ARKWOLYCSKKKOQERNGATSHPEYTIODGLSCILNFLK TREGILINDLKSTGATSHPEYTIODGLSCILNFLK TREGILINDLKSTGATSHPEYTIOLOGUMENTAKESINVIAQ SLSTENIKTKVAVLEILGAVCLVPGGHKKVLQAMLHIYGKTSKY SLSTENIKTKVAVLEILGAVCLVPGGHKKVLQAMLHIYGKTSKY TREGILINDLKSTGATSKYBEVSUKATAINSFINAVLSGCASVESL DPFHEHRYR\F\MGGHPYMBKURKHENSTIDAPSHYMSILH HELQMPYKRSGATTYRTUSTIONGGOPPSTYLEN DELEFARREUVHDITKSATQMPELITRRILTHSBAYPHYMSILH HELQMPYKRSGATVQWALLDRIIQGVORGOPBSTYLEN FIIKNVVRNLUNDENEVKOWKSQAEKMREENBELQOKLEKERSC DAKTORESEMMOTLINNEKELKSTTERKOVQOVADLTAQLIH LSPRAVCASIPGGPSGARGGPPSSVGSLLDPPPPPJLGGM LPPPPPPLPGGPPPPPPGPPPPPGPPPPPGPPPPGPPP				
KSPYTLOSLYMSVEPASSSFOSRAKAQOGEGGSVINVEBEKE REVLPOVGEBERINDOGEBERDEDEDEDDE BEKDRINEVGEPSTEG ORSPTARNARLIAQKRGALQSAMQVSSEDVRMOTTP JLGKMPR SEPRTPABLIKENTOTHLY TEVTLV NG VLLESTICK YETTLGL \CCUUSS\CINCSNSSSNFRGAPLLEARGSLH\GL\KTGLQLF SHQBIEDNSAMAFEKRGGRGISTIFCCFRNNDHPEITYRINDS NFALQTIBEDALPMP PVELEDUM SELVEDELDIDMIRERAMFALP ABKWQIYCSKKHQGENKGATSWFEFYIDQIANSHARSLIAL EKBEBEERSKTESLKTALIGGIKALMNNSGGRAHVLAMSSINVIAQ SLSTENIKTKVAVLELIGAVCLVPGGHKKVALMYGKYASER THOTLINDLAKSTGRYRDEVSLKTALMSFINAVLSQGAGVESL DPRHLRYR YHMIGHTPWMKIKKHENSTIALDPPENLRNE DELFFAKREIVHIDTKSATQMPBLTRKRLTHSEAYPHPMSILH HCLQMPYKRSGNTVQYWLLLDRIIQQVIVQNNKGQDEBTJENN FNINIVARLAVESEWKGQAEKMREENBLQKKEKKERSTED FNINIVARLAVESEWKGQAEKMREENBLQKKEKKERSTED AKTQKREEMMQTLANKKKKLEKSTTEKKQVKQQVADLTAQHE LSRRAVCASI SEGGSGAAPGPPSSVSGSLIALDEDEETFLEN FNINIVARLAVESEWKGQAEKMREENBLQKKEKKERSTE DAKTQKEEMMQTLANKKKKLEKSTTEKKQVKQQVADLTAQHE LSRRAVCASI SEGGSGAAPGPPSSVSGSLIALDEDEETFLEN FNINIVARLAVESEWKGQAEKMREENBLQKKEKKERSTE DAKTQKEEMMQTLANKKKELKENTTEKKQVKQQVADLTAQHE LSRRAVCASI SEGGSGAAPGPPSSVSGSLIALDEDEETFLEN SAYQRQQDFFVNSNSKOKRADAIDDILSSKLKVKELSVIGGRA QNCHILLSRLKISNDEIKRALITMDEGEDLE KOMMLEQLLEFVER KSDIDLLEEHKHELDRMARADRELFRERRINHYQQRLOSLYFKK KRARVABEVKEVARLSGSSEVFRSGLKALDLEAKDLIFKEV KSQDTOLLEEHKHELDRMARADRELFRERRINHYQQRLOSLYFKK KRARVABEVKEVARLSGSSEVFRSGLKALDLAGAKOLFTRAV KHGGERGKIQPDEFGIFDGFLQAVSBAQGNEMMRKKKEEEE RRAMBAQLKGRORVARSTSSSEVFRSGLKALDLAGAKOLFTRAV KHGGERGKIQPDEFGIFDGFLQAVSBAQGNEMMRKKKEEEE RRAMBAQLKGRORVARGARTKKMENSESSGERSIRHINGTVALTHAL ALSSSYSJADLDFSTEHKLDPVFDSSRRSKRSLRLATTACTLGD GEBVAQABSGTSAVSKURBARTTKORSTINSFOLVSHINGTVA ALSSSYSJADLDFSTEHKLDPVFDSSRRSKRSLRLATTACTLGD GEBVAQABSGTSAVSKURBARTTKORSTINSFOLVSHINGTVALLAV ALSSSYSJADLDFSTEHKLDPVFDSSRRSKRSLRLATTACTLGD GEBVAQABSGTASVSKORADAIDFTSEKVFLVLLTFEHLDK ACASYFLLGILRRIGAVGAVSRTAWSALMLAVVAPGRASOVF WILLGWYGPVFLISHLAVFLTTRCHRICKFRULLTPELLG LDGLKSGRAADAGGAGAGFSAVKORDSLSGCCHHERSILRETHLYKGL LDGLKSGLKSBLSSWRIVKTGCETVDAVQREMVKLLPSD QQGSLBQLLQRPSSQFVSKGDLGVVLISMIHTHAATTLEHPKTLSP VUOPDITFGRAVVSAVSBAGASGITEAQARATVARAKLYSGDKTG VUOPDITFGRAVVSAV				
BEEVLPDOVEREERNDDOERDEREDDUEDDERERRWGPFSTO ORSPTANARLLAGKRGALGSSAWOVSBYDTPP\LCRMPR SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL \(\) SCOVGS\GNCSNSSSNPRGALLGARGSL\(\) L\(\) L\(\) L\(\) COVGS\GNCSNSSSNPRGALLGARGSL\(\) L\(\) L\(\) L\(\) L\(\) C\(\) L\(\) C\(\) SCOVGS\GNCSNSSSNPRGALLGARGSL\(\) L\(\				
ORSPTARNARLIA, OKROALOGS AND VASED VIND TEV LORMER SRPRTPARE MLENDYDTUT FEW KDVL JORGE BESTCK \TDTLGE \(\) SCGVGS \(\) CONCONSSISSINFRAP LEARGS LH \(\) CL \(\) KTGLOLF \(\) SHQET END SAMAPRERGGGIST FLOCERNINHET TYTELRING \(\) SHQET END SAMAPRERGGGGIST FLOCERNINHET TYTELRING \(\) REAL CONCONSTRUCTION OF THE MARKET ALL ALL ALL ALL ALL ALL ALL ALL ALL AL				
SRPRTPAELMLENDTHVITWITWITLEORLEPSTCK \TDTIGGL \scorgs \successionsamaprergaptleagely \dignition_incole \text{AGORISMS_SINGERGAPTLEAGELY \dignition_incole \text{AEKAGY_TOSAKRAQERMSATSPETYTECFRNNDHPETTYRIRNDS} NFALQTMEPALPMPYVEELDVMFSELVDELDLIDENDARKSLIAL \text{EEEEERSKTIESLENGTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEERSKTIESLKTALRTKPMFYTRFIDLOGLOSMARKSLIAL \text{EEEERSKTIESLATHTIOMTYCKSCAUCH \text{EEEERSKTIESLATHTIOMTYCKSCAUCH \text{EEERSKTIESLATHTIOMTYCKSCAUCH \text{EEERSKTIESLATHTIOMTYCKSCAUCH \text{EEERSKTIESLATHTIOMTYCKSCAUCH \text{EEERSKTIESLATHTIOMTYCKSCAUCH \text{EEERSKTIESLATHTIOMTYCKSCAUCH \text{EEERSKTIESLATHTIOMTYCKSCAUCH \text{EEERSKTIESLATHTIOMTYCKSCAUCH \text{EEERSKTIESLATHTIOMTYCKSCAUCH \text{EEERSKAU				-
SCOUGS \ CNCSNSSSSNPRGAFLLEARGSLH\CI_XTGLOLE 6017 203 3469 SHØRIEQNSAMAPRKRGKGKSFIFCGFRNNDPEITYTLRNDS NPALQTWEPALPMPYBELDVMFSELDVLDELDLTDKHEAMFALP AEKKNQIYCSKKKOQERNKARTSWEFYIDQLUSSMARKSLLAL EKEBEBERSKITESLKTALTKPMFFYTEDLDGLSCILTHAL TIMDYBTSESRIHTSLIGCKALMINSGGRAHVLAHESINVIAG SLSTENKKTKVAURBILGAUCLVPGGHKKULQAMLHYOKYASER TRFOTLINDLDKSTGRYRDBUSLKTALMSFINAVLSGGAOVESL DFRIHLRYB\FIMLGIHPVMDKLRKHENSTLDHLDFFMLEND BELSFARRFEIJHDITSSATQMFELTSKRIJTISBRYPHFMSILH HCLQMPYKRSGMTVQYMLLDRIIQQIVJQNNKGGDESTPLEM FNIKNVVRHUVSENEVQWKEQARMKREKENBLQQKLEKKERSC DAKTQEKEBMMQTLNKKEKLEKSTTEHKQVKQQVADLTAQLHE LSFRAVCASI PGGSPPSOKGEGARMKEKENBLQQKLEKKERSC DAKTQEKEBMMQTLNKKEKLEKSTTEHKQVKQQVADLTAQLHE LSFRAVCASI PGGSPPSOKGEGARMKEKENBLQCKLEKKERSC ONCNILLSRLKSFNWSKLPENKLEGTVWTEIDDTKVKLEVIDPPPPPLPGG PTNALKSFNWSKLPENKLEGTVWTEIDDTKVKLEVIDPPPPPLPGG ONCNILLSRLKSFNWSKLPENKLEGTVWTEIDDTKVKLLEVIDERRA ONCNILLSRLKSFNWSKLPENKLEGTVWTEIDDTKVLAFGNYMN KGQRGNAYGFKISSINIADTKSSIDENIHQQRIQGLIFVFKE KEDIDLLEEKHELDRAADPFFFERSHYQQRIQGLIFVFKE KERBRVABUVRFKVSAIBSGSEBVFRSGALKQLLEVVLAFGNYMN KGQRGNAYGFKISSINIADTKSSIDENIHQQRIQGLIFVFK KFARRVABUVRFKVSAIBSGSEBVFRSGALKQLLEVVLAFGNYMN KGQRGNAYGFKISSINIADTKSSIDENIHQQRIQGLIFVFKE SVALINBELEDIPQAAVVNMTELBEISTLRSGLKAVETELEYQ KSQPPQFGDKVSVWSQFTTVASFSFSDVEDLLABARGDLIFTKAV KHGERAGKIOPDEFGIFDGPLGAVSEARQENEMMKKKEEEE RRAMMEQLKGGREREKMRAKENSESGEFDDLVSALRSGEV TISGSGGIRRREBAWFEVVNNDFSREHFMYSPGCVPENTGTYT ALSSSYSBADLPFTEHKLDPVFDSPBRERSLLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSCVSYGGTVSLQDAVTRRSPVLDBSWIRRGTTVDHFWGLDDD GDLKGGRKAAIQGNGDVGAQAATCHNOFFCSNCMILSERGDVLT AHPAADGPVSRVSRDRNQKCDDCKGRRHLDAHDGRGTMHIM ACAGYFLLGLIERIGAVGGAVSTRMSSAUAVAPGKAASGVF WLGIGHYGPVSRVSRDRNQKCDDCKGRRHLDAHDGRGTMHIM ACAGYFLLGLIERIGAVGGAVSTRMSSAUAVAPGKAASGVF WLGIGHYGPVSRVSRDRNQKCDDCKGRRHLDAHDGRGTMHIM ACAGYFLGLIERIGAVGGAVSTRMSHAUAVAPGKAASGVF WLGIGHYGPVSRVSRDRNQKCDCTGRTDTMFRHEDU LLQAKVOMBGGAAGGSASVROAVGOPRETDTMAFTGEHEVENS HLEDIIGKLERESSARIKUKGCETVDAVGSRVDLOQUFTCPTTSRLKQ LLQAKVOMBGGAAGGSASVROAVGOPRETDTMAFTGEHEVENS HLEDIIGKLERESSAIRIKSTGCSTYTSKTALBGLGGTLYFFHLUFTLL				1
SHOPT 203 SHOPT SHOPELDWAYS THE CURNINDER TYPILINDS NPALOTWERD AND PROPELDWAYS THE CURNINDER TYPILINDS NPALOTWERD AND PROPER DOWN STEP TO COLOR MARKAGING ARK WOLLD A	1			
NPALQTMEPALPMPVEELDVMPSELVDELDLTDKHREAMFALP AEKKNQIYGSKKROGENKGATSWPEFYIDQLAMAARKSLIAL EKEBEBERSKITISLIGGIKALHANNSOGRAHVLAHGESINVIAQ GLSTENLKTKVAVALEILAGAVCLVPGGAHVLAHGESINVIAQ GLSTENLKTKVAVALEILAGAVCLVPGKVAQAMLHVGKYAGER TRFQTLINDLDKSTGRYRDEVSLKTAIMSFINAVLSQGAGVESL DFRHILRYRF, FUMLGIHFVMDKUKKENSTLDRHIJDFFEMLKNE DELEFAKRFEJVHIDITSATOMETLRKKLOTHSBAYPHMSILH HCLQMPYKRSGNTVQYWLLLDRIIQQIVJONDKGQDFDTPLEN FNIKNVAMIAVENSEVKOMKEQABKMRKKHENGLOKUKKEREC DAKTQEKEEMMQTLNKMKEKLEKSTTEHKQVKQQVADLITAQLHE LSRRAVCASIFGGSFGAFGGFFFSSVGSLLPPPPPPPDPPDFDGAPFDPPPPPPPPDPPPDPPPDPPPDPPPPDP	6017	203	3469	
ARKWQLYCSKKHODERNGATSWPEPYIDQIMSMARKSLIAL EKEEEERSKTIESLKTALRTKPMFVTFIDLDGLSCILNFLK TMDYETSESRIHTSLIGGIKALMNINSQGRAHVLAHSSINVIAQ SLSTENIKTKVAVLBILGAVCLVPGGHKKVLQAMLHYQKYASER TRFOTLINDLDKSTGYRDEVSLKATMSPINAVLSQGAVESL DPRHLRYRKPLWIDTKSATQMPELTRKRLTSBAPHPMSILH HCLMPYKRSGNTVQYWLLLDRIIQQIVIQMDKGQDPDSTPLEN- FNIKNVVRMLVWENEVKQWKEQAEKMRKEHBELQQKLBKKEREC DAKTQFREBMMYTLKMKKEKLEKSTRUTGGALVIQALVALGALBER FNIKNVVRMLVWENEVKQWKEQAEKMRKEHBELQQKLBKKEREC DAKTQFREBMMYTLKMKKEKLEKSTRUTGGALBALGALGALBER FNIKNVVRMLVWENEVKQWKEQAEKMRKEHBELQQKLBKKEREC DAKTQFREBMMYTLKMKKEKLEKSTRUTGQLIVQKOKLAGLEGE DAKTQFREBMMYTLKMKKEKLEKSTRUTGQLIVQKOKLAGLEGE LSPRPPELPGGDPPPDPPLGA HOVYGVALDLITGLHE LSRRAVCASIPGGBFPSSVPGSLIPPPPPPLPLGGM LPPPPPPLPFDGGPPPPPPPPPPLAGHOVAGVAGLAGLISVTKK PARVASKALPENKLEGTVWTEIDDTKVFKILDLEDLERTF SAYGRQDFFVNSKKQEADAIDDTLSSKLKVELSVILDGERA QNCNILLSRKLKINDE IKRAILTMDEGEDLERMLEGLKFYPE KSDIDLLEBEKHBLDRMAKADRFLFFMSRINNYQQRLQSLYFKK RPARVASVFKVEAIRSGSEEVFPSSDVEDLLAEAKDLLEVLKFYPE KSDIDLLEBEKHBLDRMAKADRFLFFMSRINNIYAGRV KSQRGNAYGFKISSINKIADTKSSIDKNITILHYLITIVENKYP SVLMINBELRDJDPTGAAVNNTELDKSISTLASGIKAVETELEYQ KSQPQGGKYSVVSQPITVASFSSDVEDLLAEAKDLFTKAV KHFGERAGKIQPDEFFGIFDOFLQAVSEAKQENENMFKKKEEEE RRAMREAQLKBGREERERMRAKAENESGEFDDLVSALRISGEV PDKDLSKLKRNNRRITNOMTDSSREPPITKLMP ALSSYSDADLDFETEHKLDPVTDSFRRSRSLELATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKGRSTNKSAFSINNYSRQV TSGVSYSGGTSSLQDAVTRRPPVLDESREFDTLUTLDFKLDD GDLKGGKAAAIGONGDVCAGAATGHNGFFCSNCOMLSERRDVLT AHAPAFGVVSRVYSRORNQKCDDCKGKRHLDAHPGRAGTLMHIW ACAGYFFLIGILRRIGAVQAVSRTAWAALMLAVVARGKAASGVF WWLGIGMYOFVTLISHLAVFLLTRCLRNICKFLUYLLIPFTRLKQ PLQGDSSAFFWHMSGVEQOVASLSGGCCHHIGERLRELTTLLQK LQGDSSAFFWHMSGVEQOVASLSGGCCHHIGERLRELTTLLQK LQGDSSAFFWHMSGVEQOVASLSGGCCHHIGERLRELTTLLQK LQGLGSGAFFRENGERGARGFFGSSGCCHHIGERLRELTTLLQK LDGLGGSGAFFRENGERGARGFFGSSGCCHHIGERLRELTTLLQK LDGLGGSGAFFRENGERGARGFFGSGCCHHIGERLRELTTLLQK LDGLGGSGAFFFRENGERGARGFFGSGCCHHIGERLRELTTLLQK LDGLGGSGAFFFRENGERGARGTGAGGTCHAGARATVNSALKLYSGDKT MYDFALESGGGSILVARSSGFGYLVVALSHMIHPAFFTLEHIPKTL SPTGNISSAPKDFAVGLERGYGGEGLLGGFTYDQDGSSLQMF VUQPDIYBGNARKGSGGYLVVALSH	1			
EKEEEERSKTISSLKTALRTKPMFFYTRETDLDGLSCILNFLK TMYYETSERRIHTSLIGCIKALMINNSQRAHVLAHSESINVIAQ SLSTENIKTKVAVLEILGAVCLVPGGHKKVLQAMLHYQKYASER TRFOTLINDLDKSTGRYRDEVSLKTAIMSFINAVLSQGAGVESL DFRIHLRYEY FLMG. HPWMDKLERNSTLDRHIDPFEMLENE DELEFAKRFELVHIDTKSAATQMFELTTKRLTHSEAYPHMSILH HCLQMPYKRSGNTVQVWLLLDRIIQQIVLODKSQOPDSTLEN- FNIKNVVRMLVNENEVKQMKEGARMKEENELQQKLEKKEREC DAKTQEKEEMMQTINNKKSKLEKETTEHKQVKQQVADLTAQLHE LSRRAVCASIPGGSPGAPGGGPSYGSLDPPPPPPPDLPGGM LPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP		•		
THDYETSESRITISLIGICKALMINISGGRAVULAHSESINUTAQ SLSTENIKTKVAVLE ILGAVCLVPGGKKVLQAMLHYQKYASER TREQTLINDLDKSTGRYRDEVSLKTAIMSE INAVLSQGAGVESL DFRIHLRYB FLMIG HPYWDKLRKHRISTIDHILDPEMILRIB DBLEFAKRFELVHIDTURSATOMPHITKRITHSBAYPHMSILH HCLQMPYKRSGNTVQYWLLLDRI IQQIVIQNDKGQDPDSTPLEN- FINIKNVVRIMENEVKQWKEQAEMMKERIBLQQKUBKKRECE DAKTQEKEEMMQTILMKMKKKLEKETTERKQVKQQVADLTAQLHE LSRRAVCAS I PGGPSPGAPGGPFSSVPGSLLPPPPPPPLPGGM LPPPPPPPPPPPPGPPPPPGPPPPLGAIMPPPGAPMGLAKKKSIPQ PTINALKSFINSKLPENKLEGTVWTEIDDTKVPKILDLEDLERTF SAYQRQODFFVNSNSQKEADAIDDTLSSKIKVKELSVIDGRA QNCNILLISRIKLSNDEIRRAILTMOEDDLEPKDHECLLKFVPE KSDIDLLEEHKHELDRMAKADRFLFEMSRINHYQQRLQSLYFKK KFABRVAEVKFKVEATRSGSEVFRSGALKQLEVVLAFGNYMN KGQRANAFGKISSINKIADTKSSIDKNITLLHYLITIVENKYP SVLININESLADIPOAKVMWTELDKEISTLRSGLKAVETELBYQ KSQPPPOPDKYSVVSQFITVASFSFSDVEDLLAEAKDLFYKAV KHFGERAGKUPDEFFGIPDGFLQAVSBAKQENEINMRKKEEEE RRAMMEAQLKGQREREKMRKAKENSESSGEDDLVSALRSGEV PFOKDLSKLKRNINKTINNOMTOSBERPITKLNP 6018 13 2510 TISQSGGIRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY ALSSSYSDADLDFETHKLDPVFDSPRINSRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRSTNINSASFINIVSRGV TSSGYSYGGTVSLQDAVTRRPPVLDESWIERGTTVDHFFGLDDD GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT AHPAAPGPVSRVYSRDRIQKCDDCKGRRHLDAHPGRAGTLHHIM ACAGYFLLQILRIGAVGQAVSTRWSALMAVAPGKAASGVF WILGIGMYQFVTLISHNINFLITKCLKNICKFLVLLIPLLLIG LSLRQGQNFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSRAFFWHMMSGVSQQVASLSGQCHHHAGNIERELITTLQK LQARVDOMGGGAAGPSASVDLAVGPPRETDFMAPRGEEUVMS HLEDILKKLRKSEAIQKSGCSYGKGTSAVGROTLSPLFLLQLE LOAKVDOMGGGAAGPSASVDLAVGPPRETDFMAPRGEEUVMS HLEDILKKLRKSEAIQKSGCSTRVKAGTSAVGROLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQUREMVKLLFSED QQGGSLEQLLQRFSSGFVSKGDLQTMURDLQLQLIKNVTHHYSV TKQLPTESAVVSAVSBAGASGITEAQARATVNSALKLYSGOKTG WDFALESGGGSLILGTRCSTYFTKTALMSLFGILDWTYSOLSPR VVIQPIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAFKDFAVYGLERIFSNWGPETTCLYPRFVGGESULMF QALKEPDDTAFGIUELRIFSNWGPETTCLYPRFVGGESULMF QALKEPDDTAFGIUELRIFSNWGPETTCLYPRFVGGESULMF QALKEPDDTAFGIUELRIFSNWGPETTCLYPRFVGGESULMF]			· · · · · · · · · · · · · · · · · · ·
SLSTENIKTKVAVLELIGAVCLVPGGHKKULQAMLHYQKYASER TRYQTLINDLDKSTGRYRDEVSLKTAIMSPINAVLSQGAGVESL DFRHLRYB\FLMGIHPYMDKIKRHENSTLDRHLDFFFMLENE DELEFAKRFELVHIDTKSATOMFELTRKRITHSEAVPHYMSILH HCLOMPYKRSGNTVQWALLDRI\QQIV\QNDKGQDDGSTPLEN- FNIKNVVRMLVNENEVKQWKEQABKMRKEHNELQKLEKKEREC DAKTQEKEEMMQTLANKMEKKEKEKTEHKKYVKQQVADLITAQLHE LSRRAVCASIFGGFSGAFGGFPSSYPGSLLPPPPPPLPGGR LPPPPPPPPPPPPGGPPPPGPPPGSPPPGGAPMGGLALKKKSIPQ PTMALKSHNWSKLPMKLEGTVWTEIDDTKYPKILDLEDLERTF SAYQRQDFFVNSNSKQKEADAIDDTLSSKLKVKELSVIDGRRA QNCNILLISRLKLSNDEIKBAITHTEOGDELFKMLEGCLLKFVPE KSDIDLLEEHKHELDRMARADFJFEMSRINHYQGLQSLYFKK KFABRVAEVKPKVEATRSGSEVFRSGALKQLEVVLAFGNYMN KGQRGNAYGFKISSLNKIADTKSSIDNITLHYLITIVENKYP SVLMINBELRDIPQAAKVMYTELDKEISTLRSGLKAVETELEYQ KSQPPGGDKFVSVVSQFITVASFSFSDVEBLLAEAKDLFTKAV KHIGGERGKAPPFGFITDGPLAAVSEAKQEENMRKKKEESE RRAMMEAQLKGQRERRKMRKAKENSESGEPDLVSALRSGEV FDKDLSKLKRNRKRITNQMTDSSRERPITKLNP 13 2510 1159SGGIRRRERAWFEVVMIDDFSRHMSRPSCVPENTGYTY ALSSSYSDALDFETHHKLDPVFDSPRNSRRSLRLATTACTLGD GEMVADAGGTSSAVSUKDRAARTINGFTCOKRSTINKSAFSINIVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGRKAAIQGNGDVGAGAATCHNGFFGSNCMMSERKDVLT AHPAAPGPVSRVVSRRNRKGLTGRSTINKLSRGV WHLGIGWYQFVTLISWLNVFLLTRCINCICKFLVLLIPLFLLLG LSLRQQ\NFFSFLPVLWASMHRTQRVDDPQDVFRPTTSRLKQ PLQGDSSAFFWHMMSGVEQQVASLSGQCHHHGENLEELTTLLQK LQARVQDMGGGAAGPSASVADAVGPRETDFMAFRGLEIEVMS HLEDILKELEKSEAIQKKGGCFTVDAVQERVDVQREMVKLIFSED QQGSLEQLLGRFSSGFVSKOBLOFTCTDARATHGLEIEVMS HLEDILKELEKSEAIQKSLSGCTTRVARATGLEIEVMS HLEDILKEKSEASLSVRSHKTGCETVDAVQERVDVQYREMVKLIFSED QQGSLEQLLGRFSSGFVSKOBLOFTLENDLLQLLGILKNVTHHYSV TKQLPTESAVVSAVSBAGASGITEAQARATVNSALKLYSODKTG MYPFALESGGGSLLGRTSCTSTETKTRALMSLFGLEUTWINS HLEDILKERSGESLEGRTGRTSTRAARATUNSALKLYSODKTG MYPFALESGGGSLILGRTSCTSTFETKTALMSLFGLEUTWINS HLEDILKERSGEAIGHTENGFGCGCLGTTPLORGETQMF VVIQPITYPGNCWAFKGSGGYLVVRLSMMHPAAFTLEHIPKTL SPITNISSARKDPAVYGEEGGLLGGTTQAGTTJAUTSSLQFT QQGGSLEQLLGRTSSSGFVSKOBLOGTTNADAGGTTMYGESLQMF VVIQPITYPGNCWAFKGSGGYLVVRLSMMHPAAFTLEHIPKTL SPITNISSARKDFALTERIFSWERGETGCTTFTTETKTALMSLAGLGGTTM				
TRFQTLINDLDKSTGRYRDEVSLKTAIMSFINAVLSQCAGVESL DFRLHRYB\PLMIGIHPYMDKLRKHENSTLDRHLDFPEMLRNE DELEFAKRFELVHIDTKSATQMFELTRKRLITHSEAYPHFMSTLH HCLQMPYKRSGNTVQYWLLLDRIIQQIVIQNDKGQDPDSTPLEN FNIKNVURMLVNHEVNEMEVQKWEQARKHKEHBELQQKLEKKEREC DAKTQEKEEMMQTLNKMKEKLEKSTTEHKQVXQQVADLTAQLHE LSRRAVCASIJGGGSGCAFGGPFFSSVPGSLIPPPPPPPPPPPPLPGGM LPPPPPPLPFGGGPPPPPGPPPPLGAIMPPPGAPMGLALKKKSIPQ PTNALKSFNMSKLPENKLEGTVWTEIDDTKVFKILDLEDLERTF SAYQRQDFFVNNSKQKEADAIDDTLSKKLKVKELSVIDGRRA QNCNILLSRLKISNDEIKRAILMDEGEDLPKDMLEQLLKFVPE KSDIDLLEEHKHELDRNAKADRFLFEMSRINHYQORLOSLFYKK KPABEVAPVRVEVVZAIRSGSEEVFRSGALKQLLEVVLAFGNYMN KGQRGNAYGFKISSINKIADTKSIDKNITLHYLITIVENKYP SVLANLMEBLRDIPQAAKVNNTELDKEISTLRGGLKAVETELEYQ KSQPPOPDGKVSVVSOFITVASFSDVEDLLAERKDLFTXAV KHFGEAGKIQPDEPFGIFPOFLQAVSEAKQENEMMRKKKEEEE RRAMMEAQLKEQREREKMRKAKENSEESGEFDDLVSALRGGEV FDKDLSKLKRNRKRITMQMTDSSRENPITKLMP 6018 13 2510 TISQSGTRRREAWWEVVNMDPSRLHMYSPPQCVPENTGYTY ALSSSYSSDALDFETEHKLDPVFDSSPRMSRRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTIKQRRSTNNSAFSINHVSRQV TSSGYSYGGTVSLQDAVTRRPPVLDESBYREQTTVDHFWGLDDD GDLKKGNKAAIGORGDVGAGAATGHNGFFCSNCUMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLGILRRIGAVGQAVSRTAMSALMLAVVAPGKAASGVF WILGIGWYGPVITISHINVPLITCKRNICKFYLULIPJEFLLG LSLRGQGNFFSFP.PPLIMMASMMRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGCCHHHEENLRELTTLLQK PLQGDSEAFPWHWMSGVEQQVASLSGCCHHHEENLRELTTLLQK LARNDOMGEGAAGPSASVENDAGQPPRTDPMAPHQEHEVMS HLEDILGKLSELSWRIVKTGCETVDAVQRRVDVQVREMVKLLFSED QQGGSLBQLLQFFSSQFVSKGDLQTMIRDLQJCILRNYTHHVSV TKQLPTSEAVVSAVSBAGAGTTEAQARAIVNSALKLYSQDKTG WDFPALSBGGGSILSTRCSSTYSTKTALMSLSGIPLWYFSGSP WVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTENISSAPKDFAVYGLENEYQEEGGLLGGPTYDOGGESLQMF VVIQPDIYPGNCWAFKGSGGYLVVRLSMMIHPAAFTLEHIPKTL SPTENISSAPKDFAVYGLENEYQEEGGLLGGPTYDOGGESLQMF QALKRPDTAFGIPULERIFSNMGHPSYTCLVERFRHGEDVK	i			
DPRILIARYS\FIMIGIHPVMDKLRKHENSTLDRHLDPPMLRNE DELEFAKRFELVHIDTKSATQMFELTRRLITHSEAYPHMSILH HCLQMPYKRSGNTYQYMLLIDAIIQQIVIQNDKGQDPDSTPLEN FNIKNVVRMLVNENEVKQWKEQABKMRKEHNELQOKLBKKEREC DAKTQEKEMMQTLINKMKEKLEKBTTEHKQVKQWADLTAQLHE LSRRAVCASIBGGSPGAPGGPFSSVPGSLLPPPPPPPLPGGM LSPRAVCASIBGGPPPSPGPPLGAIMPPPADAMGLALKKKSIPQ PTNALKSFNM9KLPNKLEGTVWTEIDDTKYFKILDLEDLERTP SAYQRQDFFVNSNSKQKEADAIDDTLSSKLKKKSLEVLDGRRA QNCNILLSRLKISNDEIKRAILTMDEQEDLFKDMLEGLLKFVPE KSDIDLLEEHHELDDRAKARDRIFBMSRINHYQORLOSLYFKK KFAERVAEVKPKVEAIRSGSEEVFRSGALKQLLEVVLAFGNYMN KGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP SULNILNEELRDIPQAAKVNTEURSITSTRSCIKAVFTEELY XSQPPOPGDKFVSVVSGPTVASFSFSDVEDLLAEAKDLFTKAV KHFGEEAGKLQPDEFFGIFDQFLQAVSRAKQENEMMRKKEEES RRARMEAQLKEQREREKMRKAKENSEESGEFDDLVSALRSGEV FDKDLSKLKRNRKRITMOMTDSSREPPITKLMP 6018 13 2510 TISQSGGIRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY ALSSSYSSDALDFTEIRKLDPVDSFRMSRRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGKKAALQGNGDVGAGAATGHNGFFCSNCNNLISERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKKKRHLDAHFGRAGTLMHIW ACAGYFLLOILRRIGAVGQAVATRAPAUDPOPDVFRFTTSLLQQ WWLGIGWYGVTLISWLNVFLITRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFIPVLNWASMHRTQRVDDPQDVFRFTTSLLQQ PLQGGSEAFFWHMSGWCQQVASHOKRENELTTLLQQ LQRSCRFFFIPVLNWASMHRTQRVDDPQDVFRFYTTSLLQQ LQRGSLBQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHVSV TKQLFTEEAVVSAVSEAGASGTTEAQARAIVNSALKLYSQDKTG PLAEBSGGGSILSTRCSSTYTKTALMSLEGILHYFSGSP VVIQPTYPEBOVGANSVSEAGASGTTEAQARAIVNSALKLYSQDKTG PLAEBSGGSILSTRCSSTYTKTTALMSLKGILLQFTLYDQGESLQMF VVIQPDTYPGROWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTENISAPKDPAVTGLENEYQEEGGLLGGTTYDGGESLQMF VVIQPDTYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTENISAPKDPAVTGLENEYGEGGLEGGTTHGDESLQMF				
DELEFAKRPELVHIDTKSATQMPELTRRKLTHSBAYPHFMSILH HCLQMPYKRSGNTVQYWLLLDRIIQQIVIQNDKGQDPDSTPLEN FNIKNVVRMLVNENPVKQWKSQABKMRKEHBELQQKLEKKEREC DAKTGEKEBMMQTLNKMKEKLEKETTEHKOVKQQVADLTAQLHE LSRRAVCASIPGGPSPGAPGGPFPSVYPGSLIPPPPPPPPPGGP LPPPPPPPPPPPPPPPPPPPPPPPP				· · · · · · · · · · · · · · · · · · ·
HCLQMPYKRSGNTVQYWLLLDRIIQQIVIQNDKGQDPDSTPLEN- FNIKNVVRMLVNENEVKQWKEQAEKMREHNELQQKLEKKEREC DAKTQEKEEMMQTLINKMEKLEKETTEHKOVQGVADLTAGLHE LSRRAVCASIPGPSPGAPGGPFPSSVPGSLLPPPPPPLPGGM LPPPPPPPPPPPPGPPPPPGPPPPGP				
FRIKATVZMŁUNENEVKOWKEQABKMRKEHNELQOKLEKKEREC DAKTQEKEMMQTILKMKEKLEKKITEHKQVKQUADLITACLHE LSRRAVCASI PGGPSPGAPGGFPSSVPGSLIPPPPPPPLPGGM LPPPPPLPPGGPPPPPGPPPLGAIMPPPGAPMGLALKKKSIPQ PTNALKSPNWSKLPENDAIDDTLSSKLWYEKSUTOGRA QNCNILLSRLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFVPE KSDIDLLEEHKHELDRMAKADRFLFEMGRINHYQQRLQSLYFKK KPAREVABEVKPVEAIRAGSEEVFRSGALKQLLEVVLAFGYMM KGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP SVININBELRDIPQAAKVNMTELDKELSTLRSGLKAVETBLEYQ KSQPPOFGDKYSVVSQFITVASFSFSDVEDLLABAKDLFTYAV KHFGEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKKEEEE RRANNEAQLKEQRERERKMRKAKENSESGFDDLVSALRSGEV FDKDLSKLKRNKRKITNOMSTSREPITKLMP 6018 13 2510 TISQSGIRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY ALSSSYSSDALDFTEHKLDPVFDSPRMSRRSLRLATTACTLGD GEAVADSGTSSAVSLKNRATTYORRSTKKSAPSINHVSQQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNXAALQGNGDVGAGAATGHNGFFCSNCNNLISERKDVLT AHPAADGPVSRVSRDRNGCDDCKGRKHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVQQAVSRTAWSALMLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLIRNICKFLVLLIFLFLLIG LSLRQGQ\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSAFFWHWMSGVEQQVASLSGQCHHGGENLRELTTLLQK LQARVDOMEGGAAGPSASVRDAVGQPPRETDFMAPHQEHEVRMS HLEDILGKLREKSBAIQKELEGYTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRIVKTGCETVDAVQEREVDVQVREMVKLLFSED QGGSLEGLLQRFSSPFVSKGDLQTMLRDLQLQILRNYTHHYSV TKQLPTSEAVVSAVSAGASGITEAQARAIVNSALKLYSQDKTG MVDFALBSGGGSILSTRCSETYETKTALMSLFGIPLWTFSGSPR VVIQPDIYPGNCWAPKGSGGXLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGSSLQMF VVIQPIYPGNCWAPKGSGGSTLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGGLLGGFTYDQDGGSLQMF VVIQPIYPGNCWAPKGSGGGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGGLLGGFTYDQDGGSLQMF VVIQPIYPGNCWAPKGSGGGTLGTTTRRVHGEPVK	ļ			-
DAKTQEKEEMMQTLNKMKEKLEKETTEHKQVKQQVADLTAQLHE LSRRAVCASIPGGPSFGAPGGPFSSVPGSLLPPPPPPPPLGGM LPPPPPPLEPGGPPPPPGPPPLGAIMPPPPPPPLBGGM LPPPPPPLEPGGPPPPPGPPPLGAIMPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP				1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
LSRRAVCASIPGGPSPGAPGGPPPSSVPGSLLPPPPPPLPGGM LPPPPPLPPGGPPPLPGGPPPLASIMPPGARAPMGLALKKKSIPQ PTNALKSRNWSKLPENKKLEGTVWTEIDDTKVFKILDEDLERTF SAYQRQODFFVNSNSKQKEADAIDDTLSSKLKVKELSVIDGRRA QNCNILLSRLKLSNDEIKRAILTMDEGCDLPKDMLEGLLKFVPE KSDIDLLEBKHKELDTMAKDRFLFENSRINHYQQRLGSLFKK KFAERVAEVKPKVEAIRSGSEEVFRSGALKQLLEVVLAFGNYMN KGQRGNAYGFKISSINKIADTKSSIDKNITLLHYLITIVENKYP SVLINLMEBLEDIPQAAKAVMTSELDKBISTLRSGLKAVETBLEYQ KSQPPQPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV KHFGERGKIQPDEFFGIFPQFLQAVSEAKQENENMRKKKEEEE RRAMEAQLKEQRERERKMKAKENSESGEFDDLVSALRSGEV FDKDLSKLKRNRKRITNQNTDSSRENPITKLNF 6018 13 2510 TISGSGIRRREEAWFEVVNMDFSRLHMYSPPQCVPENTGYTY ALSSSYSSDALDFETHKLDPVFDSPRMSRRSLRATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRSTINKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCMLSERKDVLT AHPAAPGPVSRVYSRPRNQKCDDCKGKRHLDAHFGRAGTLHHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVILISWLNVFLLTRCLRNICKFDVLLTPLFLLLG LSLRGQG\NFFSFLPVLNNASMRTORVDDPQDVFFTSSLKQ PLQGDSEAFFWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHGEHEVMS HLEDILGKLREKSFAJGLEQFKYGKISAVGELLPTVEHHLGL LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHGEHEVMS HLEDILGKLREKSFAJGLEQFKYGKISAVGELLPTWFHSUSY TKQLPTSEAVVSAVSBADASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILGTLCSETYETKTALMSLFGIPLWFFSQSPR VVIQPDIYPGNCWAFKGSGGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLEERYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNNGHPBYTCLYRTRVHGEPVK	į	,		
LPPPPPPLFPGGPPPPPGPPPLGAIMPPPGAPMGLALKKKSIPQ PTNALKSFNWSKLPENKLEGTVUMTEIDDTKVFKILDLEDERTTF SAYQRQODFFVNNSKQKADAIDDTLSKLKVKELSVIDGRRA QNCNILLSRLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFVPE KSDIDLLEEKKHELDRMAKADRFLFEMSRINHYQQRLGSLYFKK KFAERVAEVKPKVEAIRSGSEVFRSGALKQLLEVVLAPGNYMN KGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP SVLNILNEELRDIPQAAKVNMTELDKEISTLRSGLKAVETELEYQ KSQPPQPGGKFVSVSVGFITVASFSFSDVEDLLAEAKDLFTKAV KHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMEKKEEEE RRARMEAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV FDKDLSKLKRNRRRITMQMTDSSRERPITKLNF 6018 13 2510 TISQSGGIRRREAVEVNMDFSRLHMYSPPQCVPENTGYTY ALSSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAIQCNGDVGAGAATGHNGFFCSNCTMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQPVTLISHAVOPVLTRICKFULLIPLFLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPDDVFRPTTSRLKQ PLQGDSEAFFWHMNSGVEQQVASLSGQCHHHGENLRSLTTLLQK LQRAVDQMEGGAAGPSASVDDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGRQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQPVSKGDLOTMLRDLQLQILRNVTHHVSV TKQLPTSEAVYSAVSARGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSGSPR VVIQPDIYPGNCNAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLEREYQEEGQLLGQFTYDQDGESLQMF SPTGNISSAPKDFAVYGLUEREYQEEGQTLGGFTYDQDGESLQMF QALKRPDDTAFQTVELRIFSNWGHPEYTCLYRRFVHGEPVK				
PTNALKSFNWSKLPENKLEGTVWTEIDDTKVFKILDLEDLERTF SAYQRQDFFVNSNSKQKEADAIDDTLSSKLKVKELSVIDGRRA ONCNILISRLKLSNDE KRAILTMDEQEDLFKUMLEQLLKFVPE KSDIDLLEEHKHELDRMAKADRFLFEMSRINHYQQRLQSLYFKK KFAERVAEVKPKVEAIRSGSEEVFRSGALKQLLEVVLAFGNYMN KGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP SVLNILMEELRDIPQAAKVNMTELDKEISTLRGGLKAVETELEYQ KSQPPOPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV KHFGEEAGKIQPDEFFGITQFLQAVSEAKQENENMRKKEEEE RRARMEAQLKEQRERERKMRKAKENSESGEFDDLVSALRSGEV FDKDLSKLKRNRRRITMOMTDSSRERPITKLNF 6018 13 2510 TISGSGIRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY ALSSSYSSDALDFFTEHKLDPVFDSPRMSRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAATGINGFFCSNCNMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLMHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLG LSLRGQG\NFFSSLPVLNWASMHRTQRVDDPDDVFKPTTSRLKQ PLQGDSEAFPWHMMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGCPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELBQTKQKTISAVGRUPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQULQRFSSCPVSKGDLOTMLRDLQLQILRNVTHIVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSSTYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCNAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGGFTYDQDGESLQMF SPTGNISSAPKDFAVYGLENEYYGEEGQTLGGFTYTQDGGESLQMF CQALKRPDDTAFQTVELRIFSNWGHPEYTCLYRFRVHGEPVK	1			
SAYQRQQDFFVNSNSKQKEADAIDDTLSSKLKVKELSVIDGRRA QNCNILLSELKLSNDEIRRAILTMDEGGDLFKDMLEGLLKFVPE KSGIDLLEEKHRELDRMAKADRPLFEMSRINHYQQRLQSLYFKK KFAERVAEVKPKVBAIRGSSEEVFRSGALKQLLEVVLAFGNYMN KGQRGMAYGFKISSINKIADTKSSIDKNITLLHYLLTIVRNKYP SVLNLNEELRDIPQAAKVNMTELDKEISTLRSGLKAVETELEYQ KSQPPQPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV KHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKKEEEE RRARMEAQLKBQRERERMKRKKENSEESGEFDDLVSALRSGEV FDKDLSKLKRNRKRITNQMTDSSRERPITKLMY FDKDLSKLKRNRKRITNQMTDSSRERPITKLMY ALSSSYSSDALDFETEHKLDPVFDSPRMSRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREGTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT AHPAAPGPVSRVYSSRDRNQKCDDCKGRRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQPVTLISHLNVFLUTRCLENICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFFWHWMSGVSQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSAVRDAWGQPFETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEGTKQKTISAYGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGSLBQLLQFFSQFVSKGDLQTTHLDQLQLILRNVTHHVSV TKQLFTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSGGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDPAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNMGHPSYTCLYRFRVHGEPVK				· · · · ·
QNCNILLSRLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFVPE KSDIDLLEEKKHELDRMAKADRRIFEMSRINNYQORLQSLYFKK KFAERVAEVKPVKEAIRSGSEEVFRSGALKQLLEVVLAPGNYMN KGQRGMAYGFKISSINKIADTKSSIDKNITLLHYLITIVENKYP SVLNLMEELRDIPQAAKVNMTELDKEISTLRSGLKAVETELEYQ KSQPPOPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV KHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKEEEE RRARMEAQLKEQRERERKMRKAKENSESGEFDDLVSALRSGEV FDKDLSKLKRNRKRITNQMTDSSRERPITKLMP 13 2510 TISGSGGIRRREAVWFEVVMMPFSRLHMYSPPQCVPENTGYTY ALSSSYSSDALDFETEKLDPVFDSPRMSRRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAALQGMGDVCAGAATGHNGFFGSNCNMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQPVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\MFFSFLPVLNWASMHRTQRVDDPQDVFFPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRRVKTGCETVDAVQERVDVQVREWVKLLFSED QQGSLBQLLQRFSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSGGYLVVRLSMMIHPAAFTLEHTPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK				
KSDIDLLEEHKHELDRMAKADRPLFEMSRINHYQQRLQSLYFKK KFABRVAEVKFVEAIRSGSEVFRSGALKQLLEVVLAFGNYMN KGQRGNAYGFKISSINKIADTKSSIDKNITLHYLITIVENKYP SVINIMEELRDIPQAAKVNMTELDKEISTLRSGLKAVETELEYQ KSQPPQPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV KHFGEBAGKLQPDEFFGIFDQFLQAVSEAKQENEEMRKKKEEEE RRARMEAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV FDKDLSKLKRNRKRITNQMTDSSRERPITKLNF FDKDLSKLKRNRKRITNQMTDSSRERPITKLNF TISQSGIRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY ALSSYSSDALDFETEHKDPVFDSPRMSRRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAALQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLOILRRIGAVGQAVSRTAWSALMLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGGG\NFFSFLPVINWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFFWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFRGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEFVK			1	•
KFAERVAEVKPKVEAIRSGSEEVFRSGALKQLLEVVLAFGNYMN KGQRGNAYGFKISSINNIADTRSSIDRNITLIHYLITIVENKYP SVLNINEELRDIPQAAKVNMTELDKEISTLRSGLKAVETELEYQ KSQPPQPGKWSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV KHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKKEEEE RRARMEAQLKEQRERERKMRKAKENSEBSGEPDDLVSALRSGEV FDKDLSKLKRNRKRITNQMTDSSRERPITKLNF 6018 13 2510 TISQSGGIRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY ALSSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLFSED QQGGSLBQLLQDFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MYDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGGFTYDDQGGSLQMF QALKRPDDTAFQIVELRIFSNWGHPETTCLYRFRVHGEPVK	İ			
SVLNLNEELRDIPQAAKVNMTELDKEISTLRSGLKAVETELEYQ KSQPPOPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV KHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKEEEE RRARMEAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV FDKDLSKLKRNRKRITNQMTDSSRERPITKLMP 6018 13 2510 TISQSGGIRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY ALSSYSSDALDFETEHKLDPVFDSFRMSRRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGYSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALMLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRIVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHEYTCLYRFRVHGEPVK				
KSQPPQPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV KHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKKEEEE RRARMEAQLKEQREEERKMRKAKENSEESGEFDDLVSALRSGEV FDKDLSKLKRNRKRITNQMTDSSRERPITKLNF 6018 13 2510 TISQSGGTRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY ALSSSYSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAIQGMGDVGAGAATGHNGFFCSNCNNLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSER VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRYHGEPVK		,		KGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP
KHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKKEEEE RRARMEAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV FDKDLSKLKRNRKRITNOMTDSSRERPITKLNF 6018 13 2510 TISQSGIRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY ALSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCTMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFFWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTVDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK	1	,		SVLNLNEELRDIPQAAKVNMTELDKEISTLRSGLKAVETELEYQ
RRARMEAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV FDKDLSKLKRNRKRITNQMTDSSRERPITKLNF 6018 13 2510 TISQSGGTRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY ALSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCTMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVTLISNLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTTDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK	I]		KSQPPQPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV
FDKDLSKLKRNRKRITNQMTDSSRERPITKLNP 6018 13 2510 TISQSGIRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY ALSSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFFWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCTTVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHYSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGGFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK				KHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKKEEEE
TISQSGGIRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY ALSSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQLLRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGGLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK		·	,	RRARMEAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV
ALSSYSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERDVVQNEEMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK	L			FDKDLSKLKRNRKRITNQMTDSSRERPITKLNF
GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK	6018	13	2510	TISQSGGIRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY
TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK	I			
GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERDVVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK	1			GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV
AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK				_
ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK	[
WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLLRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK				
LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELBQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQLIRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGGSLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK				ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF
PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK	ļ			1
LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK	1			LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ
HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK				PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK
ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK				LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS
QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK				HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL
TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK				ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED
MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK				QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV
VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK				TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG
SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK				MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR
QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK				The state of the s
				SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF
6019 2 1066 TENNORED DODD DOCUMENT OF THE ART COLUMN				
1 1000 TENDREFFERRESSKKASHLAQETISAASEGDQTQTEGSETTA	6019	2	1066	TPNDREPPPQRPPSSRRASHLAQEITSAASLGDQTQILGSLTTA

SEQ	Predicted	Predicted end	I had no need a comment of the comme
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			PVITSAIRSMPGISSQILTNAQGQVIGTLPWVVNSASVAAPAPA
		i	QSLQVQAVTPQLLLNAQGQVIATLASSPLPPPVAVRK\PSTPES
			LLKSEVQPIKPTPTVPQPAVVIASPAPAAKPSASAPIPITCSET
			PTVSQLVSKPHTPSLDEDGINLEEIREFAKNFKIRRLSLGLTQT
			QVGQALTATEGPAYSQSAICRFEKLDITPKSAQKLKPVLEKWLN
l			EAELRNQEGQQNLMEFVGGEPSKKRKRRTSFTPQAIEALNAYFE
		ļ	KNPLPTGQEITEIAKELNYDREVVRVWFCNRRQTLKNTSKLNVF
			OIP
6020	4953	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
ļ		ļ	AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
İ	l		QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
	1		RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE
			EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
			GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVBKKFNSFAE
		•	GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
	,	•	FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
			GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
			AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
			LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR
			RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
		ı	TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
			YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
		,	NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
Ì			HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP
	· ·	·	QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVBCGGERV
1 .			ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
			FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
		,	DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV
	·		DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVABFEGLT
1			DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
			RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
		* -	KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
	·		TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
'		,	RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
			FEANKILHQHLGAPEERLALHILRTQGLVPBHVETRTLHSTFQP
			NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
			NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
			SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
]			PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
	,		KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
			LFVAVLLYSLPNYLSMKIVKPNV
6021	4953	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
			AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
]	}		QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
	ł		RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE
	.		EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
j i	İ		GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
	Į		GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
. <u> </u>	{		FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
			GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
		-	AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
]]			LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR
.			RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
		j	TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
	•		YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
			NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
			HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP
			QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV
			ESVVIKNLKKTPNPPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
			FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
			

	Dwodiato-	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:			H=Histidine, I=Isoleucine, K=Lysine,
1	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV
			DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT
1	1		DFSDTFKI,YRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
1		1	ROFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
1		1	KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
ļ.		1	TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
			RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
			FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
1	1		NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
			NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
			SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
			HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
i			PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
1			KLDLPNRPBTSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
			LFVAVLLYSLPNYLSMKIVKPNV
6022	4953	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
0022	4755	543	AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLOTNIEALKSGI
			OGKIPANOLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
1]	1
ŀ			RKLRSRSLSQIHEAAVRMRSEATDVKSTLABIEDWLDKLMQLTE
1	Į	}	EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
	į	-	GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
l	İ		GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
1			FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
I			GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
1			AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
	1		LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR
1			RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
1		1	TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
1			YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
1		1	NPPKVIMELFDNDOVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
1	į.		- ·
ŀ			HPVMNGDKACGDVLVTABLILRGKDGSNLPILPPQRAPNLYMVP
1			QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV
1		1	ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
1		1	FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
1	1	1	DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV
1			DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT
	1		DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
ì	1		RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
1			KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
1			TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
		1	RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
			FEANKILHOHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
1	1		NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
1		1.	NKOKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
1			NKQKTDVHYRSLDGEGNFNWRFVFFFDIDFAEQLCIVARREHFW SIDOTEFRIPPR\LIIOIW\DNDKFS\LDDYLGFPRTLTCRHTI
1 .	1		
1			HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
1			PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
ł			KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
			LFVAVLLYSLPNYLSMKIVKPNV
6023	102	916	SQELGMFVELNNLLNTTPDRAEQGKLTLLCDAKTDGSFLVHHFL
			SFYLKANCKVCFVALIQSFSHYSIVGQKLGVSLTMARERGQLVF
			LEGL/IVCSGR\VFQAQKEPHPLQFLREANAGNLKPLFEFVREA
			LKPVDSGEARWTYPVLLVDDLSVLLSLGMGAVAVLDFIHYCRAT
1			VCWELKGNMVVLVHDSGDAEDEENDILLNGLSHQSHLILRAEGL
			ATGFCRDVHGQLRILWRRPSQPAVHRDQSFTYQYKIQDKSVSFF
L	<u> </u>		AKGMSPAVL
6024	3	3260	FLSFLCYPRFRCLFCLQFAIPASRMEQLNELELLMEKSFWEEAB
			LPAELFQKKVVASFPRTVLSTGMDNRYLVLAVNTVQNKEGNCEK
1			RLVITASQSLENKELCILRNDWCSVPVEPGDIIHLEGDCTSDTW
1			IIDKDFGYLILYPDMLISGTSIASSIRCMRRAVLSETFRSSDPA
	1		TROMLIGTVLHEVFOKAINNSFAPEKLOELAFOTIOEIRHLKEM
L			.10

mulectide location corresponding to first anino acid an	SEQ	Predicted	Predicted end	T >
Molectide Cortesponding to first amino acid residue of residue of amino acid residue of amino acid sequence Sequenc	_		ľ	Amino acid segment containing signal peptide
Cortesponding to first amino acid Security Security		, , ,		Clubation Acid R Physical R 2
to first amino acid residue of residue of amino acid residue of sequence Se		1	B '	W-Wightiding T-Tapleweins W towns
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence 8-Sectien, T-Threenine, V-valline, w-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop Codon, (-possible nucleotide lenertion) YEMINGOBE KORDENDYPS-FCKMAGE/FMKHSTSTDFPGMISL PEDNSKONSTCHIEVYKHMIESSISSERSCOUVLTILISGERSCH REGYEKYKKIMPLELIKTEKSSISIBERSCHULTURGKEN ATROKTOLASION INVEKTIMBLELIKTEKSSISIBERSCHULTURGKEN ATROKTOLASION INVEKTIMBLE LIKERSSISIBERSCHULTURGKEN ATROKTOLASION INVEKTIMBLE LIKERSSISIBERSCHULTURGKEN ATROKTOLASION INVEKTIMBLE LIKERSSISIBERSCHULTURGKEN ATROKTOLASION INVEKTIMBLE LIKERSSISIBERSCHULTURGKEN ATROKTOLASION INVEKTIMBLE LIKERSSISIBERSCHULTURGKEN ATROKTOLASION INVEKTIMBLE LIKERSSISIBERSCHULTURGKEN ATROKTOLASION INVEKTIMBLE LIKERSSISTERSCHULTURGKEN ATROKTOLASION INVEKTIMBLE LIKERSSISTERSCHULTURGKEN ATROKTOLASION INVEKTIMBLE LIKERSSISTERSCHULTURGKEN ATROKTOLASION INVEKTIMBLE LIKERSSISTERSCHULTURGKEN ATROKTOLASION INVEKTIMBLE LIKERSSISTERSCHULTURGKEN AND IN LIKERSSISTERSCHULTURGKEN	1			h-histidine, i=isoleucine, k=Lysine,
Saszine, Tethreonine, U-Valine, amino acid amino acid sequence Sequence	-			P-Proline O-Clubanine D. Ameirica
residue of amino acid sequence				S-Carina T-Thronning W.Waling
amino acid sequence Codon, /=possible nuclectide deletion. -possible	i			W-Trotophan V-Trocine V Halance t Char
Sequence \possible nucleotide insertion	j	1		Codor /-noggible muglestide deletide
YRLMISODE KQEVEDYLESSYCKMAGDFMIKNTSTDFPOMILSI. PEDMSKONSTCHISE PREGIGKEN DUTVGVKI HEGYKTKYK IMPLELKTIGKESNSI BRISGOVUTYLLISGBERADP BEGLLIJKKTOGMYPVANHLIDKESLIKKINOMAPSHHISES ATROKTOLASI-QI IEEEKTCKYCSQIGNCALYSRAVEQOMOCS SVETUVLIJKK IEEEKTCKYCSQIGNCALYSRAVEQOMOCS SVETUVLIJKK IEEEKTCKYCSQIGNCALYSRAVEQOMOCS SVETUVLIJKK IEEKTCHKKYTLELYSRIKCHILITESSGKONKIN HONINIMPASEMEKSGICIGH LEMENVKIVUCDGOVLINFOCCH GAI PVYNIMAGDRIVINGSGERSI JEHENVKIVUCDGOVLINFOCCH BULI DEPREPOFISTI SVLPHDAKDTVACILLGIAN PROGAMKK VLISKDYTIL VOMMOTISKTTI CTLVRILJYAGGFSVLLTSYTHS AVANILLIKLAKKKIGHERSR QIGVGNIPALOCHERE ICESKSI KSQLALLEBLYTSQLIDATTOMISHHIPFSRRIFDECIVDENSQ ISOPICICAPIFFSRRIFORIUNGHOOLDPIVLINEBRARLOGSSVLUTSYTHS AVANILLIKLAKKKIGHERSR QIGVGNIPALOCHERE ICESKSI KSQLALLEBLYTSQLIDATTOMISHHOFTSRRIFDECIVDENSQ ISOPICICAPIFFSRRIFORIUNGHOOLDPIVLINEBRARLOGSSDKVA NAVINLAHFEDVIKLEBEFYLDSYSDHYMAOVERNIPYCILMTS KVPAPEQVERGGVSINVTEAKLITYLTSIFVXAGCSSSDIGIITAP FOQUKLINDILARSKILIDIDSGRAVENTYOKYOP DRINKITYLYSPIPLSKL LIMHISSKLIIDLISSGRAVENTYOKYOP DRINKITYLYSPIPLSKL LIMHISSKLIIDLISSGRAVENTYOKYOP DRINKITYLYSPIPLSKL LIMHISSKLIIDLISSGRAPHSICICAPITSTSPPPPRELBELDGOPG GLAWMOATAVAQLIKPAGLGOPGOSRAAVLVQOMYSYADTELIP AACCATLPAJGIRSSGRHISSICIPLSTSTSPPPPRELBELGOPG GLAWMOATAVAQLIKPAGLGOPGOSRAAVLVQOMYSYADTELIP AACCATLPAJGIRSSGRAPISGROGGORGARAJLINGVOMYSYADTELIP PERKKUSKGROMOSPSBRIVENAMYPEMSCOPPERVERGEPRIVS AANBROVENKCI PPRIVTOSIAHGRALTNALQDSLITRHHMRGE EKKERKOOKKI QQQOPPOGKKERPERGOPGITTDLDTP PERKKUSKGRMODSPSBRIVENAMYPEMOQGPFREGEPRIVS AANBROVENKCI PPRIVTOSIAHGRALTNALQDSLITRHHMRGE TIMMPGCODRAGIATNYCKKURSGISHQLGREGGFRIVOSW KWKEEKGDRITYIQLKKLGSSIDEWVANTTRETMLADVAVAV HENDITTYCHILKKORVI VERKINEBGGISHQLGREGFRIVOSW KWKEEKGDRITYIQLKKLGSSIDEWVANTTRETMLADVAVAV HENDITTYCHILKKORVI VERKINEBGGISHQLGREGFRIVOSW AANBROVENKCI PPRIVTOSIAHGKATTARPYTORAVITI PAHDONDYEWGGORGIGEAISI MOSGGALINDVAN HENDITTYCHILKKORVI VERKINEBGGISHQLGURGAVISTA KAREPOUSDBUS SIDVELDENTAVOSQOSPORDSHVONGANIANING KWKEEKGDRITYIQLKKLGSSIDEWONDOPTICHSEVUHAH LIGTHFTOKLIVANIANING KRITARDOPPORTISHANING HANDING WISKLIFAVILASGROPPOORV			acquence	\-nossible nucleotide deletion,
FEDNSKORSTONIEVVRPMOLESINSPREGIKKI DUTVGVKI HEGYKTKKIMEJEKTKGKENSI SIERGYOUTILLIGERRADP BAGLLIJIKTOGMYPVPANHLDKRELLKIERIOWAPSLPHRIESES ATROKTOLASLOJI LEBERTCKKCSGIONALTSRRAYSOMDOS SVPIVALPKI EBETQHLKOTILLEYPSLMCLMILTUSOSKONKON HONIKIMPASEMEKSIGGIOKILTSREVIKIVUOOQOJUNFOCCH GAIPVTNIMAGDRIVISGERSSIJFALSRGVYKEINNTTVTCLLD RILSVIPESTICHRIDGERNOLDIDTPGINISLIMEMETYVSKILR DLIIDPREPOJISTLSSVLPHDAKDTVACILLIGINPOPROAMK VLISKOYTLIVOMOPOTKYTITICTUSTIJSAOGSVUTUSTYHS AVONILLIKLAKRIGPISRROJOKVHPATOQPTEHBICSISKI SILALLEBELYTSGIDIATTOMOINPITPSRRIPDEJ VORBAQ ISQPICLOPIJFPSRRYVLVGHOOLPPIVARERARLIMESIJF RRLEGORSAVVOLTVOYRNNEK MBICHITISTVRAGCSBIVA NAVINLRIPEDVKLBEPYADYSDNPHLMOVPENNPVCHATU KVRAPEOVERGGVSNVTVERKITUSTIJSTVRAGCSBIVA NAVINLRIPEDVKLBEPYADYSDNPHLMOVPENNPVCHATU KVRAPEOVERGGVSNVTVERKITUSTIJSTVRAGCSBIVA NAVINLRIPEDVKLBEPYADYSDNPHLMOVPENNPVCHATU KVRAPEOVERGGVSNVTVERKITUSTIJSTVRAGCSBIVA NAVINLRIPEDVKLBEPYADYSDNPHLMOVPENNPVCHATU KVRAPEOVERGGVSNVTVERKITUSTOVAPPENPAPEIDLITAP YROOKHIINDILARSIOMVENTVERKITUSTOVAPPENPAPEIDLITAP YROOKHIINDILARSIOMVENTVERKITUSTOVAPPENPAPEIDLITAP YROOKHIINDILARSIOMVENTVERKITUSTOVAPPENPAPEIDLITAP YROOKHIINDILARSIOMVENTVERKITUSTOVAPPENDATOVAPENCI KVRAPEOVERGGVSNAVATATAAHLILLIGCVPBLICKYPDPEKL VRAPETALLAAVILLILLIPEVVLIDPPRICAPPEPEIDLITAP YROOKHIINDILARSIOMVERKITUSTOVAPPENDATOVAPPENDE ANCARTIPALIAMANATAAOLINAPATOVAPERKITUSTOVAPPENDATOVAPPENDE ANCARTIPALIAMANATAAOLINAPATOVAPERKITUSTOVAPPENDATOVAPPINDIP POERKOVAGIMODEYSERVYSAANIYPHNOOCHEPYLDEVITULDIPP POERKOVAGIMODEYSERVYSAANIYPHNOOCHEPYLDEVITULDIPP POERKOVAGIMODEYSERVYSAANIYPHNOOCHEPYLDEVITULDIPP POERKOVAGIMODEYSERVYSAANIYPHNOOCHEPYLDEVITULDIPP POERKOVAGIMODEYSERVYSAANIYPHNOOCHEPYLDEVITULDIPP POERKOVAGIMODEYSERVYSAANIYPHNOOCHEPYLORUSATIATIVALODILITARINIADADA XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX		Boquonec		VPLNI CODET VOEVEDAT DE ECAMACIDEM NOME COLOR COL
HRØYKTKYKIMPLEKTIKESNSIEHRSGVYLTILLSGBERADP BAGLLIYLKTQDYPVPANILDKERLIKLRNQPASPLEHRISKS ATROKTQLASLPQIIEEEKTCKYCSQIGNCLYSRAVEQOMD SVPLVALPKIEBETGHLKQTHLEVSIMCLAULTLSGSKNNKKN HQNINLMASEMBERGGSCIONLIRMENVXIVCDGQYLBNDQCG SVPLVALPKIEBETGHLKQTHLEVSIMCLAULTLSGSKNNKKN HQNINLMASEMBERGGSCIONLIRMENVXIVCDGQYLBNDQCG GAIPVTNIMAGORVIVGGERSLAUSANGYVERIUNTTVTCLLD RNLSVLPBSTLFRLDQEENKCDIDTPLGNLSKLMENTFVSKLKK DLIIDFRRPQFISTLSSVLPHDAUDTVACILLKLMENTFVSKLKK PLIIDFRRPQFISTLSSVLPHDAUDTVACILLKLMENTFVSKLKK VLLSKDYTLIVGMPGTGKTTTCTURILVACOFSVLLTSYTHS AVDMILLKLAKFGLFLRSN, 100KVHPAIQGTEGSKSI KS\LALLBELYTSQLIDATTCMGIMPIFSRKIFDGCIVDENS AVDNILLKLAKFGLFLRSN, 100KVHPAIQGTEGSKSI KS\LALLBELYTSQLIDATTCMGIMPIFSRKIFDGCIVDENS KS\LALLBELYTSQLIDATTCMGIMPIFSRKIFDGCIVDENS KS\LALLBELYTSQLIDATTCMGIMPIFSRKIFDGCIVDENS KS\LALLBELYTSQLIDATTCMGIMPIFSRKIFDGCIVCHTY KVPAPEQUVEKGGVSNVTEAKLIVELISFIFVXAGCSSPSIGIIAP YRQQLKIINDLARSIGMWANTAKKKILLIGCVSSLNCYPPLEKL LIMINSERLIIDLABSTGMWANTAKKILLIGCVSSLNCYPPLEKL LIMINSERLIIDLABSTGMWANTAKKILLIGCVSSLNCYPPLEKL LIMINSERLIIDLABSTGMWANTAKKILLIGCVSSLNCYPPLEKL LIMINSERLIIDLABSTGMWANTAKKILLIGCVSSLNCYPPLEKL LIMINSERLIIDLABSTGMWANTAKKILLIGCVSSLNCYPPLEKL LIMINSERLIIDLABSTGMWANTAKKILLIGCVSSLNCYPPLEKL ARCHADAVAQLLMPAGIGGGGGSRAAVLVQONVSYADTELI AACQATLPAGLGURSSAQDPQAVLGAGGGGGRAVALVQONVSYADTELI AACQATLPAGLGURSSAQDPQAVLGAGGGGASAAVLVQONVSYADTELI AACQATLPAGLGURSSAQDPQAVLGAGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA				
REGILLYLKTOGNYEVPANILDKRELLKLRIGNERSPEDGENGES APROKYOLASIDJE IEBERCKYCSGOGNOCLSBRAVEOGNOCS SYPTUMLPKIEBETGHLKOTHLEYPSIMCIMITESSGSKONKOK HONNIMPASEMEKSGSCIONILINBREWKIVCOGOTUNOCKH HONNIMPASEMEKSGSCIONILINBREWKIVCOGOTUNOCKH GAIPYNIMAGDRUVUSGERSLFALSRGYVKSIMNTTYCILLD RNLSVLPSSTLFBLDGERNCDIDTPLGMISKIMKENTYUSKILR RNLSVLPSSTLFBLDGERNCDIDTPLGMISKIMKENTYUSKILR DLIIDFRRPGFISYLSSULPHDAMDVAGILKGLNKPORGAMKK VLLSKOYTLIVGMOPGTOKTTICTURUIXAGOFROAMKK VLLSKOYTLIVGMOPGTOKTTICTURUIXAGOFROAMKK VLLSKOYTLIVGMOPGTOKTTICTURUIXAGOFROAMKK VLLSKOYTLIVGMOPGTOKTTICTURUIXAGOFROAMKK VLLSKOYTLIVGMOPGTOKTTICTURUIXAGOFROAMKK VLLSKOYTLIVGMOPGTOKTTICTURUIXAGOFROAMKK VLLSKOYTLIVGMOPGTOKTTICTURUIXAGOFROAMKK VLLSKOYTLIVGMOPGTOKTTICTURUIXAGOFROAMKK VLSKOYTLIVGMOPTOKTOTURUIXAGOFROAMKK ISQPICLAGPLEFENDETTITTURUITARIAGOSLIVA RAVINLRIPKOVELELBEYADVSINDPIMMGVEPRINPVCLTURUIX RVAPPOOVEKGGVSVVTEAALIVUTISTEVASCASSIOIGITAP YROOLKITINDLARSIGMOVAVTATURUITARIAGOSLIVASVESSI NAVINLRIPKOVELELBEYADVSINDPIMMGVEPRINPVCLTURUIX VROOKATINDLARSIGMOPTURUITARIAGORIVATURUIXAGORIVAT				HDGAKAKAKAMDI SI KACKESHETERIDEOTARI AMILI CODDUSED
ATROKTOLASLAPQI I EEEKTCKYCSQIGNCLISRANYROMOKS SVPTVALPKI EERTCHALKOTHLESGSKONKKN HQNINLMAPASEMSKSGSCIGNLI RMSENVLIVGOGQYLBINOGCO GAI PVYNLMAGDSVV VSGGERS LABASGYVYSIINTTVTCILLD RNLSVLPSSTLFRLDQEENCCI DTPLGNLSKLMEXTFVSKLNL DLI LIDERBOPG I SLSSVLPHADAUTVACILIKALIKHPORQMKK VLLSKDYTL VGGMERS LABASGYVKSIKHPORQMKK VLLSKDYTL VGGMERS LABASGYVKSIKHPORQMKK VLLSKDYTL VGGMERS LABASGYVGSTLCSKSI SVANLILKLARFGEFRENVLODIOLOPPLVMERSERICSSKSI KSALALLERLYTSQLIDATTCHG INME I PSEKT PPECTUVDANS I SQPICLAPLE PERFENVLODIOLOPPLVMERSERIC CSSISI KSALALLERLYTSQLIDATTCHG INME I PSEKT PPECTUVDANS I SQPICLAPLE PERFENVLODIOLOPPLVMERSERIC CSSISI KSALALLERLYTSQLIDATTCHG INME I PSEKT PPECTUVDANS I SQPICLAPLE PERFENVLODIOLOPPL LABASIAL COSSISION NAVINLRIFEROVALLER PAULS DEPLACEMENT AND SERVICE AND				
SVPIVALPKIEBETQHLKUPSIMCHALITLESGSKONKUL HONNIMMAGENEKGSGCIONILIMENEKVIVOGOZHANPOCKH GAI PVINILMAGENEKGSGCIONILIMENEKVIVOGOZHANPOCKH GAI PVINILMAGENEKGSGCIONILIMENEKVIVOKOZHANPOCKH GAI PVINILMAGENEKGSGCIONILIMENEKTVEKKLR DLI IDERREGETYLSSULPHDAKDIVACILKELHKPOROMKK VLLSKOYLLIVGHOPTOKTTICILVELIVACOPROMKK VLLSKOYLLIVGHOPTOKTTICILVELIVACOPROMKK VLLSKOYLLIVGHOPTOKTTICILVELIVACOPROMKK VLLSKOYLLIVGHOPTOKTTICILVELIVACOPROMKI KYALALIBELVIPAGILDIATTOK IMPUFSEKIPOCTURDAG ISQPICLIGPLEPSREPVLVIGHOQLPPLVINREARALOMSEGLE KRLEGNKSAVVQLIVOZINNEKINISLSKILTIGGILGCOSINCI KRIEGNKSAVVQLIVOZINNEKINISLSKILTIGGILGCOSINCI KRIEGNKSAVVQLIVOZINNEKINISLSKILTIGGILGCOSINCI KRIEGNKSAVVQLIVOZINNEKINISLSKILTIGGILGCOSINCI KRIEGNKSAVVQLIVOZINNEKINISLSKILTIGGICGSCOSINCI KRIEGNKSAVVQLIVOZINNEKINISLSKILTIGGICGSCOSINCI KRIEGNKSAVVQLIVOZINNEKINISLSKILTIGGVESINCYPPLEKL LIMHINSEKLI IDLOSERBEISLCHINDIYOZINOZIPELEKI YRQQLKIINILLISARSIGMVENITIVALDDYGR GGFFAQSBOHDPVPFLESDLLITMSTLYVSSHIDAPSGERALIA ARVGEAGGGOMGANBRICICIPPSTRISTSPPEBLALEGOP GLAWMGATAVAQLUMPAGIGGGGGSRAAVLVQOMVSYADTELI AACCATLERAGIGISSSADDPOAVLAGIGGRALSINCHINTILA GEAPTLADIAAVTALLIPPRVVLDPPARRINNAVTRIPVTCVRQ GEAPTLADIAAVTALLIPPRVVLDPPARRINNAVTRIPVTCVRQ PERRAVLGEVVLYSSAPDSHOPESPAAPLETANGKARAK EKLEKROGOKKIQOQOP POPEKKKYREKKEKERDPAVTTYDLYP PGEKKONSGMPHOSYSSPVVBARAVRIMOZOGISRALSUKRAKK EKLEKROGOKKIQOQOP POPEKKYREKKERDPAVTTYDLYP PGEKKONSGMPHOSYSSPVVBARAVRIMOZOGISRALSUKRAKK EKLEKROGOKKIQOQOP POPEKKYREKKERDPAVTTALISVP AANDRAVERMCI PPROVTSILIICHALITAATQUSITRHEMMGE TTIMMPGCDHAGIATOVVVEKKIMREGGLISRICHERILISVP VKREEKGBRITYHQLKKIGSSLDMDRACPTMPPELSAMYTBAVR AARDRAVERMCI PPROVTSILIICHALITAATQUSITRHEMMGE TTIMMPGCDHAGIATOVVEKKIMREGGLISRICHERILISVP VKREEKGBRITYHQLKKIGSSLDMDRACPTMPPELSAMYTBAVR KKREEKGBRITYHQLKKIGSSLDMDRACPTMPPELSAMYTBAVR KKREEKGBRITYHQLKKIGSSLDMDRACPTMPPELSAMYTBAVR KKREEKGBRITYHQLKKIGSSLDMDRACPTMPPELSAMYTBAVR KKREEKGBRITYHQLKKIGSSLDMDRACPTMPPELSAMYTBAVR KKREEKGBRITYHQLKGLASTATARAVR KKREEKGBRITYHQLKGLASTATARAVR KKREEKGBRITYHQLKGLASTATARAVR KKREEKGBRITYHQLEGATARAVR KKREEKGBRITYHQLEGATARAVR KKREEKGBRITYH				
HONTHUMPASEMEKSGSCIONLIRMENTUTICLID GAIPVINIMAGORIV UVSGERSILABISGYVEININTUTICLID RINLSVLIPSTLIFALDQEENICDIDTPLGHLSKIMENTFUTKLIL BLIIDFREDPISTUSSVLJEHDADATVACILKSKIMENTFUTKLIL DLIIDFREDPISTUSSVLJEHDADATVACILKSKIMENPORGAMKK VULSKOYTLIVGMPGTGKTTTICTUREILYACGFSVLLTSYTHS AVUNILLKLAKFUGFIRSRINJOKVHPATQOJETICSKISI KS\LALLEELYTSQLIDATTCHGINHPIPSKIFTPCIUDEASQ ISQPICLOPLIFSRERPIVLOSHQUAPPLUMPERSKIELGSKISI KS\LALLEELYTSQLIDATTCHGINHPIPSKIFTPCIUDEASQ ISQPICLOPLIFSRERPIVLOSHQUAPPLUMPERSKIELSKISKI KS\LALLEELYTSQLIDATTCHGINHPIPSKIFTPCIUDEASQ ISQPICLOPLIFSRERPIVLOSHQUAPPLUMPERSKIERGGSDLOFILAP RELEONKSAVVQLTVQYNMSKINSLSNKLITYSGKLEGGSDLOIIAP RELEONKSAVVQLTVQYNMSKINSLSNKLITYSGKLEGGSDLOIIAP VEQQLKIINDLIABEIGMPUNTUKYQD\DADATUSYPENPOCTLATT KVPAPEQVEKKGGVSNVTEAKLIVULTSIFVYSAGGSBDIGIIAP YEQQLKIINDLIABEIGMPUNTUKYQD\DADATUSYPENPOCTLATI KVPAPEQVEKKGGVSNVTEAKLIVULTSIFVYSHPDAFFSLRALIA ARTIGEAGGSGKGGGHREILODFRENELLDFORR GGFPANGHENDATTALLABTRAKULTLICGVPSINCYPPLEKI LAMINSEKLIJOHPROFFSTSTSYPPRALPALEGGG GLAWMGATAVQLIHPAGIGGGFGSKAVLVQGWYSYADTELDIP ARCONTLERAGISHSAQDPQAVLGALGRALFULTSIPSTELDIP ARCONTLERAGISHSAQDPQAVLGALGRALFULTSIPTEDIP ARGONTLERAGISHSAQDPQAVLGALGRALFYCOKYPTUCHTYDLFTP PGEKKDVSGMPDSYSPRVERAMYDWEQGGFFREYGGRNV AAMPROVENGT PEPNVTCSILLICHALITATAIQSITTSHRIPKNEG TITMPGGGDAGIATQVVVEKKLMRSQGLSRHQLGREBAFLOKY KAKEKERODIYNGLKKKLGSSLDMPARCFTMOPELAAVITEAPVX KAKEKERODIYNGLKKKLGSSLDMPARCFTMOPELAAVITEAPVX KAKEKERODIYNGLKKKLGSSLDMPARCFTMOPELAAVITEAPVX LHEEGITYRSTELVMMSCTLANSASDIEVVORKELGRATILSVPG YKKKVEFGVUJSTARVYQGSSDSDEVVVATTIR ETRICHTENVA KAKULVALKEEGIFRGIEDHMVVPLCNISKOVVEPLLARPGWYDG YKKKVEFGVUJSTARVYQGSSDEDEVVVATTIR ETRICHTENVA HPKOTRYOHLKOKNVIHPLISKSLPTVPDSFULGREFSAR KALVALKEEGIFRGIEDHMVVPLCNISKOVVEPLLARPGWYDG KLMWGHRA, YPAYFVTVSDPAVPGGDPDGRYAVSGRNERARRE KARKEFGVGSPDISKIGNVDFLANGTHAMMETNIN NICHTENGOSED LSVFYFGTLLETGHDLIFFWARNVALGLKICATGLPFBEVTUN RIGHTSHPCHKKURGARGAPTOTULDUR RIGHTSHPCHKINGARGAPTOTULDUR RIGHTSHPCHKINGARGAPTOTULDUR RIGHTSHPCHKINGARGAPTOTULDUR RIGHTSHPCHKINGARGAPTOTULDUR RIGHTSHPCHKINGARGAPTOTULDUR RIGHTSHPCHKINGARGAPTOTULDUR RIG		1	ŀ	
GAIPVINIMAGDRIIVSGERSIJFALSRGYVKEINMITTUTCLLD RNLSVIJFBSTLFRIDDEEKINCD DIPTLEINLSKINEPTVSKLKE DLIIDFREPOFISTLSSVLPHDAKDIVACILKGLNKPORGAMKK VILSKYTLIVGMEGTGKTTITCITURILAGEVSLILTSYTHE AVDNILLKLAKFKIGPLGSROJGKVHPATOQPTHBICGSKSI KS\LALEBLITSQLIDATTVGLHSROJGNEKE LSQDICLGPLFFSRRFVLVGDHQQLPPLVLNRSARALGMSESIP KRLEDNKSAVVQLTVQYRNBKSKIMSLGNKLTYSKGTSDKVA NAVINLHPKDVKLELEFYADISDNPALMGVEFRNRVCFLNTI KVPAPGVEKGGVSVAVTAKLLIVFILGSIFVARGCSPSDIGITAR YRQGKRINDLLARSIGNVAVNTVKKQDLOKSIVLVSFVESN KDGTVGELLKDWRRLMVATTRAKHLLILLGCVPSINCYPPLEKL LINHINSEKLI IDLDFSREHESLGHLILGPGVGS GFFAQSSHDLDPVFPLRSDLLTMSTLTVSFPHPDAFPSLRALIA ARVGRAGSGFORGGAPHPICLGPPTSRTSPPPRLPBALEGGFG GLAWWAGATAVAQLLMFAGLGGFGGSRAAVLVQOWSYADIFLIF AACGATLFALGLESSAQDPQAVLGALGRALSJEEMURLHTYLA GEAPTLADLAAVTALLLFFRYUDDPPARRIWNNYTRYFTYCORQ PEFFRAVLGSVVLYSGARPLSHGGPGBAPALFJEMGKKEAKKR EKLEKFOQKOKLOQQQPPPGEKKFRFKRDPQVITTDLDFT PGEKKDVSGMFDDSSYRPYVERAMYPWWEGQFAGLKKEAKKR EKLEKFOQKOKLOQQQPPPGEKKFRFKRDPQVITTDLDFT PGEKKDVSGMFDSSYRPYVERAMYPWWEGGRAAKKEAKKR KKEKGRGTYHQLKKLGSSLOWDRACFTMDPKLGAAVTRAFVR LHEBGIIVSGTLATOVVVEKKIMBEGGLSIPGRAFALGEWIN KWEEKGGRTYHQLKKLGSSLOWDRACFTMDPKLGAAVTRAFVR LHEBGIIVSGTLATOVVVEKKIMBEGGLSIPGRATLGEVK KWEEKFGVLVSPAKYOGGSDSEVVVATTRIETMLGDUAVAV HEKOTYOHLUKGNVIHPFLSRSLDIVDFELGTRATLLSVPG VKEKVFFGVLVSPAKYOGGSDSEVVVATTRIETMLGDUAVAV HEKOTYOHLUKGNVIHPFLSRSLDIVDFELGTRATLLSVPG CGRAQAASAAVTRODLKIIDPELGRREDVUSPLLRRGYVIH CGRAQAASAAVTRODLKIIDPELGRREDVUSPLLRGMYVH CGRAQAASAAVTRODLKIIDPELGRREDVUSPLLRGMYVH CGRAQAASAAVTRODLKIIDPELGRREDVUSPLLRGMYVH CGRAQAASAAVTRODLKIIDPELGRREDVUSPLLRGMYVH CGRAQAASAAVTRODLKIIDPELGRREDVUSPLLRGMYVH CHAMGRIKHSKLANTYFDLAYAGAGADLINGMNDDS LSVFYGGTLEGTHDILFFRAVRAMVMIGLKLGSLEPFREYVHH IVERDARGKWSKLGNVIHPFSSGCFTALGARSGCREBLIVON RILGYHHCKKMANTKFALGRIGGFVPSPTOFGGGGHSLVON RILGYHHCKKMANTKFALGRIGGFVPSPTOFGGGGHSLVON RILGYHHCKMANTKFALGRIGGFVPSPTOFGGGGHSLVON RISKLTBAVRLSNOGGQAVDFAATTAQYSFWLYBLÜE LKPRNPQAPPSLCVTFYPSPSGCSWEDBBABALBLALSTRR VRP\LABAYHLBESGTPCLGAVAGCGRDILLON RILGYHHCKMANTKFALGRIGGFVSPSPTOFGGHESLVON VESKLTBAVRLSNOGGAALGRIGGFTSPPTOFUELGVILL TNNTAKLEYSTDFFWITTGLDGA				HONTHI MDA CEMEVOCCCTONI I DMEINIVI NODGOVI I DIEGOVI
RNLSVI_RESTLFRIDDEEKNCD_DTPLOANS_KAMENTFVSKKLE DLIIDFRERGPISTLSSVLPHDAKDTVACLKAKENPORAMKK VLLSKSYTLIVGMEGGKTTICTLVRIACGESVLLTSYTHE AVDMILKKLAFK[GFLESR_VALORAVPHA_OQFPILITSYTHE AVDMILKKLAFK[GFLESR_VALORAVPHA_OQFPILITSYTHE ENDILITERSPRIVENCHOOLDEP_LVINREARALIGMSESIF KS\LALLEELTTSOLLDATTCMSINHPIPFSKRIFPLOEMSSIF KRLEONKSAVVQLTVQYRMSKIMSLSNKLITEGKLECSSDKVA NAYINLRIPKDVIKLBLEFYAD YSDMPHIMOVEPPRINVCFLINTD KVPAPEQUEKGSVNTTSAKLVIPTISTFVAHGSCPSDIGIIAP YRQQLKIINDLLARSIGWZVNIVVDKYQD\RDKSIVLVSFVEN KOTVEELKUMRRINVAITRAKHKLILLCVFSINCYPPLEKL LINHINSEKLIIDLPSRETESLCHILGDFQRE GLWWGATAVAOLLHPAGKIGGGGSRAVLVOYSTOPELTP ARVGAGECFOWGAHIPRICLQPPTSRTSPPPRIPALEGOPG GLWWGATAVAOLLHPAGKIGGGGSRAVLVOYSTOPELTP AACGATLPALGLESSADOPOAVGALGRAISPLEEWURHHTYLA GEAPTIADLAAVTALLLPFRYUDDPARR EWENDRYTTYDLPTP PAACGATLPALGLESSADOPOAVGALGRAISPLEEWURHHTYLA GEAPTIADLAAVTALLLPFRYUDDPARR EWENDRYTTYDLPTP PGEKKDVSGPMDSYSPRYVEAAWYPWEGOGFFKVEKGRDVYSTOPELTP PGEKKDVSGPMDSYSPRYVEAAWYPWEGOGFFKVEKGRDVYTTYDLPTP PGEKKDVSGPMDSYSPRYVEAAWYPWEGOGFFKVEKGRDVITYDLPTP PGEKKDVSGPMDSYSPRYVEAAWYPWEGOGFFKVEKGRDVITYDLPTP PGEKKDVSGPMDSYSPRYVEAAWYPWEGOGFFKVEKGRDVITYDLPTP PGEKKDVSGPMDSYSPRYVEAAWYPWEGOGFFKVEKGRNINTERFYG KWKEEKGORIYHQLKKLGSSLDWDRACFTMDPKLSAAVTERFYG KWKEEKGORIYHGLKKLGSSLDWDRACFTMDPKLSAAVTERFYG KWKEEKGORIYHGLKKGGSSLDWDRACFTMDPKLSAAVTERFYG HENDRYGCHGLEAISIMSGGALINVPPPFLGLERFERA KAULVALKERGIKGNVIHPPLSASIDLEVKERTGRTLLSVPG YKKWEFKOVLVSFAYKVOGSDSDEEVVVATTRIETMIGDVAVAV HPKOTTYGHLKGNVIHPLSSRIDLETDFTAVAVENTLLBVGC GGBAQAASAAVTRGDLRIJPSHGTENDWPLCKGRSGVADPPLGLRROWYNE CGBAQAASAAVTRGDLRIJPSHGTENDWPLCKGRSGVADPPLGLRROWYNE CGBAQAASAAVTRGDLRIJPSHGTENDWPLCKGRSGVANGRAGRAF KAULVALKERGJFGGIENGWPLFARAVENDILLFROWYVE CGBAQAASAAVTRGDLRIJPSHGTENDWPLCKGRSGVANGRAGRAF KAULVALKERGJFGGIENGWPLFARAVENDILLFROWYVE CGBAGAASAAVTRGDLRIJPSGLAPBEGDPDARWWGRENGRARAR KAULVALKERGJFGGGGRAAULPARAMGGRIDLINDW RILGTHPCKLMNATKPALRGLGKGVPSPFTSGGGGRBSLVOR RILGTHPCKLMNATKPALRGLGKGVPSPFTSGGGGRBSLVOR RILGTHPCKLMNATKPALRGLGKGVPSPTSGGGGRBSLVOR RILGTHPCKLMNATKPALRGLGKGVPSPTSGGGGRBSLVOR RILGTHPCKLMNATKPALGLGKGVPSPTSGGGGRBSLVOR RILGT				
DLIIDFREPGISILSVLPHDAKDTVACILKGINNERGAMKK VULSKYTILVGMPGTGKTTICTURILVACCESVLITSYTHS AVDNILLKLAKFKIGFLGSROIGKVMPATQQFTSHEICESKSI KS\LALEBLIYGOLIDATUGHIPIPIPSKPIPFCIVDENG ISQPICLGPLFFSREPVLVCDHQQLPPLVINREARALGMSESIF KRLEQNKSAVVQUITVQYMMSKIMSLSNKLITEGKLECSSDVA NAVINLRIFKDVKLBLEFYJAVSDNPHMMSVETVLVSFVENS KRLEQNKSAVVQUITVQYMMSKIMSLSNKLITEGKLECSSDVA NAVINLRIFKDVKLBLEFYJAVSDNPHMMSVETVLVSFVENS KOTTVEELLKDWRRLNVAITTRAKHKLILLCCVPSINCYPPLEKL LINHINSEKLI IDLDFREREBLICHIGDFORG GEPFAGSDBLDPVFPLRSDLLITMSTTLVSFPHPDAFFSGRALIA ARVGEAGEDEGWGGAHPRICLGHIGDFORG GLWWGATAVAQLLWFAGLIGSDGSRAVLVQOWVSYADTELIP ARCCATLPALGLRSSAQDPQAVUGALGRALS PLEEMILHTYLA GEAPTLADLAAVTALLDFFRYVLDPPARRI WMNVTRKFVTCVRG PERRAVLGEVVLYSGARFLSHQGGBAPALPKTAQGLKRAKK EKLEKFQUKKGIQQQPPFCEKKPPEKRKRAKDGVITTDLFTP PGEKKDVSGPMPDSYSPRYVEAAWYPWWEQQGPFKDFYGRNVS AAMPROVPMGLOQQOPPPGEKKPPEKRKRAKDGVITTDLFTP PGEKKDVSGPMPDSYSPRYVEAAWYPWWEQQGPFKDFYGRNVS AAMPROVPMGLOQQOPPDGKKPPEKRKRAKDGVITTDLFTP PGEKKDVSGPMPDSYSPRYVEAAWYPWWEQQGPFKDFYGRNVS AAMPROVPMGLOQQOPPDGKKPPEKRKRAKDGVITTDLFTP PGEKKDVSGPMPDSYSPRYVEAAWYPWEQQGPFKDFYGRNVS AAMPROVPMGLOQQOPPDGAVENDFAGTHUNGDSLTRWRRNGGE TTIMMPGCDHAGIATQVVVEKKLWBEGGLSRHIGGBRAFLIGWW KWKEEKGDRITHQLKGASSIADDRACFTMPGHSAAVYTADLFTP PGEKKDVSGPWPDSYSPRYVEAAWYPWEQQCPFKDFYGRNVS AAMPROVPMGLSAAVYTAGKUSTAWAY HENDTFYOHLKGRNVIHPFLSSISIVDRACFTMPGHSAAVYTADLFTP PAHDQMDVEVGQRRILERISIMDRRACHTWGDAVAXVI PHOTTYOHLKGRNVIHPFLSSISIVDRACFTMPGHGDAVAXVI CGEMAQAASAAVTRODLRIIPPERSILITMGDVAAVXI PHOTTYOHLKGRNVIHPFLSSISIIVDDEFVDMDFGTCAVKIT PAHDQMDVEVGQRRILERISIMDRRACHTWMGDNIERICHGRADARR KAAKERGVSPDKISIQQDEVULDTHFSSGLFPLSILGWBNOSED LSVPYFGTLLETHOHLFFWAYMYMGLKLGFLFREYVLHA IVRADAGRASKASLGNVIDPLDVIYGTSLQGIHNQLLMSNLDDP EVKRAGGGGADPFAGTPEGGTDARRGCARMGGRBINLDVW RILGYRHPCHKLMNATKFALRGLGKGVPPPPTSQDGGHSLVDR RILGYRHPCHKLMNATKFALRGLGKGVPPPPTSQDGGHSLVDR WIRSCHTADVISLANGPQADPPATTAQYSHVISLCUVLEC LKPVLNGDQDQAABCAACLAGCAGCAGCAGLABABCSI (HLQLGG\LLDP ARELOCALLDPSPPPVUTGLIGLIGGANLSSVTNARDPVLVDLLQ VREADBALLQOTABLERNENTHRESTYDCNDLIGLIFPPRPVTEELPQ PARRICANAGAGGAGARVALVORLCHUPPRETURENTENT LLEENKLTELNGGPATARGAGRA				
ULLSKYTLIVGMEGTGKTTICTURIACGESULITYTHS AVUNILIKLARKIGGLESK ROJGKVHRAIQGFHEDICRESG KS\LALLERLYTSGLIDATTCMGINHPIFGRKIFPGCIUDEASQ ISQPICIGPIFFSRRFULVGMCDQPPLUTBARAGMSEBLEF KRLEDNKGRVVQLTVQYRMNSKIMSLGNKLTYEGKLECGSDKVA NAVINLRHFKDVKLELEFYADYSDRPHLMGVFEPRRFVCFLNTD KVRAPEQUEKGGVSNVTRAKKIVPLISTSTYRAGCSPEDIGIIAP ROGUKIINDLLARSIGMVZWNTVDKYQD\RDKSIVLYSPUSN KDGTVEGLIKDMRRINVAITRAKHLILLACVPSINCYPHERL LINHANSEKLIIDLPSREBSLCHILGPGRE GEFRAGSBELPVPPLRSBLLITMSTLYVSPHPDAFFSLRALIA ARVGRAGECPGMGGAHPRICLQPPTSRTSPPPRLPALEGGCG GLWWGATAVAQLLHPRAUGGGGSRAALVVSYXDTELIF ARCGATLPALGLESSAODPOAVGALGRAISPLEEMURHHTYLA GEAPTIADLAAVTALLLPFRYVUDPPRAT BURLERHTYLA GEAPTIADLAAVTALLLPFRYVUDPPRAT BURLERHTYLA GEAPTIADLAAVTALLLPFRYVUDPPRAT BURLERHTYLA GEAPTIADLAAVTALLLPFRYVUDPPRAT BURLERHTYLA GEAPTIADLAAVTALLLPFRYVUDPPRAT BURLERHTYLA GEAPTIADLAAVTALLLPFRYVUDPPRAT BURLERHTYLA GEAPTIADLAAVTALLLPFRYVUDPPRAT BURLERHTYLA GEAPTIADLAAVTALLLPFRYVUDPPRAT BURLERHTYLA GEAPTIADLAAVTALLLPFRYVUDPPRAT BURLERHTYLA GEARTIADLAAVTALLLPFRYVUDPPRAT BURLERHTYLA GEARTIADLAAVTALLLPFRYVUDPPRAT BURLERHTGRTTADVTO PERKENDYGEMPDSYSPRYVEARWYPWWEQQGFPKPEKGRNVS AANPROVPMCI PPNTVGSLHIGGRAFALGEVW KWEEKGRIYTHQLKKLGSSLDWDRACFTYNDPKLSAAVTHAPVA LHEBGIIVRSTRIVWSGCTILBASIDLEVDREGHGRAFALGEVWA KWEEKGRIYTHQLKKLGSSLDWDRACFTYNDPKLSAAVTHAPVA HPKONTYGHLKGGNVIHPPLSAASIDLEVDREGHGRAFALGEVWA HPKONTYGHLKGGNVIHPPLSAADTHAPVA HPKONTYGHLKGGNVIHPPLSAADLAAVAV HPKONTYGHLKGGNVIHPPLSAALDERHTGATAVAVA HPKONTYGHLKGGNVIHPPLSAALDERHTGATAVAVA HPKONTYGHLKGGNVIHPPLSAALDERHTGATAVAVA HPKONTYGHLKGGNVIHPPLSAALDERHTGATAVAVA KAKUPAGVAGNASAAVTRODLRILPRHOVYHTGARAGARATAVARGARATAVARGARATAVARGAADAVAAVA HPKONTYGHLKGGNVIHPPLSAALDERHTGATAVAVA HPKONTYGHLKGGNVIHPPLSAALDERHTGATAVAVA HPKONTYGHLKGGNVIHPPLSAADLAAVAA KAULALEKEGLFGGTENGAADABAALGARGAVAAAA KAULALEKEGLFGGTENGAADAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA				
AVDMILLKLAFKKIGFLRSR\OIGKVHPAIQQPTEHBICRSKSI KS\LALLEBLYTSGLIDAFTCMGIMHPICHTOMPIONE ISQICLGGLFFSRFYLVODHQGLPEVLINREARALGMSESLF KRLEDNKSAVVQLTVQYRMNSKIMSLSNKLTYGKKIGGSDKVA NAVINLRHFKDVKLBLEFTADYSINPULKHGYBERNBYCFLNTD KVRAPEQVEKGGVSNVTEAKLIVELTSIFVKAGCSSDKVA RAYINLRHFKDVKLBLEFTADYSINPULKHGYBERNBYCFLNTD KVRAPEQVEKGGVSNVTEAKLIVELTSIFVKAGCSSDKVA PROQLKII TONLLARSIGMVENVITUKYGYPENSPVCFLNTD KVRAPEQVEKGGVSNVTEAKLIVELTSIFVKAGCSSPBIGII IAB YRQGLAKI TONLLARSIGMVENVITUKYGYPENSPVCFLNTD KVRAPEQVEKGGVSNVTEAKLIVELTSIFVKAGCSSPBIGII IAB YRQGLAKI TONLLARSIGNGVO PROKUNCYPELKEL LINHINSEKLI TOLLAGPSTSTTYSPPPDAFPSLRALLA ARYGEAGEGPGGABIPRICLOPPTSTSTYPPSPRAPARGOPE GLAWWGATAVAQLUMPAGLGGPGGSRAAVLVQQWSYADTELIP AACCATLPALGLARSSAQDPAVIGALGRALSPENDLETWRFYTCVRC PERRAVLGEVVLIYSGARPISKIQEOPBAPALEKTAAQCKEAKKA EKLEKFQGKQKIQQQOP PEGSEKKPEREKERDBGVITTULPTP PGEKKNVSGOPNPDSYSPRTVSRAAVTWMSQGFFKPEVGRINVS AAMPROVEMEN IPPRIVICISHLICHALTINGDLTRMERRINGG TILMINGCDHAGIATQVVVEKKLMRRQGLSRHQUKERAKRY KRIEEKGBRITYHQLKKLGSILDMRACFTIETHLGUDAVAV KRIEEKGBRITYHQLKKLGSILDMRACFTIETHLGUVAVAV HEKDTSTRLUNNSCTILNSATSDIEVDKKELTGRTTLSVPG YKERVEFGVUSSPRYVSGASDBEVVVAFILSTHICHLGUNAVAV HEKDTSTRLUNNSCTILNSATSDIEVDKKELTGRTTLSVPG YKERVEFGVUSSPRYVSGASBDBEVVAFILSTHICHLGUNAVAV HEKDTSTYGHLKGKNYTHPLSRSI.PIVPDEFVUMDRGTGAVKIT PAHDOMDVEVGORRIGLEATS KMOSGGAL INNUPPIGGAPRFEAR KAVLVALKERGLFRGIEDNPMVVPLCNSKNVVEPILRRQMYVR CGEMAQAASAANTRTSOLET IDBERGRTHHAMMINISH (MCMPFG KLAMGHRA IPATYFVTVSDPAVPOEBDPDGTGAVKSTREABARE KAAKERGVSPDKISLQQEDVLDTWSSGLEPISLIGHROLISNIDDS EVEKAKEGGKAPPAG1EFCTTALFFGLGTANFAKNYGRGRDINIDAV RILGYRHCKNLMNARKFALBGLSKGFVPSSTSSGGGRESUVOR WISSLTEAVLESNOP OAND PAVPTTAGYASGGRESUVOR WISSLTEAVLESNOP OAND PAVPTTAGYASGGRESUNDR WISSLTEAVLESNOP OAND PAVPTTAGYASGGRESUNDR VERSLTEAVLESNOP OAND PAVPTAGYASGALASITER VRP\LEADYNLHPESGFTCHEVAD LAGUNINGKMPOLLEY TURNARIESTSDPVNATIGELGSONNALHKESGISTRADILLSTTRA VRP\LEADYNLHPESGFTCHEVAD CATCALASGRVSGYVQGFG QAQVVAVAPEPMLEPS TYPKARMONDRALTITUOANDEKVDCLLGV TURNARGHSPSTIPWARMONDRALDERNINGKSYPHOULLEY VLEENKTPESDPVNA	1			
KS\LALLERITTGCLIDATTCMCINHE FISRATIONGESULF ISQPICLAGEPFSREPVI/CODEQUEPTUNERARALGMSESULF KRLEONKSAVVQLTVQTRMNSKINSLSNKLTYEKKLECGSDKVA NAVINLERHEKOVKLELEFYADYSDNPWLMGYPEPNNPVCFLNTD KVPAPEQVEKGGVSNVTEAKLIVELTSITVKAGCSBDIGITAP YRQQLKIINDLLARSIGMVENTIVDKYQD\RDKSIVLVSFVESN KDGTVGELIKUMRIRINVAITRAKKIKLIVSLTSITVKAGCSBDIGITAP YRQQLKIINDLLARSIGMVENTIVDKYQD\RDKSIVLVSFVESN KDGTVGELIKUMRIRINVAITRAKKIKLIVSPUSPLNOYPLEKL LNHLNSEKLIIDLDSREHBSICHILGDFQRE GFPAQSDBIDPVPPERSBLLITMSTIVVSPHPDAFPSLRALLA ARYGEAGEDCHGGABIPRICLQDPPTSRTSPPPDRIPALEGOPC GLWWGATAVAQLUMPAGLGGGGGSGRAPLWORDVSYADTELIP AACGATLPALGLRSSAQDPQAVLGALGRALSPLEWIRHHTYLA GEAPTLADLAAVTALLLPFRIVLDPPARRINNNYTHEVTCVRG PEFRAVLGEVVLYSGAR PLSSIGGPGSRAPALHKTAAQLKKEAKKR EKLEKPQKQKIQQQPPGEKKRKPEKKERDDGVTTDLPTT PGEKKDVSGAWPDDSYSPRIVSRAPYWEMOQOPFKDEVGRIPNVS AAMPROVFMGIPPPBVTGSILHLANTALQDSLTRMFRINGG ETILMINGCOLAGAIATOVVEKKLINRGGLARHOGGREAPLGEW KWKEEKGDRIYHQLKKLGSSLDWDRACPTMDPKLSAAVTEAFVR LHEEGIIVFSTLUMSGCTLINSAISDIEVDKLETTGRITLSVPG YKEKVEFGVLVS FAYKVQGSDSDEWVATIRIETHBLGDVAVAV HRKUTRYGHLEGKRVIHPPLSRSIPIVFDEFVUNDGFGAVKIT PAHDQNDVEVGONGLEBISITMSGRGALINVPPPFIGLBRFERA KANLVALKERGLFRGIEDNPMVVPLCNRSKDVUEPLLRRQMYVR CGGMAQAASAAVTRGDLRILDEPHQRTWHONIEW (MYPPG KLMWGHR\IPAYTVVSDPAVPPGEDPDGRYWSGREBARR KAAKEGVSPRKISLQQDEDVLDTWSSGLPPLSILGWBNOSED LSVFYPGTLLETGHDILFPWVARWAVLGLKUTRILDFRRGVYLHA IVROHAGRKMSKSLGNVIDPLDVIYGISLQGLINDLINSNLDPS EVEKAKEGQKADPPAGITTGLYMSGGGFISLIVTR WIRSKLTEAVRLSNOGFQADVDPAVTTAGLYSPFILERLOVVLEC LKPULNGVDQVAABCARQTIVTCLDVGLRLLSPPMFTEELFG RLPRRMPGDAPSLCVTPFPEPSSCSWKNDEREBARR VARVELVALSONGGPADPFACTTAGLASAVSGVYGGP QAQVVVAVABPERGLPROGORGACARGTLYTCLDVGLRLLSPPMFTEELFG RLPRRMPGDAPSLCVTPPFPSSTSCSWGGRESILVD WIRSKLTEAVRLSNOGFQADPFACTLAGLASAVSGVYGGP QAQVVVAVABPERGLPROGORGACARGTLYTCLDVGLRLLSPPMFTEELFG RLPRRMPGDAPSLCVTPPFPSSTSCSWGGRESILVT VRYLRADYNLHPESGPTCPLEVAD\EATGALASAVSGVYGGP QAQVVVAVABPERGLPROGORGANACHTRICEMPTIRIKDVHLL LERLHINSHLQMINKKYDDLARNILGHISTIPFALIRCHPTIRIKDVHLL VALQKVVOLLEFLIDENGLSELSHLUGLAITTINGKSYTPLOGLLSV VLEENKLTELPPERCLICESLINGESILVNINGKSTPLICPULTERSIMIN	1			
ISOPICLGPLFFSRRFVLUGDHQLEPLVLINREARALGMSESLIF KREDNIKSAVVOLTVOYENINSKIMSISHISHITTEGKLEGCSDKVA NAVINLRHFKDVKLUELFYADYSDNPPLMGVPEDNRPVCFLMTD KVPAPEOVEKGGVSNVTEKALTUPLTST TYMGGSPBIGITAP YRQOLKIINDLLARSIGMVEVNTVDKYQD\RDKSIVLVSFVRSN KDGTVGELLKDWRRIANTATRAKKILLIGCVPSLNCYPLEKL LINHINSKLIIDLDSRRHFSLCHLLABFOKAGSPBIGITAP YRQOLKIINDLLARSIGMVEVNTVDKYQD\RDKSIVLVSFVRSN KDGTVGELLKDWRRIANTATRAKKKLILLGCVPSLNCYPPLEKL LINHINSKLIIDLDSRRHFSLCHLLABFOKAGSPBIGITAP ARVGEAGEGFGGMGAHFRICLQPPPTSRTSTPPPRLPALBOGGE GLWWGATAVAQLLWPAGLGGGGGSRAAVLVQONVSYADTELIF AACGATLPALGLRSSAQDPOAVLGALGRTSTPPPRLPALBOGGE GLWWGATAVAQLLWPAGLGGGGGSRAAVLVQONVSYADTELIF AACGATLPALGLRSSAQDPOAVLGALGRTSTPPPRLPALBOGGE GLWWGATAVAQLLWPAGLGGGGGSRAAVLVQONVSYADTELIF AACGATLPALGLRSSAQDPOAVLGALGRTSTPPPRLPALBOGGE GLWWGATAVAQLLWPAGLGGGGGSRAAVLVQONVSYADTELIF AACGATLPALGLRSSAQDPOAVLGALGRTSTPPPRLPALBOGGE GEPTLADLAAVTALLLPPRVULDPPARRIWMNTRRFTCVDRC PEFRAVLGEVVLYSGARPLSHQDEXADVATEVTLEP EKLENOQKOKIQOQDPPGEKKPEKRERDDGVITYDLPTP PGEKKDVSGPWDDSYSPRYVSAAAVTWWBCOGFFKERVSCRNNV AAMPROVEPMCI PPRNVTGSLHLGHALTNALQDSLTRMERRGGG TTLMNGCDHAGLATQVVVEKLMRRQGGSHRLOGARFLOGWW KWKEEKGBTYHQLKKLGSSLDMDRACFTMPKLSAAVTRAFVR LHEGGITYSSTRLVMSCTILNSATSIDEVDKKELTGRTLLSVPG YKERVEFGVLVSSAYAVUNSCTILNSATSIDEVDKKELTGRTLLSVPG YKERVEFGVLVSSAYAVUNSCTILNSATSIDEVDKKELTGRTLLSVPG YKERVEFGVLVSSAYAVUNSCTILNSATSIDEVDKKELTGRTVLSVPG YKERVEFGVLVSSAYAVUNSCTILNSATSIDEVDKKELTGRTVLSVPG YKERVEFGVLVSSAYAVUNSCTILNSATSIDEVDKKELTGRTVLSVPG YKERVEFGVLVSSAYAVUNSCTILNSATSIDEVDKKELTGRTVLSVPG YKERVEFGVLVSSAYAVUNSCTILNSATSIDEVDKKELTGRTVAV KREEGGETTALARGATARAMTAGALGLGKOVVEPLLRRQMYVR CGSMAQAJAAAVTRGDLR ILMSPRRYTLSTMLLERQMYVR CGSMAQAJAAAVTRGDLR ILMSPRRYTLSTMLLRRQMYVR CGSMAQAJAAAVTRGDLR ILMSPRRYTLSTMLRRQMYNR KREEGGETALGALSTATAA YRPLAGAAAVTRGDLR YMPROSTEDETARAMAMAMAAAAVTRGDLR ILMSPRMSGGRDINLDVN RILGYRHCCHARAMAAAAVTRGDLR YMPROSTEDETARAMAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1			KS\LALLERLYTSOLIDATTCMGTNHDIPSPKIEDECIUDPAGO
RRLEQNISAVVQLIVQYRNNSKINKLTYEGKEGSDRVA NAVINLRHERVDVKLELEFYADYSDNPUNGENDRVCFLNTD KVPAPEQVEKGGVSINVTEAKLIVELTSIFVKAGGSPBJGIIAP YRQOLKIINDLLARSIGMVEVNTUKYQD\ROKSIVLVSFVRSN KDGTVGELLKDWRELWATTRAKKLILIGCVPSLINCYPPLEKL LINHINSEKLIIDLPSREHBSLCHILGBYQRE GSFPAQSDRLIPVPVFLRSBLLITNSTITVYSPHPDAFFSLRALIA ARVGEAGEGPGWGGAHPRICLQPPPTSRTSPPPPRLALEQGFG GLWWGATAVAQLUWPAGLGGGGGSGRAVLVQQWSYADTELIP AACARLPALGLRSSAQDPOAVLALGARLSPLEEMLHTYLA GEAPTLADLAAVTALLIP PRYVLIPPPARKINOVRSYADTELIP AACARLPALGLRSSAQDPOAVLALGARLSPLEEMLHTYLA GEAPTLADLAAVTALLIP PRYVLIPPPARKINOVRSYADTELIP PEGEKKOVSGPMPDSYSPRYVSARAYYWMENGQFFKPEYGRPNVS AAMPROVFMMCIPPPNVTGSLHLGHAITNATQDSLTRMFRIKGE TITMINGGCHAGAITQVVVEKKLINRQGLARGGERAPLGEW KWKSEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR LHEEGIIVRSTRLINNSCTLINSAISIEVERLGGREARLGEW KWKSEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR LHEEGIIVRSTRLINNSCTLINSAISIEVERLGGREARLGEW KWKSEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR LHEEGIIVRSTRLINNSCTLINSAISIEVERLGGREARLGEW KWKSEKGRORIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR CGEMQAASAAVTRODLRILDSAINDSKALINVPPFIGGPRFEAR KANLVALKERGLFRGIEDNPMVVPLCNRSKOVVEPLLRPQMYVR CGEMQAASAAVTRODLRILDSENGKOVEPLLRPQMYVR CGEMQAASAAVTRODLRILDSENGKOVEPLLRPQMYVR CGEMQAASAAVTRODLRILDSENGKOVEPLLRPQMYVR CGEMQAASAAVTRODLRILDSENGKOVEPLLRPQMYVR CKEMPOPPSPRIDDINGSED LSVFYGGTLESTHOTLDFFNVARMVELGLKUTGRLDFFRSVLIHA IVRDARGKRWSKSLGMVIDDFDMYTSGLFPGLINGNOLINDON RILGTRHCUNLINHATKPALKGLISKFPVSPTSTOPGGERSLVOR WIRSRLTEAVKLSNOGPGAVDPPAVTTAGYTSPHLVELCDVVLEC LKVILNGVDQVAAECARGTLYTCLDVGLRLLSSPIPMTELEG RLPRRMPQDPSLCVTPYPFBSTSCSKMOPBERSARAR VRP\LRADYNIHPESGPTCFLEVADLEATGALASAVSGVYQFG QAQVVAVAVAPEWGLAPPOLOCAVALASGRAVHOLLSSITRA VRP\LRADYNIHPESGPTCFLEVADLEATGALASAVSGVYQFG QAQVVAVAVAPEWGLAPPOLOCAVALASGRAVHOLLSSITRA VRP\LRADYNIHPESGPTCFLEVADLEATGALASAVSGVYQFG QAQVVAVAVAPEWGLAPPOLOCAVALASGRAVILDLGGLLSTTRA VRP\LRADYNIHPESGPTCFLEVADLEATGALLASAVSGVYQFG QAQVVAVAVAPEWGLAPPOLOCAVALASGRAVILDLGGLASTTRACLLLSP PLINLSSLVIAGGIITEIPDPALLUGLATTTLOGAVDKKVDCLLSV VLEENKLTELDPEKCLSELSNLQBLIVNINLLSTIBSPTIRLIKUSHL LLELHINNSHLQMINKTHOLGNINFKYTHOLGNIPTIR LKOMPIK PLINLASLVIAGGI	1)		ISOPICIOPI.FFSPDFVI.VCDVOOT.DDI.VI.NDFXDAT.CMCDGI.P
NAVINLEHPEDVKLELEFYADYSDNPWLMGYPERNRPUCFLINTD KVPAPEGVERGGVSNVTEAKLIVPITVAGCSPS DIG IAD YRQQLKIINDLLARSIGMVEVNTVDKYQD\RDKSIVLVSFYRSN KDGTVGELLKDWRRINVAITRAKHKLILLGCYSINCYPPLEKL LINHINSEKLIIDLDSREHSSLCHILDFQRE 6025 3977 89 GGPPAGSDHLPPVFPLESDLLITMSTLYVSSHPPAFFSLRALIA ARYGEAGGEFOWGGAHRPICLCQPPTSTSPPPRIPABLEGGRE GLWWGATAVAQLWPAGLGGPGGSRAVLVQOWSYADTELIP AACCATLPALGLRSSAQDPQAVLGALGRALSFLEEWIRLHTYLA GEAPTLADLAAVTALLLPFRYVLDPPARRIWNYTHWFVTCVRQ PEFRAVLGSVVI.YSGARPLSHQGGEAPALDKTAAQLKKEAKKR EKLEKRQOKKIQQQP POEKKENPERERDPGVITTUD.PTP PGEKKDVSGPMDBSYSPRYVERAMYPWMEQQGSPKEYCRPNVS AANPRGVFMCIPPPNVTSSLHIGHAINOGDSITRHRRGGE TTLMNPGCDHAGIATQVVVEKKLMRBQQLSRHQLGREAPLQEVW KWKEEKGDRIYHGLKKLGSSLDWDRACFTMDFNSGAVTERFRY LHEBGIIYRSTRLVMWSCTINSAISDIEVDKKELGRATLLSVPG YKEKVEFGGVLVSFAYKVQGSDBDEVVVATTRIETMLEDVAVAW HPKOTRYOHLKGKWVIHPFLSKSLDVFDVMDFGGTGAVKIT PAHDQMDVEVGGRIGLEATSINDSRGALINVPSPLEPPGPVVR CGEMAQAASAAVTRGDLRIPPISSLSPFUNDFGTGAVKIT PAHDQMDVEVGGRIGLEATSINDSRGALINVPSPLEPPGVVR CGEMAQAASAAVTRGDLRIPPISSLSPFUNDFGTGAVKIT PAHDQMDVEVGGRIGLEATSINDSRGALINVPSPLEPPGVVR CGEMAQAASAAVTRGDLRIPPISSLSPFUNDFGTGARKT LYRDAMGRAMSKIGNVIPPLDIVTGISLGGLHNQLLNSNLDPS EVEKAKEGGKADPFAGTPEGGTDALRFGLCAYMSGRDINLDVN RILGYHRFCNLMMATRFALRGLGKGPPSTGPGGGESLVDR WIESGLTEAVELSNOGFQAYDPPAYTTQYSPMLYSLCDVYLEC LKPVLNGVDQVAAECARQTLYTCLDVGLRILSPFPFVYTEELFQ RLPRRWPQAPPSLCVTYPYEPSSCSWKDPBERBALELAISITAA VRP\LRADYNLHPESGPTCFLEVAD\EATHTAQYSPMLYSLCDVYLEC LKPVLNGVDQVAAECARQTLYTCLDVGLRILSPFPFVTTEELFQ RLPRRWPQAPPSLCVTYPYEPSSCSWKDPBERBALELAISITAA VRP\LRADYNLHPESGPTCFLEVAD\EATHTAQYSPMLYSLCDVYLEC CCERPWETPRSTYMBASTVDCNDLGLITPFRELPATQLLLLQ MNIAKIESTDFPVAUTGLDLSQNNLSSVTINNGKKWPGLLSUT VJEENKLTELPEKKLDELISHLQELYTHNILLSTTSPGAFTGLLIN LERLHINSHLQMINSKWFADLAPHLISTITANTOKLUNDFLL URLEHLINNELQHINSKWFADLAPHLISTITANTOKLUNDFLL STDSLAVDALPWGLFRUDELSTHNINGSTYTINNGKKWPGLLSUL MNIAKISTDFPVAUTGLDLSGONLSSTYTINNGKKWPGLLSUL MNIAKISTDFPVAUTGLDLSGONLSSTYTINNGKKWPGLLSUL MSNALSALYRGTITESLPNIKEISTHSNFILESTGPPTGLLLKUPH VALUKVVNLKFLDLUNNPINIRTRRGDFSNIMLLKEISTHNMFKLESLEFUH MSNALSALYHGTITESLPNIKEISTHSNFILLESTGPTWRILLKUPH LER				
RVPAPEQVERGOVENVTEAKLIVPLTSIFVRAGCSBEDIGIIAD YRQOLKINDLIARSIINDLIARSIGMEWRYNTVOKOP RDKSIVIVSFVREN KDGTVGELLKDWRRINVAITRAKHKLILLGCVPSINCTPPLEKL LINHLINSEKLIIDLESREHESLCHTHISTLYSPHPDAFPSLRALIA ARYGEAGEOFGKGGAHPRICLGPPTSRTSFPPRIPALEGGEG GLWWGATAVAQLUMPGLGPPTSRTSFPPRIPALEGGEG GLWWGATAVAQLUMPGLGPGGGSARAVLVQOMVSYADTELIP ARYGEAGEOFGKGAHPRICLGPPTSRTSFPPRIPALEGGEG GEAPTLADLAAVTALLLPFRYVLDPPARRIWNYTMFVTURG PEFRAVLGEVVLYSGAR PLSHQEGGEAAVLVQOMVSYADTELIP AACGATLPALGLRSSAQDPQAVLGALGRALSFLEEWLRLHTYLA GEAPTLADLAAVTALLLPFRYVLDPPARRIWNYTMFVTURG PEFRAVLGEVVLYSGAR PLSHQEGGEAPLATKAQLKKEAKR EKLEKFQOKOKLQQQPPDGEKKPKPEERERKPDGVITTDLPTP PGEKKDVSGAPPDGSVSFRYVEAAWYPWEQQGFFKDEVGRIPNVS AANDEGVFMMCIPPDNVTGSLHLGHALTNALGDSLTRHHRWRGE TTILMNPGCDHAGIATQVVVEKKLMREGGLSRHQLGREAFLQEW KWKEERGORIYHQLKKLGSSLDWDRACGTMDFKLSAAVTEAFVR LHEEGIIVRSTRLDWWSCTLINSAISDLEVDKREHIGRTLLSVPG YKEKVEPFGVLVSFAYKVGGSBDEBEVVATTRIETMLGDVAVAV HPKOTRYOGHLKGKAVIHPPLSSISJEVPDEFVDMDFGTGAVKIT PAHORDVEVGGRIGLEAISIMDSRGALINVPPPFLGLRPFWAVR CGEMAQAASAAVTRGDLRILPERHQRTWHAMMDNIRE WCMPPG KLAWGHW, 1PAYPVTVSPDAVPGGBORTWYSGRRBARE KAAKEGVSPDKISLQQDEBVLDTWFSSGLFPLSILGWPNOSED LSVFYGGTLLSTGHDILFFWARMWLGLYTGTREPFEVYLHA IVRDAIGRRMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS EVEKAKEGOKADPPAGIPECGTDALREGLCAYMGGBDISLUVR RILGYKHCNIKMMATKFALRGLGGYGVPSPTSQGGGHESLVDR WIESRLTBAVZLSNQGFQAYDPPAVTTAQVSFWLJELCDVYLEC LKPVLNGDVQVAASCARCTLYTCLDVGLINGTREPFERSULDT RIPSRTPDQAPBGLCVTPYPEPSECSWKDPBABALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYYQGPG QAQVVAVAPBWGLPAP\QGCAVALASDRGST HHQLQG\LLDP ARREGG KLQ\AKRVEAQ\RQAQ\RAQVSKKYDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPRRIPANTQLLLQ TNNIARIEYSTDPFVRLTYBLDLSQMNSSYTINNKKMPQLLSV YLEENKLTELPERKLDSSTNINDEKTPRILLEGFPPFYTGEBLO TNNIARIEYSTDPFVRLTYBLDLSGARTTHURGENFITRINGENFITRINGMPK PLLINGSLVLAGIANITETPDNALVGLENLESISFYDNRLKVPLL URADAGSARAVERQLAGHELERINGENTIHR KOMPK PLLINGSLVLAGIANITETPDNALVGLENLESISFYDRRLKKPDH VAALGVUAULFLDLINKNPLINGESTHFNINGENFITRINGENFITH IRPMEDDSCORPOGGONGOVINGUNGLILLEESIFP	1]		
YRQCIKIINDLLARSIGMYZUNTVKYQD\ADKSIVIVSFVRSN KDGTVGELLKOWRRINVAITRARHKILGCYPSLNCYPPIEKL LNHLNSEKLI IDLPSREHESLCHILGCYPSLNCYPPIEKL LNHLNSEKLI IDLPSREHESLCHILGCYPSLNCYPPIEKL LNHLNSEKLI IDLPSREHESLCHILGCYBERGER GSFPAGSDHLPPVFPLESDLLITMSTLYVSBHPDAFSIRALIA ARYGEAGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			
KDGTVGELLKÜNRRILNVAITRAKHKILLIGCUYSINCYPPLEKI LIMHLINSKLI IOLDFGREBEISCHLIDFORDE 6025 3977 89 GGFPÄQSDHLPPVFPIRSDLLITMSTLYVSPHPDAFFSLRALIA ARYGEAGEGPGIGGAHPRICLQPPPTSRTSPPPRIPALEGGEG GLWWGGATAVAGLUHPRAGIGGPGGSRAVLVOQMVSJADTELIF AACCATLPALGURSSAODPOAVLGALGRALSPLEWIRLHTYLA GEAPTLADLAAVTALLPFRYLDPARI WINNVTEWBVTCVRQ PEFRAVLGEVVLYSGARPLSHQPGPBAPALPKTAAQLKKRAKKR EKLEKRQOKOKIQQQDPPGEKKPKPEKREKDFQVTTYDLPTP PGEKKOVSGPMPDSSYPRYVBAAVPBQQGFFPEFGRNVS AANDRGVFMMCIPPNVTGSLHLGHALTMAIQDSLTRMHRINGE TTIMNPSCCHAGIATOVVVEKKLMGSLSRHQLGREPLQEWW KWKSEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTBAFVR LHEEGIIYRSTRLVMWSCTINSAISDIEVDKRLTGRTLLGVAVAV HPKOTRYQHLKOKNVIHPFLSRSLPIVPDEFVDMDFGTGAVKIT PAHODNIPEVGGRHCLEAISIMOSGLSRHQLGREAPLQEWW KAVEVEFGVLVSFAYKVQGSDSDEBVVVANTTRIETMLGDVAVAV HPKOTRYQHLKOKNVIHPFLSRSLPIVPDEFVDMDFGTGAVKIT PAHODNIPEVGGRHCLEAISIMOSGLAINVOPPELLGDWFRAR KAVLVALKERGLFRGIEDNDMVVPLCNRSKDVVEPLLRPQWYVR CGEMAQAASAAVTRGDLRILPERHQRTWHAWDDNIRE\WCMFPG KLMWG\HR\IPAYFVTVSDPAVPPGEDPDGRWWSGRNEBABE KAAKEGUSPDKISLQQDEDVLDTWFSSGLFFLSILGWFNQSED LSVFYFGTLLETGHBILFFWVARMIKJKLTGGLFPFEVYLIA IVKDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLINSNLDBS EVERAEGGKADPPAGIPECGTDALRFGLCAYMSQGRDINLDVN RILGYRHFCNKLWARTKPALRGLGKFVPSPTSDGGHBSLVDR WIRSRLTBAVRLSNAGFQAVDFPAVTTAQYSBMLYELCDVYLEC LKPVLMGDVQAVAZEARQTLYTCLDWGLKLSPFMPFYTEELFG RLPRRNPQAPPSLCVTPYPEPSSCSKKDPEAPAALELALSITAA VRY\LBAVNLHPBSGPTCFLEVADLASDRCSI\LHQLQG\LLDD ARRLG\KLQ\AKRVEAQ\RQAQ\RL*\ERRAAASSNVKOYVQED QAQVVVAVAPBWGLPPP\QCACVALASDRCSI\LHQLQG\LLDD ARRLG\KLQ\AKRVEAQ\RQAQ\RL*\ERRAAASSNVKVPLE VQEADERALQGTABLKKVDEAILADFXNL TCHRPWFPPPRSIYMBASTVUCDLBLLLSFPMPFYTEELFG TCHRPWFPPPRSIYMBASTVUCDLBLLLSTSTPAFGIHN LLRHIHMSNRIQMINSKWFDALPHAAASGNVKVPLE TCHRPWFPPPRSIYMBASTVUCDLBLLLSTSTAFFIPKLEGHN LLRHIHMSNRIQMINSKWFDALPHAANGLINGKMPGLLEV YLEENKLIFELEKLSSELSHLORLYINNLLSTISPGAFTGHN LLRHIHMSNRIQMINSKWFDALPHATHYLIGHNITHI KOMMPK PLLNIRSSLVIAGINLTFIPDNALVGLERLESISFYDNRLIKVPH VALOKVVUKLSFILDINKNPINKITRINGENDHLHKELGINNMPEL ISIDSLAVDNLPPLIKRIETSIPNLEGISIHMEILGUNFRINKTN				
LIMHINSEKLI IDLPSREHESICHTLGDFQRE				
6025 89 GGFPAQSDHLPPYFPLRSDLLTMSTLYVSPHPDAFFSLRALIA ARYGEAGEGPPGWGGAHPRICLQPPFTSRTSPPRLENGGGG GLWWGGTAVAGLLWFAGLGGGGGGRAVLVQGWVSYDTELIF AACCATLPALGLRSSAQDPOAUGALGRALSPLESULRLHTYLA GEAPTLADLAAVTALLLPFRYLDAPRIWMNVTRWFUTCVRQ PEFRAVLGEVVLYSGARPLSHQPGPEAPALPKTAAQLKKEAKKR EKLEKRQQKQKIQQQPPPGEKKPKPEKKRPGVTTYDLPTP PGEKKDVSGPMPDSYSPTYDEAAVWECQGFFPEPGGRNVS AANPRGYFMCIPPNVTGSLHLGHALTNALQDSLTRWHRWRGE TTLMNPGCDHAGIATQVVVEKKLWREQGGFRQLGSRQLGW KWKEEKGDRIYHQLKKLGSSLDWDRACFTMDEKLSAAVTERFUR LHEEGIIYRSTRLVWWSCTLNSAISDIEVDKKBLTGRTLLSVPG YKEKVEFGULVSFAXVQGSDSDEWVATTRIETMLGDVAVAV HPKDTRYQHLKGKNVIHPFLSRSLPIVFDEFVDMDFGTGAVKIT PAHDQRDYEVGGRHGLEAISIMDSRGALINVPPFLGLPRFWRY CGEMAQAASAAVTRGDLRILDERHQRTWHAWMDNIRE WCMPPG KLWWG\HR\IPAYFYVSDPAVPPGEDPDGRYWVSGRNEBARE KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPMQSED LSVFYGGTLLETGHDILFFWVARMVMLGLKLTGRIPPREVYLHA IVRDAMGRKMSKSLGNVIDPLDUYSGAGLFULNSNLDPS EVEKAKEGGKADFPAGIFECGTDALRFGLCAYMSQGRDINLDVN RILGYRHFCNKLMNATKFALGGLGGFFVPSFTSQPGGHBSLVDR WISSRLTEAVRLSNQGFQAVDFPAVTTAQYSFWLFELCDVYLEC LKPVLNGVDQVABCCARALSDRCSI\HLQGGLLLDP AREIGKLO\AKRVEAQ\RQAO\RAPATTAQYSFWLFELCDVYLEC LKPVLNGVDAVBCEARGTLYTCLDUGLRLLSPMPFVTEBLPQ RARGKAGKLO\AKRVEAQ\RQAO\RAPATTAQYSFWLFELCDVYLEC LKPVLNGVDQVABCCAVALASDRCSI\HLQGGLLDP AREIGKLO\AKRVEAQ\RQAO\RAPEATTAQYSFWLFELCDVYLEC LKPVLNGVDQVABCCAVALASDRCSI\HLQGGLLDD AREIGKLO\AKRVEAQ\RQAO\RAPEATTAQYSFWLFELDOTYLEC CERPWFTPRSIYMEASTVDCHDLLLTFPARIPANTOLLLIQ TNNIAKIBYSTDFPVNLTGLBLSONNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINNLLSTISPGAFIGHIN LIRLHENSNLAGINNTERSTVDCHDLSLTTFPARIPANTOLLLIQ TNNIAKIBYSTDFPVNLTGLBLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINNLLSTISPGAFIGHIN LIRLHENSNLAGINNTERSTVDCHDLSLTTFPARIPANTOLLLSV YLEENKLTELPEKCLSELSNLQELYINNLLSTISPGAFIGHIN LIRLHENSNLAGINNTERSTVDCHDUGLSTFPARIPANTOLLLSV YLEENKLTELPEKCLSELSNLQELYINNLLSTISPGAFIGHIN LIRLHENSNLAGINNTERSTVDCHORGINHIPLECININFEKLINDER PLINLRSSLVIAGINLTEIPDNALVGLENESSFYDNRIIKVPH VALOKWUKKFELLNKPHNINFIRSTISPINHEICHTIALDESSFYDNRIIKVPH VALOKWUKKFELLNKPHRISTISHERSTISHTINDERCOVIRKWMMNINTN IRFMEDDDSLCVOUPPEPGOGNUWQHFRDMMEICLELLJAESEF	ļ			
ARYGEAGEGRGWGAHPRICLQPPTSRTSPPPPRLPALEQGEG GLWWGATAVAQLLWFAGLGGRGGSRAAVLVQGWYXDTELLIP AACCATLPALGLESSAQDPQAVLGALGRALSPLEEWLRHITYLA GEAPTLADLAAVTALLLPRYVLDPPARHIWNNTRWFVTCVRQ PEFRAVLGEVVLYSGARPLSHOFGPBAPALPKTAAQLKKEAKKR EKLEKFQQKQKIQQQPPGEKERPRERRERDGVTTYDLPTP PGEKKDVSGMPDBYSSPRVEAAWTPWEQQFFKEPSCRNVS AANPRGVFMMCIPPDWTTGSLHLGHALTNATQGSLTRWHRWRGE TTLWNPGCDHAGLATQVVVEKKLMREQGLSHRQLGREAPLQEW KWKEEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVA LHEEGIIYRSTKLVSWSCTLNSAISDIEVDKKBLTGRTLLSVPG YKEKVEFGVLVSFAYKVQGSDBDEEVVYATTRIETMLGDVAVAV HPKDTRYQHLKGKNUTHPPLSSLPIVPDEFVDMDFGTGAVKIT PAHDQNDYEVGGRHGLEAISIMDSRGALINVPPPPLGLPPERR KAVULVALKERGLFRGIEDNPMVVPLCNRSKDVVEPLLRPÇWYVR CGEMAQAASAAVTRGDLRILPERHQRTWHAMMDNIRE\WCMPFG KLAWGHRIJPAYFVTVSDPAVPPGEDPGRYWVGGRNEABARE KARKEFVSSPDKISLQODBDLVFSSGLEPUSLIGWPNQSED LSVEYPGTLLETGHDILFFWVARMWMLGLKLTGRLPFREVYLHA IVRDAHGRKMSKSLENVIDPLDVYGIGLGLHNQLINSNLDPS EVEKAKEGGKAPPAGIFECTDALRFGLCAYMSQGRDINLDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSTSGGGHESLUDR WISSRLTEAVRISNGGFQAVPTATQYSFBHLYBLCDVUYLEC LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ RIPRRYPQAPPSLCVTPYPERSECSWKDPBEBABALBLAISITRA VRF\LRADVINLHPESGPTCTELVAD\EARTGLAGARVGGVOGFG QAQVVVAVAPPGGLPAYQGCAVALASDRCSI\HLGLGGLLLDY ARBLGKLQLAKRVEAQ\RQAQRAD\RLSCTIHLGLIGGLLLDY TNNIAKIEYSTDFPVMLTGLDLSQNNILSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSEKLDLLILTTITUQAUKKKVDCPRIC TCSIRPWFTPRSIVRASTVOLDLLLTTITUQAUKKKVDCPRIC TCSIRPWFTPRSIVRASTVOLDLLLSTIFTRARDATGLLLLQ TNNIAKIEYSTDFPVMLTGLDLSQNNILSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNILGELYILMISTISTBATIGHUN LLRLHLINSNRLQMINSKNFDALPRILETINGERPSPITIKWPH LLRLHLINSNRLQMINSKNFDALPRILETINGERPSPITIKWPH PLINLRSLVIAGINLTBIPDMALVGLENLESISTYNNRILKVPH PLINLRSLVIAGINLTBIPDMALVGLENLESISTYNNRILKVPH VALQKVVALKEPLDLIKKIISTINFREGFSPOMHHLKEGINNMPEL ISIDSLAVDNLPDLRKIENTNRPLSYIHPNAFFRLPKLESIML NSNALSALYHGTIESLENLIKEISINSHDRICDCUTRWMINNINTIN RRMBPDSLFCVOUPPETGGGOWNGVYHFROMMETCLELLERSSFP	6025	3977	89	
GLMYWGATAVAQLLMPRGLGGPGGSRAAVUQQMYSYADTELIE AACGATLPALGLRSSAQDPQAVLGALGRALSPLEEWLRLHTYLA GEAPTLADLAAVTALLLPRYVLDPPARRIWINNTRMFVTCVRQ PEFRAVLGEVVLYSGARPLSGCPEAPALPKTAAQLKKEAKKR EKLEKFQOKGKI QOQOPPGEKEKPKPEKEKRPDEVTTYDLPTP PGEKKDVSGPMPDSYSPRYVEAAWYPWWEQQGFPKPEYGRPNVS AANPRGVFMMCI PPRNVTGSLHLGHALTINALQDSLTRWHEMRGE TTLWNPGCCHAGIATQVVVEKKREQGLSRHQLGREAFLQEW KWKEEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTBAFVR LHEEGI IYRSTRLVWWSCTLNSAISDIEVVDKKELTGRTLLSVPG YKEKVEFGULVSFAYKVQGSDSDEVVVATTRIETMLGDVAVAV HPKDTRYGHLKGRNYLHPPLSRSLPIVPDFWDMDFGTGAVKIT PAHDQNDYEWGGRGLGAIS INDSGALINVPPPLGLPRPERA KAVLVALKERGLFRGI EDNPMVVPLCNRSKDVVEPLLRPQWYVR CGEMAQAASAAVTRGDLRILDERHQRTHAMMDNIRS\MCMFPG KLMWG\HR\IPATYTVSDFAVPPOEDPDGRYWVSGRNEABARE KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPRQSED LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYHHA IVRDAHGRMMSKSLGNVIDPLDVYGGISLGQHNQLLNSNLDDS EVEKAREGGKADFPAGI FPCGTDALRFGLCAYMSQGRDINLDVN RILGYHFCNKLWMATKRALRGKFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFMLYELCVVYLEC LKSVLNGVDQVAAECARGTLYTCLDVGLRLLSPFMPFVTEELFQ RLPRRMPQAPPSLCTYPPEFSECSWKDPEABABLELAISITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAPBWGLFAP\QGCAVALASDRCSI\HLGLGG\LLDP ARRLGK KQ\ARVEQAQ\CAVALASDRCSI\HLGLGG\LLDP ARRLGK KQ\ARVERAQQ\CAVALASDRCSI\HLGLGG\LLDP ARRLGK KQ\ARVERAQQ\CAVALASDRCSI\HLGLGG\LLDP ARRLGK KQ\ARVERAQQ\CAVALASDRCSI\HLGLGG\LLDP ARRLGK KQ\ARVERAQQ\CAVALASDRCSI\HLGLGG\LLDP ARRLGK KQ\ARVERAQQ\CAVALASDRCSI\HLGLGG\LLDP TTNIARIETSTDFFVNLTIGLDLSQNNLSSVYNINGKKMPDLFRC TCEIRBWFTPRSIYMEASTUVDLIGLLTFPARLPANTOILLLQ TNNIARIETSTDFFVNLTIGLDLSQNNLSSVYNINGKKMPDLFRC TCEIRBWFTPRSIYMEASTUNDLIGLITPARLPANTOILLLQ TNNIARIETSTDFFVNLTIGLDLSQNNLSSVYNINGKKMPDLFGLHN LLRLHLNSNRLQMINKSKFPALFUREITINGKEMPLLEGINNMPK PLINLRSLV IAGINLTBIPDNALVGLENLESISFFYDNRIKVPH PLINLRSLV IAGINLTBIPDNALVGLENLESISFFYDNRIKVPH PLINLRSLV IAGINLTBIPDNALVGLENLESISFFYDNRIKWPH ISDBLAVONLEPDLIKKPISISHNHILKSISHSPRPHLEKLGLINMPEL ISDBLAVONLEPDLIKKPISHTNERDYCHPROMECICLLELISFSFP				
ACCATLPALGLESSAQDPQAVLGALGRALSPLEEWIRLHTYLA GEAPTLADLAAVTALLL PFRYVLDPPARR IWNNVTRWFUTCVRQ PEFRAVLGEVVLYSGARPLSHQPGPEAPALEKTAAQLKKEAKKR EKLEKFQQKKLQQQQPPGEKKPKPEKREKDPGVTTYDLPTP PGEKKDVSGMPDSYSPRYVEAAWYPWHEQQGFFKPEYGRPNVS AANPRGVFMMCI PPPNVTGSLHLGHALTNALQDSLTRWHEMRGE TTLWNPGCDHAGLATQVVVEKKLMREQGLSRHQLGREAPLQEWW KWKEEKGARTYHQLKKLGSSLDMRACFTMDPKLSAAVTEAFVR LHEEGI IYRSTRLVNWSCTLNSAISDIEVDKKELTGRTLLSVPG YKEKVEFGVLVSFAYKVQGSDSDEEVVVATTRIETMLGDVAVAV HPKDTRYQHLKKGNVIHPPLSSRJPIVPDEFVDWDFGTGAVKIT PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPPPLGLPRFEAR KAVLVALKERGLFRGIEDNPMVVPLCNSKDVVEPPLLRPGWYVR CGEMAQASASANTRGDLRILDERGTHAMMONIEN\CMPPG KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEABARE KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNQSED LSVFYFGTLLETGHDILFFWAMYMMLGLKLTGRLFPFREVYHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLINSNLDPS EVEKAKEGQKADFPAGIPECGTDALFFGLCAYMSQGRDINLDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSFTSQPGGHESLVDR WISSRLTEAVRLSNQGFQAYDFPAUTTAQVSFWLYELCDVYLEC LKPULMGVDQVAABCARQCTLYDGLGRLLSPMPFVTEELFQ RLFRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATAGLASAVSGYVQGFG QAQVVAVAPEPBGLPP\GCGVAVLASDRCSI\HLDLQGLLDD ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEABLRKVDBAIALFQKML 6026 2674 514 GPITFLKKKAKMKDWPLRTHULGITTTUQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNIGLLTTPTALPANTQILLLQ TNNIAKIEYSTDFFVNLTGLDLSQNNLSSYNINIKRWPGLLSV YLEENLITLEPEKCLSELSNLOELYINNINLISTISPAFTGHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMFK PLINLRSLVIAGINLTBIPDMALVGLENLESISFYDNRLIKVPH VALQKVVNLKFFLDLKKNININGSTGPSNIHLHKEGINNMPEL ISJDLAVONLPDLKKIE ATNIPRLSYTHPNAFFRLPKLESLML NSNALSALYHGTIESLPNKEISISHSPIRCDCVIRWMMKNKTN IRFMBPDSLFCVUPPPEPGGGNVRQVPRDMMETCLELIAPESSP				
GEAFTLADLAAVTALLLPFRYVLDPPARRIWNNYTRMFVTCVEQ PEFRAVLGEVVLYSGARPLSHQPGBEAPALPKTAAQLKKEAKKR EKLEKFQQKQKIQQQPPPGEKKPKPEKREKRPGVITYDLPPP PGEKKDVSGPMDDSYSPRYVEAAWYDWEQQGFPKPEYGRPNVS AANPRGVFMMCIPPPNVTGSLHLCHALTNAIQDSLTRWHRMGE TTLWNPGCDHAGIATQVVVEKKLWREQGLSRHQLGREAFLQEVW KWKEEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR LHEEGIIYRSTRIVNWSCTLINSAISDIEVDKKBLTGRTLISVPG YKEKVEFGVLVSFAYKVQGSDSDEEVVVATTRIETMLGDVAVAV HPKDTRYQLLKGKNVIHPFLSRSLPIVFDEFVDMDFGTGAVKIT PAHDQMDYEVGQRHGLEAISIMDSRGALINVPPPFLGLPFFAR KAVLVALKERGLFRG IEDNPMVVPLCNRSKDVVEPLLRPQWYVR CGEMAQAASAAVTRGDLRILPENQRTWHAWMDNIRE\WCMPPG KLWMG\HR\TPAYFVTVSDPAVPFGEDPDGRYWVSGNREBEARE KAAKEFGVSPDKISLQQDEDVLDTWFSGLFPLSILGWPNQSED LSVFYFGTLLEFTHOTLIFFWVARMVLIGLKLTGRLFFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS EVEKAKEGQKADFPAGIPEGGTDALRFGLCAYMSQGRDINLDVN RILGYRHFCKLKUNATKFALRGLGKGFVPSPTSQDGGHBSLVDR WIRSRITEAWRLSNQGFQAYDFPAVTTAQYSPMLYBLCDVYLEC LKPVLNGVDQVAAECARQTLYTCLDGLRLLSFFMFFVTEELFQ REPRRMPQAPPSLCVTFYFEPFSCSKKDPEABABLELAISITRA VRP\LRADVNLHPESGFTCPLEVAD\EATGALASAVSGYVQGFG QAQVVVAVAPPWGLPAP\QGCAVALASDRCSI\HLQGLSLLDP ARELGKKQ\KQ\AKKVEAQ\RQAQ\RLE\ERRA\ASGNPVXVPL\E VQEADBARLQQTEAELRKVDEATALACKML GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCMDLGLLTFPARLEANTQLLLQ TNNIAKIEYSTDFPVNITGLDLSQNILSSVTNINGKMPQLLSV YLEENLITELJBERCLSELSHLKUEISIHLSISFPDRFIGHN LLRHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKVMPK PLINLRSLVIAGINLTEIPDNALVGLEENLESISFTDNRLIKVPH UALQKVVNLKFLDLINNDINGT REGOFSOMHLIKEGIGINMPPL 1SIDSLAVDNLPDLRKIESIHLKEISIHNPELSIML				AACGATLPALGLRSSAODPOAVIGALGRALSPIEEWLRI.HTVI.A
PEFRAVLGEVVLYSGAR PLSHQPGPBAPALPKTAQLKKEAKKR EKLEKFQQKQKIQQQPPDGEKKPYBEKREKRDGVITYDLPTP PGEKKDVSGPMPDSYSPRYVEAAMYPWWEQQGFFKPEYGRPNVS AANPRGVFMMCIPPNVTGSLHLGHALTNAIQDSLTRWHHMRGGE TTLWNPCCDHAGIATQVVVEKKLWREQGLSRHQLGREAPLQEVW KWKEEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTBAFVR LHEEGIIYRSTRLVNWSCTLINSAISDIEVDKKBLTGRTLLSVPG YKEKVEFGVLVS FAYKVQGSDSDEEVVVATTRIETMLGDVAVAV HPKDTRYQHLKGKNVIHPFLSRSLPIVFDEFVDMDFGTGAVKLT PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPPFLGLPRFEAR KAVLVALKEEGLFRGI EDNPMVVPLCNRSKDVVEPLLRPQWYVR CGEMAQAASAAVTRGDLRILPERHQRTWHAWMDNIRE\KCMFPG KLWMG\HR\TPAYFVTVSDPAVPPGBDPDGRYWVSGNBEAREE FAAKEFGVSFDKISLQQDBDVLDTWFSSGLPFLSILGWROGSD LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS EVEKAEGGKADPFAGIPEGGTDALRFGLCAYMSQGRDINDDN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAOTPEGTDALKFGLCAYMSQGRDINDLDN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAOTPEGTDALSSFNFYVTEELFQ LKPVLNGVDQVAAECARQTLYTCLDUGLRLLSFPMFFVTEELFQ RLPRRMPQAPPSLCVTPYPPEPSECSWKDPEABALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGVQGPG QAQVVAVAEPWGLPAP\GCAVALASDRCST\HLGLGG\LDP ARELG\KLQ\ARRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEALQGTEAELRKVDEAIALFGKML 6026 2674 514 GPTTFLKKKKMKMDMPLRITVLLGLAITTUVQAVDKKVDCPRLC TCBIRWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQLLLQ TNNIAKIEYSTDFPVNILTGLDLSQNILSSVTNINGKKMPQLLSV YLEENKLTELPERCLSELSHLGELYINHMLLSTIFGAPTGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENFIIRIKDMFK PLINLRSLVIAGINLTEIPDNALVGLEALESTEFDNRLIKVPH VALQKVVNLKFLDLWNDIRGT RRGDFSNMLHKEIGINNMPEL ISIDSLAVDNLPDLRKIESTHNNFRLSYTHPNAFFRLYKLESLML NSNALSALYHGTIESLPNLKEISTISNPIRCDEVIRMMNKTN IRFMBEDSLFCVDPPEFGQQNVRQVHFRDMMDICLPLLAPSSFP				GEAPTLADLAAVTALLLPFRYVLDPPARRIWNNVTRWEVTCVPO
EKLEKFQXKOKIQQQPPGEKKPKPEKREKRDPGVITYDLPTP PGEKKDVSGPMPDSYSPRYVEAAMYPWWEQQGFFKPEYGRPNVS AANPRGVFMMCIPPPNVTGSLHLGHALTMAIQDSLTRWIMRMGE TTLWNPGCDHAGIATQVVVEKLWREQGLSRHQLGREAPLQEVW KWKEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR LHEEGIIYRSTRLVNWSCTLNSAISDIEVDKKELGTATLLSVPG YKEKVEFGVLVSFAYKVQGSDSDEEVVVATTRIETMLGDVAVAV HPKDTRYQHLKKKRAVIHPFLSRSLPIVPDEFVDMPGTGAVKLT PAHDQNDYEVGQRIGLEAISIMDSRGALINVPPPFIGLPRFEAR KAVLVALKERGLFRGIEDNPMVVPLCNRSKDVVEPLLRPQWYVR CGEMAQAASAAVTRADLRILDERRHGRTHHAWMDNIRE\WCMPPG KLWMG\URFLAYPVTVSDPAVPPGEDPDGRTWVSGRNEBARE KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNQSED LSVFYPGTLLETGHDILFFWVARWMLGLKLTGRIPFFREVYLHA IVRDAHGRKWSKIGNVIDPLDVIYGISLGGLHNGLINSNLDPS EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVN RILGYRHFCNKLWMATKFALRGLGKGFVPSPTSQPGGHESLUDR WIRSRIFEAVRLSNOGFQAVDFPAVTTAQYSFMLVELCDVYLEC LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ RLBPRRMPQAPPSLCVTFYPEFSESCEWKDPEABAALGLALISITRA VRP\LRADVHHPESGPTCFLEVAD\EATGALASANSGVYQGGG QAQVVVAVAEPWGLPAP\QCCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\BERRA\ASGNPVKVPL\E VQEADRAKLQQTEAELRKYDEAIALFLYAGNVKVDCPRLC TCSIRPWFTRSIYMEASTVDCNDIGLITFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPBERCLSELSNLQELYINNINLSTISPGAFIGLHN LLRLHLMSNRLQMINGSWFDALPNLEILMIGRNPIRIKDMFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRGDDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYHPPNAFRELESLML NSNALSALYHGTIBSLPNLKEISIHSNPIRCDCVIRWMMNKTN IRFMEPDSLFCUDPPEFQGQNVRQVHFRDMEICLPLTAPRSFP	1			
PGEKKDVSGMPDSYSPRYVEAAWYPWEQQEFKPEYGRPNVS AANPRGVFMMCIPPDNVTGSLHLGHALTNAIQDSLTRWIRMRGE TTILMNPGCDHAGIATQVVVEKKLNREQGLSRHQLGREAFLQEW KWEEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR LHEEGIIYRSTRLVNWSCTLNSAISDIEVDKKELTGRTLLSVPG YKEKVEFGVLVSFAYKVQGSDSDEEVVVATTRIETMLGDVAVAV HPKDTRYQHLKGKAVIHPPLSRSLPIVPDEFVDMDFGTGAVXIT PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPPFLGLPRFEAR KAVLVALKERGLFRGIEDNPMVVPLCNRSKDVVEPLLRPQWYVR CGEMAQAASAAVTRSDLRILPERHQRTWHAMMDHIRE\MCMPFG KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEABARE KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWBNQSED LSVFYPGTTLETGHDILFFWVARMMULGLKLTGRLPFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS EVEKAKEGGKADFPAGIPECGTDALRFGLCAYMSGGRDINLDVN RILGYRHFCNKLWMATKFALRGLGKGFVPSPTSQPGGHESLUDR WIRSRLTEAVRLSNQGPQAYDFPAVTTAQYSFWLYELCDVYLEC LKPULNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFTVTEELFQ RLPRRWPQAPPSLCVTPYPEPSECSWKDPEABAALELAISITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QCGAVALASDRCSI\HLQLGS\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLA\SERAALASANSGYVQGPG QAQVVVAVAPBWGLPAP\QCGAVALASDRCSI\HLQLGS\LLDQ TCSIRPWFTPRSIYMEASTVDCNDLGLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPERCLSELSILQELYININLLSTISPGAFIGLHN LKRLHLNSNRLQMINSKWFDALPRILBILMIGENPIRIKDMFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLXFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYHPPAFFRLESIML NSNALSALYHGTIBSLPNLKEISIHSPIRCDCVIRWMNMKTN IRFWEPDSLFCUDPPEFGGGONVRQVHFRDMEICLPLTAPRSFP				
AANPRGVFMMCI PPPNVTGSLHLGHALTNAIQDSLTRMIRMRGE TTLWNPGCDHAGIATQVVVEKKLWREQGLSRHQLGREAFLQEVW KWKEEKGDRIYHQLKKLGSSLDMDRACFTMDFKLSAAVTEAFVR LHEEGIIYRSTRLVXWSCTLNSAISDIEVDKKELTGRTLLSVPG YKEKVEFGVLVSFAYKVQGSDEEVVVATIRIETMLGBUAVAV HPKDTRYQHLKGKNVIHPFLSRSLPIVFDEFVDMPGTGAVKIT PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPPFLGLPRFEAR KAVLVALKERGLFRGIEDNPMVVPLCNRSKDVEPLLRPQWYVR CGEMAQAAAAVTRGDLRILPERHQRTWHAMMDHIRE,WCMPPG KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEABARE KAAKEFGVSPDKISLQQDEBVUDTWFSSGLFPLSILGMPNQSED LSVFYPGTLLETGHDILFFWVARWMLGLKLTGRLPFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNGGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVLNGVDQVAAECARCTLYTCLDVGLRLLSPFMPFYTEELFQ RLPPRMPQAPPSLCVTPYYFEPSECSWKDPEABAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAAPBWGJPAP\GGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADBAKLQQTEAELRKVDBAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCSIRPWFTPRSIYMEASTVDCONLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGHN LLRLHLNSNRLQMINSKWFDALPNLESILFRIGRIFIRIKVDHFK PLINLRSLVIAGINLTBIPDNALVGLENLESISFPJDNRLIKVPH VALQKVVNLKFLDLINKDPINRIRRGGFSNMLHKELGINNMPEL ISIDSLAVDNLPPLIRKIESISHNLERISFPJNRLEKLESIML NNALSALYHGTIESLPNLKEISISNPIRCDCVIRWMMMKTN IRFWEPDSLFCVDPPEFFGQNVRQVHFRDMMEICLPLIAPESFP				
TTIMPGCDHAGIATQVVVEKKLMREQGLSRHQLGREAPLQEVW KWKEKKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR LHEEGIYRSTRLJWWSCTINSAISDIEVDKKBLTGRTLLSVPG YKEKVEFGVLVSFAYKVQGSDSDEEVVVATTRIETMLGDVAVAV HPKDTRYCHLKGKNVIHPPLSRSLPIVFDEFVDMDFGTGAVKIT PAHDONDVEVGGRHGLEAISIMDSRGALINVPPPFLGLPRFEAR KAVLVALKERGLFRGIEDNPMVVPLCMRSKDVVEPLLRPQWVVR CGEMAQAASAAVTRGDLRILPERHQRTWHAMMDNIRE\WCMPPG KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEABARE KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNQSED LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLMSNIDPS EVEKAKEGGKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRITEAVKLSNQGFQAYDFPAVTTAQYSFMLYELCDVYLEC LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ RLBRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAPBWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARRLG\KIQ\LQ\KVEAG\RQAQ\RAQ\RACSAPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLIGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFFVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQBLYINHNLLSTISPGAFIGLHN LERLHLMSNRLQWINSKMFDALPNLETLMTGEMPIIRIKDMPK PLINLRSUVIAGINLITEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPPLIRKIESISLPNLKEISISHSDPIRCDCVIRWMNMKTN IRFMEPDSLFCVDPPEFGGQNVRQVHFRDMMEICLPLIAFESFP	1			AANPRGVFMMCIPPPNVTGSLHLGHALTNAIODSIJTRWHRMRGE
KWKEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR LHEEGIIYRSTRLVNWSCTLNSAISDIEVDKKELTGRITLLSVPG YKEKVEFGVLVSFAYKVQGSDSDEEVVVATTRIETMLGDVAVAV HPKDTRYQHLKGKNVIHPFLSRSLPIVFDEFVDMDFGTGAVKIT PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPPFLGLPRFEAR KAVLVALAKERGLFRGIEDNPMVVPLCNRSKDVVEPLLRPQWVR CGEMAQAASAAVTRGDLRILPERHQRTWHAWMDNIRE\WCMFPG KLWWG\HR\IPAYFVTVSDPAVPGGDPDORYWVSGRNEABARE KAAKEFGGYSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNQSED LSVFYPGTLLETGHDILFFWVARWMLGLKLTGRLPFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIVGISLGGLHNQLLNSNLDPS EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVLNGVDQVAAECARQTLYTCLDVGIRLLSFFMPFVTEELFQ RLPRRMPQAPPSLCVTPYPBPSECSWKDPEAEBALBLALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVABEWGLPAP\QCCAVALASDRCSI\HLGLGG\LLDP ARRLG\KLQ\AKRVEAQ\RQAQ\RLR\ERA\ASGNPVKVPL\E VQEADEAKLQQTEABLRKVDEAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRHVLGGLAITTLVQAVDKKVDCFRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LRRHLHLNSNRLQMINSKWFDALPNLEILMIGKMPPLLSV PLINLRSLVIAGININSKWFDALPNLEILMIGKMPPLLSV PLINLRSLVIAGININSKWFDALPNLEILMIGKMPPLLSV PLINLRSLVIAGININSKWFDALPNLEILMIGKMPPLLSV PLINLRSLVIAGININSKWFDALPNLEILMIGKMPPLLKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLKKIEATNNPRLSYTHPNAFFRLPKLESIML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMKTN IRFWEPDSLCVUDPEFQQQNVRQVHFRDMMEICLELLAFESFP				TTLWNPGCDHAGIATOVVVEKKLWREOGLSRHOLGREAFLOEVW
LHEEGI IYRSTRİJVNMSCTINSAISDIEVÜKKELTGRTILSVPG YKEKVEFGVLVSFAYKUQGSDSDEBUVDATTRIETMIGDUAVUX HPKDTRYQHLKGKNV1HPFLSRSLPIVFDEFYÜMDFGTGAVKIT PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPPFLGLPRFEAR KAVLVALKERGIFRGIEDNPMVVPLCNRSKDVVEPLLRPQWYVR CGEMAQAASAVTRGDLRILPERHQRTWHAMMDNIRE\WCMFPG KLWMG\HR\IPAYFVVSDPAVPPGEDPDGRYWVSGRNEABARE KAAKEFGYSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNQSED LSVFYPGTILLETGHDILFFWVARMYMLGIKLTGRLPFREVVLHA IVKDAHGRKMSKSLGHVIDELDVIGISLQGLHNQLLNSNLDPS EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVLNGVDQVAAECARQTIYTCLDVGGRLLSPFMPFVTEBLFQ RLPRRMPQAPPSLCVTPYPEPSECSWKDPEABAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARRLG\KLQ\AKRVERQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADBAKLQQTEAELRKVDBAIALFQKNL 6026 2674 514 GPITFLKKKARMKDMPLRITULGLAITTLVQAVDKKVDCFRLC TCSIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINNNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINIKTEIPDNALVGLERLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYTHPNAFFRLPKLESIML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMKTN IRFMEPDSLCVDPPEFQQQNVRQVHFRDMMEICLELLAFESFP				
YKEKVEFGULVSFAYKVQGSDSDEEVVVATTRIETMLGDVAVAV HPKDTRYQHLKGKNVIHPLSRSLIPIVPDEFVDMDFGTGAVKIT PAHDONDVEVGQRGLEAISIMDSRGALINVPPPFLGLPRFEAR KAVLVALKERGLFRGIEDNPMVVPLCNRSKDVVEPLLRPQMYVR CGEMAQAASAAVTRGDLRILPERHQRTWHAMMDNIRE\WCMFPG KLWWG\HR\IPAYFVTVSDPAVPPGEDPDRTWVSGRNEABARE KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNQSED LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLFFREVYLHA IVRDAHGRKMSKSLGNVLDPLDVIYGISLQGLHNQLLNSNLDPS EVEKAKEGQKADFPAGIPECTDALRFGLCAYMSGGRDINLDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVLNGTDQVAAECARQTLYTCLDVCLRLLSPFMPFVTEELFQ RLPRRMPQAPPSLCVTFYPEPSECSWKDPEABABELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEABLRKVDBAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMBASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMIFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYJHPNAFFELPKLESLEML NSNALSALYHGTIESLPNLKEIS ISNPIRCDCVIRWMNMKTN IRFMEPDSLFCVDPPEFFQGNWRQVHFRDMMEICLPLIAPESFP	1			
HPKDTRYOHLKGKNVIHPPLSRSLPIVPDEFVDMDFGTGAVKIT PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPPFLGLPRFEAR KAVLVALKERGLPRGIEDNPMVVPLCNRSKDVVEPLLRPQWYVR CGEMAQAASAAVTRGDLRILPERHQRTWHAWMDNIRE\WCMPPG KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEAEARE KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNQSED LSVFYPGTLLETTHOILFFWVARMVMLGLKLTGRLPFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDPPAVTTAQYSFWLYELCDVYLEC LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ RLPRRMPQAPPSLCVTFYPPESSCSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPMGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFCKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISFGAFTGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYTHPNAFFRLPKLESLML NSNALSALYHGTIESJPNLKEIS ISNPIRCCVIRWMNMKTN IRFMEPDSLFCVDPPEFQGNVRQVHFRDMMEICLPLIAPESFP	}			
PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPPFLGLPRFEAR KAVLVALKERGLFRGIEDNPMVVPLCNRSKOVVEPLLRPQWYVR CGEMAQAASAAVTRGDLRILPERHQRTWHAWMDNIRE\WCMFPG KLWWG\HR\IPAYPVTVSDPAVPPGEDPDGRYWVSGRNEABARE KAAKEFGVSPDKISLQQDBDVLDTWFSSGLFPLSILGWPNQSED LSVFYPGTLLETGHDILFFWVARMWMLGLKLTGRLPFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS EVEKAKEGGKADFPAGIPEGGTDALRFGLCAYMSGGRDINLDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAVTTAQVSFWLVELCDVYLEC LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ RIPRRMPQAPPSLCVTPYPEPSECSWKDPEABAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGHN LLRLHLMSNRLQMINSKWFDALPNLBILMIGENPIRICHDHNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYTHPNAFFRLPKLESIML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLTAPESFP	:	;		
CGEMAQAASAAVTRGDLRILPERHQRTWHAWMDNIRE\WCMFPG KLWWG\HR\IPAYFYTVSDPAVPPGEDPDGRYWVGRNEABARE KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNQSED LSVPYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVINGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEARLQQTEAELRKVDEAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLATTTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGDLLSQNNLSSVTNINGKKNPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLMSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWNMNKTN IRFMEPDSLFCVDPPEFQGONVRQVHFRDMMEICLPLIAPESFP				
KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEAEARE KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWENQSED LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINIDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKFVLINGVDQVAAECARQTLYTCLDVGLRLLSPFMPFYTEELFQ RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADVANLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQCQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML GPITFLKKKAKKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLLAPESPP	1 1		•	KAVLVALKERGLFRGIEDNPMVVPLCNRSKDVVEPLLRPOWYVR
KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEAEARE KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWENQSED LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINIDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKFVLINGVDQVAAECARQTLYTCLDVGLRLLSPFMPFYTEELFQ RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADVANLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQCQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML GPITFLKKKAKKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLLAPESPP				CGEMAQAASAAVTRGDLRILPERHQRTWHAWMDNIRE\WCMFPG
KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNQSED LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLFFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLMSNLDPS EVERAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QCCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML 6026 2674 514 GPITFLKKKARMKDMPLRTHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISFGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNPK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESIML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESPP			•	KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEABARE
IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVLNGVDQVAAECARQTLYTCLDVGLRLSPFMPFVTEELFQ RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVBAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINRNLLSTISPGAFIGHN LLRLHLNSNLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESIML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNNNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP			•	
EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVN RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVONLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	1			LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA
RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	,	ŀ		IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS
WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ RLPRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP		ŀ	ı	
LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR
RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP]	f		wirsrlteavrlsnogfoaydfpavttaqysfwlyelcdvylec
VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				
QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LIDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				
ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQQTEAELRKVDEAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESIML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP		}		
VQEADEAKLQQTEAELRKVDEAIALFQKML 6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGHIN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	ļ l			
GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	1 1			
TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	<u> </u>			
TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP	6026	2674	514	
YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP			İ	
LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				
PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP		•	,	
VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				
ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				
NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				
IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP				
		1		
SNLNVEAGSYVSFHCRATA\EPQPEIYWITPSGQKLLPNT\LTD				
	LL	<u></u>		SNLNVEAGSYVSFHCRATA\EPQPEIYWITPSGQKLLPNT\LTD

Predicted in moleculed contemporary in moleculed contemporary in moleculed contemporary in moleculed contemporary in the first main acid residue of amina acid sequence Preplic medicine Medicine medicine Medicine medicine Medicine medicine Me			31 - 5 - 5	The same and the same and the same as a same a
No: nucleotide corresponding to first anine acid residue of saints acid residue of saints acid residue of saints acid sequence se	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first anino acid amino			l '	
to first anino acid Sequence Seque	NO:	ł	1	
to first amino acid residue of anino acid sequence ##Tryptophan, %=Tyrosine, %=Unknown, *=Stop coden, %-possible nucleotide deletion, %-possible nucleotide innertion) ##Tryptophan, %=Tyrosine, %=Unknown, *=Stop coden, %-possible nucleotide innertion) ##Tryptophan, %=Tyrosine, %=Unknown, *=Stop ##Tryptophan, %=Tyrosine, %=Unknown, *=Stop ##Tryptophan, %=Tyrosine, %=Unknown, *=Stop ##Tryptophan, %=Tyrosine, %=Unknown, *=Stop ##Tryptophan, %=Tyrosine, %=Unknown, *=Stop ##Tryptophan, %=Tyrosine, %=Unknown, *=Stop ##Tryptophan, %=Tyrosine, %=Unknown, *=Stop ##Tryptophan, %=Tyrosine, %=Unknown, *=Stop ##Tryptophan, %=Tyrosine, %=Unknown, %=Stop ##Tryptophan, %=Tyrosine, %=Unknown, %=Stop ##Tryptophan, %=Tyrosine, %=Unknown, %=Stop ##Tryptophan, %=Tyrosine, %=Unknown, %=Stop ##Tryptophan, %=Tyrosine, %=Unknown, %=Tyrosine, %=Unknown, %=Tyrosine, %=Unknown, %=Tyrosine, %=Unknown, %=Tyrosine, %=Unknown, %=Tyrosine, %=Tyros		location	corresponding	
anino acid residue of amino acid sequence ##TTP/EQDAIN, **Introsine, Kuthknown, **Stop Codon, /*possible nucleotide deletion, V=possible nucleotide disection) ##TTP/EQDAIN, **Introsine, Kuthknown, **Stop Codon, /*possible nucleotide disection) ##TTP/EQDAIN, **Stop Codon, /*possible nucleotide disection) #	1	corresponding	to first	
residue of amino acid sequence (Codon, *possible nucleotide deletion,	1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence Codom, /=possible nucleotide deletion, -possible nucleotide insertion) RFYVISSETIDINOVTREGRUTCHATMINGADLKSVMIKUO SPOROMSISINIKIROIDASSULMSKANSKILKISSVMIKUO SPOROMSISINIKIROIDASSULMSKANSKILKISSVMIKTAPVK TENSHAAQSARIFSDWAYNIKIRAPSTEYKICIDIFTIYQKOR KKCVNYVTKSIMPDOKEYSENNYTIKALCIGILLISIVCLIS CLSFERNCOSGISIVVENVIKOKPTRAJGRIVPPI,INLHERGKEKS TSLKVKVATVIGIPTINS GORRAPGREDESTIDEBERVYREWYSPSPDPIPVRYYNKOTIK GORRAPGREDESTIDEBERVYREWYSPSPDPIPVRYYNKOTIK TIPPVGWATNIARIBERJELDGON/PLETALCROPPISSOPPRI LLCHMMOSYLDDEFIQOSVVOTPYAPYHMOCIUDPVYRSHITU TIPPVGWATNIARIBERJELDGON/PLETALCROPPISSOPPRI TIPPVGWATNIARIBERJELDGON/PLETALCROPPISSOPPRI TIPPVGWATNIARIBERJENGAGERRADVYQOVDYRARONVVOGRPTO DKVOGGFPRASGSVOTVOLGFITITAMBEGGRICEAFIAGDRESY OAVARDIVOTTYRFFFIGMIINIENSISISAAVGMIMPPIRVTT TIPPVGWATNIARIBERJENGAGGRRADVYQOVDYRARONVVOGRPTO DKVOGGFPRASGSVOTPJGSPHIADHEFSCRIGEDFSTACEG FYNYMEEELLERRILGOAGERRADVYQOVDYRARONVVOGRPTO DKVOGGFPRASGSVOTPJGSPHIADHEFSCRIGEDFSTACEG FYNYMEEELLERRILGOAGERRADVYQOVDYRARONVVOGRPTO DKVOGGFPRASGSVOTPJGSPHIADHEFSCRIGEDFSTACEG FYNYMEEELLERRILGOAGERRADVYGOVDYRARONVOGRPTO NILGABOTIAVASRPSILLIDTVI-GOIDERKYFANSWINREGIII LIDJAKGFPKKSVETKINRIKKYKTVLEEABINAA MEPINSIKJOPPIK WILTQABOTIAVASRPSILLIDTVI-GOIDERKYFANSWINREGIII LIDJAKRESVETKINRIKKYKTVLEEABINAA MEPINSIKJOPPIK TOLAGREFTSKUNGSOOVULIRULISVOSRAKVVOGNINREGRIADHIALDI LIDJAKEFPKKLEEKRASIANAATTMOOTVALAICHDSITTIKHW LIRARGESTIAVASRPSILLIDTVI-GOIDERKYFANSWINREGIII LIDJAKEFPKKLEEKRASIANAATTMOOTVALAICHDSITTIKHW TITLARAPERVILAMAAGNOOVULIRULISVOSRAKVVOGREDALAACU NARTTILTDKKEVIPOBIISVIKANGAGGMAAFPROKRAKREPASASITYPSGOT QIETNINPRVALLUVSKOQOVMALABERRRILADALDRILEELEEFA RIPPDIB MEKKYRWHWAKKORMOMPERDIDADHIALDRILEELEEFA RIPPDIB MEKKYRWHWAKKSROWDPFERDIDADHIALDRILEELEEFA RIPPDIB MEKKYRWHWAKKSROWDPFERDIDADHIADHIALDRILEELEEFA RIPPDIB MEKKYRWHWAKKSROWDPFERDIDADHIADHIADHIADHIADHIADHIADHIADHIADHIA		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence Codom, /=possible nucleotide deletion, -possible nucleotide insertion) RFYVISSETIDINOVTREGRUTCHATMINGADLKSVMIKUO SPOROMSISINIKIROIDASSULMSKANSKILKISSVMIKUO SPOROMSISINIKIROIDASSULMSKANSKILKISSVMIKTAPVK TENSHAAQSARIFSDWAYNIKIRAPSTEYKICIDIFTIYQKOR KKCVNYVTKSIMPDOKEYSENNYTIKALCIGILLISIVCLIS CLSFERNCOSGISIVVENVIKOKPTRAJGRIVPPI,INLHERGKEKS TSLKVKVATVIGIPTINS GORRAPGREDESTIDEBERVYREWYSPSPDPIPVRYYNKOTIK GORRAPGREDESTIDEBERVYREWYSPSPDPIPVRYYNKOTIK TIPPVGWATNIARIBERJELDGON/PLETALCROPPISSOPPRI LLCHMMOSYLDDEFIQOSVVOTPYAPYHMOCIUDPVYRSHITU TIPPVGWATNIARIBERJELDGON/PLETALCROPPISSOPPRI TIPPVGWATNIARIBERJELDGON/PLETALCROPPISSOPPRI TIPPVGWATNIARIBERJENGAGERRADVYQOVDYRARONVVOGRPTO DKVOGGFPRASGSVOTVOLGFITITAMBEGGRICEAFIAGDRESY OAVARDIVOTTYRFFFIGMIINIENSISISAAVGMIMPPIRVTT TIPPVGWATNIARIBERJENGAGGRRADVYQOVDYRARONVVOGRPTO DKVOGGFPRASGSVOTPJGSPHIADHEFSCRIGEDFSTACEG FYNYMEEELLERRILGOAGERRADVYQOVDYRARONVVOGRPTO DKVOGGFPRASGSVOTPJGSPHIADHEFSCRIGEDFSTACEG FYNYMEEELLERRILGOAGERRADVYQOVDYRARONVVOGRPTO DKVOGGFPRASGSVOTPJGSPHIADHEFSCRIGEDFSTACEG FYNYMEEELLERRILGOAGERRADVYGOVDYRARONVOGRPTO NILGABOTIAVASRPSILLIDTVI-GOIDERKYFANSWINREGIII LIDJAKGFPKKSVETKINRIKKYKTVLEEABINAA MEPINSIKJOPPIK WILTQABOTIAVASRPSILLIDTVI-GOIDERKYFANSWINREGIII LIDJAKRESVETKINRIKKYKTVLEEABINAA MEPINSIKJOPPIK TOLAGREFTSKUNGSOOVULIRULISVOSRAKVVOGNINREGRIADHIALDI LIDJAKEFPKKLEEKRASIANAATTMOOTVALAICHDSITTIKHW LIRARGESTIAVASRPSILLIDTVI-GOIDERKYFANSWINREGIII LIDJAKEFPKKLEEKRASIANAATTMOOTVALAICHDSITTIKHW TITLARAPERVILAMAAGNOOVULIRULISVOSRAKVVOGREDALAACU NARTTILTDKKEVIPOBIISVIKANGAGGMAAFPROKRAKREPASASITYPSGOT QIETNINPRVALLUVSKOQOVMALABERRRILADALDRILEELEEFA RIPPDIB MEKKYRWHWAKKORMOMPERDIDADHIALDRILEELEEFA RIPPDIB MEKKYRWHWAKKSROWDPFERDIDADHIALDRILEELEEFA RIPPDIB MEKKYRWHWAKKSROWDPFERDIDADHIADHIALDRILEELEEFA RIPPDIB MEKKYRWHWAKKSROWDPFERDIDADHIADHIADHIADHIADHIADHIADHIADHIADHIA		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence	1		1	
FPVNISESTIDLINOVPREGGLYTCLATTALUGADLKSWIKTOW SPPONNOSIAINIKINGLASSILLISSKYKNTAPVK TENSHAAQSARI PSDWVYNLHALPSTRYKICID I PTIYQONN KRCVNYTKISHIPDQOKESKNYTTUMACLGGLLI I GULCLIS CLSPENNCOSGHSVVSINVLOKPTRALGGLIA GULCLIS CLSPENNCOSGHSVVSINVLOKPTRALGGLIA GULCLIS CLSPENNCOSGHSVVSINVLOKPTRALGGLIA GULCLIS CLSPENNCOSGHSVVSINVLOKPTRALGGLIA GULCLIS CLSPENNCOSGHSVVSINVLOKPTRALGGLIAPILA GULCLIS CLSPENNCOSGHSVVSINVLOKPTRALGGLIAPILA GULCLIS CLSPENNCOSGHSVVSINVLOKPTRALGGLIAPILA GULCLIS CLSPENNCOSGHSVVSINVLOKPTRALGGLIAPILA GULCLIS CLSPENNCOSGHSVVSINVLOKPTRALGGLIAPILA GULCLIS CLSPENNCOSGHIA CLSPENNCOSGHIA GULCLIS CLSPENNCOSGHIA GULCLIS CLSPENNCOSGHIA GULCLIS CLSPENNCOSGHIA GULCLIS CLSPENNCOSGHIA GULCLIS CLSPENNCOSGHIA GULCLIS CLSPENNCOSGHIA GULCLIS CLSPENNCOSGHIA GULCLIS CLSPENNCOSGHIA GULCLIS CLSPENNCOSGHIA GULCLIS CLSPENNCOSGHIA GULCLIS CLSPENNCOSGHIA GULCLIS CLSPENNCOSGHIA GULCLIS CLSPENNCOSGHIA GULCLIS CLSPENNCOSGHIA			sequence	1 ' ' 4
SPRODNINGSINITIRDIQAISULVISHKASSKILKSSVRYTAFVUK TENSHANQSARI PEDNIVOVINITHUM PSTRYKLICIO FITYIONIR KKCVAVTTKIAHPDOKEVERNYTITHACLGGILGI IGVICLIS CLSPERMCOGGISS VENTVIKOKPTRAJELEVPPLINUMEAKKK TSLKVYATVIGIPTIMS GGRAPGGEGES ISVENIVOKOPTRAJELYPPLINUMEAKKK TSLKVYATVIGIPTIMS 10020	<u> </u>	sequence		l · ·
TENSHAQSAR I PSDWAYNLIKHANPSTEYKICI DI TYTYONR KCVAVYTKISHIP DOKE PSENNTTIAN CLIGILAI I TSUI-LIS CLSPENNCOSCHSI VENNYLOKPTRALGELIJA I TSUI-LIS CLSPENNCOSCHSI VENNYLOKPTRALGELIJA I TSUI-LIS CLSPENNCOSCHSI VENNYLOKPTRALGELIYPPINIMAGOKEKS TSLKVKAVATUOLPTINIS 6027 5254 4148 6GREADGROEDS I KDEREETY REVVS PS PDEPLYTYKONTIK TI PSVISLELLIAMPKIPLEDGRYWALPLACKOP PILSOK PRE LL-CHOMMOSCH LODE PI COSVUOTEVAR PYRHOCI LUP VYTSHHITU TI PRVOWNTVARHIRIDE VALOTIVATE PILSOK LOUGHVAPSHANTIT ONADELVOI TV.R PPERIONIL INI ENSLSLAAVGIND PETLAYLIT ONADELVOI TV.R PPERIONIL INI ENSLSLAAVGIND PETLAYLIT ONADELVOI TV.R PPERIONIL INI ENSLSLAAVGIND PETLAYLIT ONADELVOI TV.R PPERIONIL INI ENSLSLAAVGIND PETLAYLIT ONADELVOI TV.R PPERIONIL INI ENSLSLAAVGIND PETLAYLIT ONADELVOI TV.R PPERIONIL INI ENSLSLAAVGIND PETLAYLIT ONADELVOI TV.R PPERIONIL INI ENSLSLAAVGIND PETLAYLIT ONADELVOI TV.R PPERIONIL INI ENSLSLAAVGIND PETLAYLIT ONADELVOI TV.R PPERIONIL INI ENSLS LIALAKA MEPERISLIQOPI IN NILKEKMESUSTIKANING NATAL LIALAVA MEPERISLIQOPI IN NILKEKMESUSTIKANING NATAL LIALAVA MEPERISLIQOPI IN NILKEKMESUSTIKANING NATAL LIALAVA MEPERISLIQOPI IN NILKEKMESUSTIKANING NATAL LIALAVA MEPERISLIQOPI IN NILKEKMESUSTIKANING NATAL LIALAVA MEPERISLIQOPI IN NILKEKMESUSTIKANING NATAL LIALAVA MEPERISLIQOPI IN NILKEKMESUSTIKANING NATAL LIALAVA MEPERISLIQOPI IN NILKEKMESUSTIKANING NATAL LIALAVA MEPERISLIQOPI IN NILKEKMESUSTIKANING NATAL LIALAVA MEPERISLIPANING NATAL LIALAVA MEPERISLIPANING NATAL HARVA MENTAL LIALAVA MEPERISLIPANING NATAL HARVA MENTAL LIALAVA MEN	}		<u>}</u>	· · · · · · · · · · · · · · · · · · ·
KKCVNYTIKSLHPOOKSYEKNNYTHANGLIGSLIGIUTIANGAGERS CLSPENNCCIGISTYNNYLOPTRAGESTENDISTINGAGERS TSLKVKATVIGIPTMMS GGRAPAGRAPS LOSEBETYPREVVSYSPDPLPVRYYKKYTK PISPYLSSLEELLAWKPRLEDGRWALEPLACROPPLSSOSPT LLCHMMGGVLODRY TGSVVOYDYNSYHROTT TIPYOWNYNTARREGOVALOFTITEMNSGGRICGRAPLAGDERSY OAVADELVQTT, PEPREVENLINI TENSLISLAWAGNUNGGRICKAPLAGDERSY OAVADELVQTT, PEPREVENLINI TENSLISLAWAGNUNGGRICKAPLAGDERSY TOLHROVPGGILVAMYDEVOGGGLKWODELNOHNVEYPISCHOF PTHYNWREELLARMLOGAGERRADVVOVOVDVAGAGNVOGRIPOT DKVGGGFPRAGGOVPPLGPHFLHOLPPSAPORNOSCSSOS DPUALANNCCAPARLCH 120 3432 NCLLLQARGFPRAGETEDLOGWLTDTERHILLASKELGGLPETAKSO DPUALANNEVCAPERENETYSISLAWCOGQUALARCKSAPTURODI NNIKEKMESVSYKLAREN VITY SLEENLILA MEFHRILLOPUR LLDARGTHANDARENTLYSINGKOGQUALARCKSAPTURODI NNIKEKMESVSYKLAREN VITY SLEENLILA MEFHRILLOPUR LLDARGTHANDAREN SLEENLIP COLDENHVYRANSKIRKOLI LLDARGTHANDAREN LLDAVINGCOGQUALARCKSAVTOLOBER VITY SLEENLILA MEFHRILLOPUR LLDARGTHANDAREN LLDAVINGCOMALA MEFHRILLOPUR SLEENLIP SLEENLIP SLEENLIP SLEENLIP DON'LK TQLARKER POKSLGARKSVOTTER TRESLIKKTILADONIKLD DMLSELERBKODT COKK VERONIKATERA LLESSYSTENTIVALASI MELTREF CALSOLOPHODIO WERLITAKTER VITY TURBH LTTI TARREVEN LAMARKHOO CHARA PASQUER FERTY TURBH LTTI TARREVEN LAMARKHOO CHARA PASQUER FERTY TURBH LTTI TARREVEN LAMARKHOO CHARA ALGAL TARGTTEREDED ALFET NEDER TORK VERWAMINKS SKUPP KRAINDALDRICH TRESTTREPTON VITY KRRAADPSELGHT PUT KRAINDALARLA TARGTTERE SETTREPTON VITY KRRAADPSELGHT PUT KRAINDALARLA TARGTTERE SETTREPTON VITY KRRAADPSELGHT PUT KRAINDALARLA TARGTTERE SETTREPTON VITY KRRAADPSELGHT PUT KRAINDALARLA TARGTTERE SETTREPTON VITY KRRAADPSELGHT PUT KRAINDALARLA TARGTTERE SETTREPTON VITY KRRAADPSELGHT PUT KRAINDALARLA TARGTTERE SETTREPTON VITY KRRAADPSELGHT PUT KRAINDALARLA TARGTTERE SETTRE TARGTTERE TORGTTERE SETTRE TARGTTERE TOR	1			1
CLSPEMNCDGGISTYURNYLORPITALGELTPPLINIMEAGKEKS TSLKVKATVIGLPTIMS GGRADGREGS IKOERESTYTREVVSSSPDLEVRYTYKDYTT GREYLSLEBLIAMKERLEGERTYTE IKOERESTYTREVVSSSPDLEVRYTYKDYTT TI PPVSUSTINIARIEM KORLEGERTYTTE ILLEGIMMAGNILDBER IGGSVVQTPVAPYHWQCIDVFVYSSHYTT TI PVSWATNIARIEM KOVLGGT TI TENBROGRICLEGA PLAGDERSY OANDELDVITT, RPERTEKULINI ENGISLLANCOMPP PISSORPET LLCHIMMAGNILDBER IGGSVVQTPVAPYHWQCIDVFVYSSHYTT TOLMROY POGULANTEDVVOGGOLOMQDELIMORINY PPDSCORPET FINYRWREEHLERMLGQAGERRADVYVGVDVARGRVVGGSPDT DKVGGGPR PRAGGEVPP LOPPFLMOLP PSARQRNVGGSPDT DKVGGGPR PRAGGEVPP LOPPFLMOLP PSARQRNVGGSPDT DKVGGGPR PRAGGEVPP LOPPFLMOLP PSARQRNVGGSPDT DKVGGGPR PRAGGEVPP LOPPFLMOLP PSARQRNVGGSPDT DKVGGGPR PRAGGEVPP LOPPFLMOLP PSARQRNVGGSPDT MKLEKEWSSVETKLIBEN LATT KLEERLILLAMERINSLOOD IN MILKEKWSSVETKLIBEN LATT KLEERLILLAMERINSLOOD IN MILKEKWSSVETKLIBEN LATT KLEERLILLAWERINSLOOD IN MILKEKWSSVETKLIBEN LATT KLEERLILLAWERINSLOOD IN MILKEKWSSVETKLIBEN LATT KLEERLILLAWERINSLOOD IN MILKEKWSSVETKLIBEN LATT KLEERLILLAWERINSLOOD IN MILKEKWSSVETKLIBEN LATT KLEERLILLAWERINSLOOD IN MILKEKWSSVETKLIBEN LATT KLEERLILLAWERINSLOOD IN MILKEKWSSVETKLIBEN LATT KLEERLING LATT KLEER	1		1	TENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNR
TSLIKVKATVIGLPTMMS	ł		ļ	KKCVNVTTKGLHPDQKEYEKNNTTTLMACLGGLLGIIGVICLIS
6027 6027 6027 6027 6027 6028			İ	CLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKS
PISFYLSSLERILANKPRIEDGFFVALBELAGGPFLSGPFTT LLCHMMGGYLDDFTIGSSWYDTPAFYHMGGRICCBATLAGDESY OAWADELVOIT-PEFFEDGELIUTENSLESALAVONNPPFLEYLT TIPPVGWTWTAHHHGVULGTFITENNEGGRICCBATLAGDESY OAWADELVOIT-PEFFEDGELIUTENSLESALAVONNPPFLEYLT TOLHROYPGGLUEWTDSVOSGGLKRODELNOCHNEVPFDSCOPF FTWYNWREEHLERNLGQAGERRADVYVOVDVFARGNYVGGRFDT DKVGGGFPFRENGOPVPFLOPHFLHDLPFPSAPGRNDSSCSSGG DPVALRINGERMENSLOPHFLHDLPFPSAPGRNDSSCSSGG DPVALRINGERMENSLOPHFLHDLPFPSAPGRNDSSCSSGG LNVHMEVCAAFEAKEETYKSLHQKSQGMLARCPKSAETHIODI NNLKEKWESVETKLERENKY, KLEEALINLA MERENSLOPPIN WLTQAROTIANVASRPSLILDTVLFQIDEIKVFANEVNSHERGII ELBKTSTHLKYSGKQDVLINLINLISVOSGAREVVQGLVERGR SLDDARKRAKQPHEAWSKLMEHLESSKSLDSELEINDDPKIK TQLAGKHEFKGSGAGHAVYTTHROTESLKERALDDNIKLD DMISELRPKMDTICGKSVERQNKLEEA-LLFSGGFTDALQALID WLVREPGLABADOPVHGDILUMMLINNIKAPGELIGKRTSVQ ALKKSARRLISGSRDDSSWVKVOMQELSTRWETVCALSISKQTR LEAALROAEFHSVVHALLEBLARAEQTTERFULDEDDELTITKWH ITTILRAFPEFLVAHAKGHQGYLGKASALGGLIARGAULD WARTITUDKDEVIPOJEISEVKALIAHOTPHEEMTKRQUEDDELTITKWH ITTILRAFPEFLVAHAKGHQGYALAAREACTITRGVLDDDELTALAHAMU WARTITUDKDEVIPOJEISEVKALIAHOTPHEEMTKRQUDDK WARTITUDKDEVIPOJEISEVKALIAHOTPHEEMTKRQUDDK WARTITUDKDEVIPOJEISEVKALIAHOTPHEEMTKRQUDK WARTITUDKDEVIPOJEISEVKALIAHOTPHEEMTKRQUEDDK WYKYYKRRANDPSSGGBIE UPULDKGRAGKRERPASSLIYSGGGT OIETWIPRVHLUNSKQOVALLALERSRKINDALDRIBELEEPA NFDFDI HRKVYMRRMHKKSERWAPFFRICHSULTHALHAUDA YKPITDADKIEDBVTRQVAKCKCARPOVEQIGDNKYRFPIGNQ RGDSGGALRIVEHIRSTWAWELGKGGARAFERSESSRGSDASSIFTISG SGAQAAASGOVATTFEKLIHELTINGKWHTTSKWETPICKAA ECSDFPVDSAGGTPIQGSKLRLEGVLIGGKPHISGEDGGITTTAA ARVETQFADEVITARAAGGAGATAPLEITARGAAAAAVAVGIFP PNSCAGHGGLUPDIQFRARMQAIQCHACQNILUDFGGSBSVLSAA TIVAKHTSALACHAGATASTATAPLATRAGAAAAYAVGIFP PNSCAGHGGLUPDIQFRARMQAIQCHACQNILUDFGSBSSVLSAA TIVAKHTSALACHAGAAATAPLETARAGAAAAYAVGIFP PNSCAGHGGLUPDIGFRARMQAIQCHACQNILUDFGSBSSVLSAA TIVAKHTSALACHAGAAATAPLEGGRIFARAQAAAYLVGIFP PNSCAGHGGLUPDIGFRARMQAICHACGNILUDFGSBSSVLSAA TIVAKHTSALACHAGAAATAPLEGGRIFARAGAAAATUVGIFP PNSCAGHGGLUPDIGFRARMQAICHACGGRIFARAGAAAATUVGIFP PNSCAGHGGLUPDIGFRARMGATTARAAGAAATURGAAAAAAAAAAAAAAAAAAAAAAAA	ì			TSLKVKATVIGLPTNMS
PISFYLSSLERILANKPRIEDGFFVALBELAGGPFLSGPFTT LLCHMMGGYLDDFTIGSSWYDTPAFYHMGGRICCBATLAGDESY OAWADELVOIT-PEFFEDGELIUTENSLESALAVONNPPFLEYLT TIPPVGWTWTAHHHGVULGTFITENNEGGRICCBATLAGDESY OAWADELVOIT-PEFFEDGELIUTENSLESALAVONNPPFLEYLT TOLHROYPGGLUEWTDSVOSGGLKRODELNOCHNEVPFDSCOPF FTWYNWREEHLERNLGQAGERRADVYVOVDVFARGNYVGGRFDT DKVGGGFPFRENGOPVPFLOPHFLHDLPFPSAPGRNDSSCSSGG DPVALRINGERMENSLOPHFLHDLPFPSAPGRNDSSCSSGG DPVALRINGERMENSLOPHFLHDLPFPSAPGRNDSSCSSGG LNVHMEVCAAFEAKEETYKSLHQKSQGMLARCPKSAETHIODI NNLKEKWESVETKLERENKY, KLEEALINLA MERENSLOPPIN WLTQAROTIANVASRPSLILDTVLFQIDEIKVFANEVNSHERGII ELBKTSTHLKYSGKQDVLINLINLISVOSGAREVVQGLVERGR SLDDARKRAKQPHEAWSKLMEHLESSKSLDSELEINDDPKIK TQLAGKHEFKGSGAGHAVYTTHROTESLKERALDDNIKLD DMISELRPKMDTICGKSVERQNKLEEA-LLFSGGFTDALQALID WLVREPGLABADOPVHGDILUMMLINNIKAPGELIGKRTSVQ ALKKSARRLISGSRDDSSWVKVOMQELSTRWETVCALSISKQTR LEAALROAEFHSVVHALLEBLARAEQTTERFULDEDDELTITKWH ITTILRAFPEFLVAHAKGHQGYLGKASALGGLIARGAULD WARTITUDKDEVIPOJEISEVKALIAHOTPHEEMTKRQUEDDELTITKWH ITTILRAFPEFLVAHAKGHQGYALAAREACTITRGVLDDDELTALAHAMU WARTITUDKDEVIPOJEISEVKALIAHOTPHEEMTKRQUDDK WARTITUDKDEVIPOJEISEVKALIAHOTPHEEMTKRQUDDK WARTITUDKDEVIPOJEISEVKALIAHOTPHEEMTKRQUDK WARTITUDKDEVIPOJEISEVKALIAHOTPHEEMTKRQUEDDK WYKYYKRRANDPSSGGBIE UPULDKGRAGKRERPASSLIYSGGGT OIETWIPRVHLUNSKQOVALLALERSRKINDALDRIBELEEPA NFDFDI HRKVYMRRMHKKSERWAPFFRICHSULTHALHAUDA YKPITDADKIEDBVTRQVAKCKCARPOVEQIGDNKYRFPIGNQ RGDSGGALRIVEHIRSTWAWELGKGGARAFERSESSRGSDASSIFTISG SGAQAAASGOVATTFEKLIHELTINGKWHTTSKWETPICKAA ECSDFPVDSAGGTPIQGSKLRLEGVLIGGKPHISGEDGGITTTAA ARVETQFADEVITARAAGGAGATAPLEITARGAAAAAVAVGIFP PNSCAGHGGLUPDIQFRARMQAIQCHACQNILUDFGGSBSVLSAA TIVAKHTSALACHAGATASTATAPLATRAGAAAAYAVGIFP PNSCAGHGGLUPDIQFRARMQAIQCHACQNILUDFGSBSSVLSAA TIVAKHTSALACHAGAAATAPLETARAGAAAAYAVGIFP PNSCAGHGGLUPDIGFRARMQAIQCHACQNILUDFGSBSSVLSAA TIVAKHTSALACHAGAAATAPLEGGRIFARAQAAAYLVGIFP PNSCAGHGGLUPDIGFRARMQAICHACGNILUDFGSBSSVLSAA TIVAKHTSALACHAGAAATAPLEGGRIFARAGAAAATUVGIFP PNSCAGHGGLUPDIGFRARMQAICHACGGRIFARAGAAAATUVGIFP PNSCAGHGGLUPDIGFRARMGATTARAAGAAATURGAAAAAAAAAAAAAAAAAAAAAAAA	6027	5254	4148	GGRRAPGRPGRSIKDEEEETVFREVVSFSPDPLPVRYYDKDTTK
LLCHDMMGGYLDDRFIGGSWQTFYAP YHMQCIDVFVYFSHITY TIPPVGWTNTAHHRWGYULGTTIENNEGGILCAPIAGDERSY OAVADELVOIT\PFREPGGILINIENSLSIAAVGNMPPIRYIT TQLHRQYPGGUVUNTDSWUSGGUKAGDELNGAPERAPYTOT DKWGGFPRRASGYPPILGHPIJGHEFPARGRINVSGGFDF PTMYMREEHLBRMILGGAGERRADVYVGWDVFARGNVVGGRFDT DKWGGFPRRASGYPPILGHPIJGHFIJABGFPARGRISSSGGS DPWALRINCPARALCPH 6028 120 3432 NCLLLGAKGFHGEIBDLGGWLTDTERHLLASKFLGGLPETAKGO LNYMBYCAAPEAKEETYKSLMQKGQMLARCPKSAETNIOQDI NNLKEWESVETKLIMER\KT\SLEGALIAA\MEPHNSL\OPPIN WLTQAROTINVARSPISLLITUT\CGIDERKYPSAETNIOQDI NNLKEWESVETKLIMER\KT\SLEGALIAA\MEPHNSL\OPPIN WLTQAROTINVARSPISLLITUT\CGIDERKYPSAETNIOQDI NNLKEWESVETKLIMER\KT\SLEGALIAA\MEPHNSL\OPPIN WLTQAROTINVARSPISLLITUT\CGIDERKYPSAETNIOQDI NNLKEWESVETKLIMER\KT\SLEGALIAA\MEPHNSL\OPPIN WLTQAROTINVARSPISLLITUT\CGIDERKYPSAETNIOQDI NNLKEWESVETKLIMER\KT\SLEGALIAA\MEPHNSL\OPPIN WLTQAROTINVARSPISLLITUT\CGIDERKYPSAETNIOQDI NNLKEWESVETKLIMER\KT\SLEGALIAA\MEPHNSL\OPPIN WLTQAROTINVARSPISLITUT\CGIDERKYPSAETNIOQDI NNLKEWESVETKLIMER\KT\SLEGALIAA\MEPHNSL\OPPIN ULTYRORGIADOPHNGTICGKSVERGAKLEER\LITUT\CGIDERLATAL ULTYRORGIADOPHNGTICGKSVERGAKLEER\LITUT\CGIDERLATAL ULTYRORGIADOPHNGTICGKSVERGAKLEER\LITUT\CHASISYOT ALKRARALLIESSKESOSSWWWOMOGLISTWETALSISKQTE LEAALRQAEEFISVVALLEERLAKATTWGOTVALAICHDDSTITTIRM ITTI TRAFFEEVILAAAKGHOGGIASALAGIIAKGALLEALIAATQ WARTITLDEKKEVIJAGNAGHOGGIASALAGIIAKGALLEALIAATQ WARTITLDEKKEVIJAGNAGHOGGIASALAGIIAKGALLEALIAATQ WARTITLDEKKEVIJAGNAGHOGGIASALAGIIAKGALLEALIAATA UTUKTKRALAAANGAAYATATALAAANGAATATARAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1 0027	3231	1	i i
TIPPVGWINTAHHRIGULGTFITENNEGGILCRAFLAGERSY OANDELVOIT, PERFORGILLINIENSLEJAAUVINDPPPLRYIT TOLHROYPOGULWYDSVUOSGILKHODELNOHRIVPEPSCOPF FTWYNWREEHLERMLGQAGERRADVYVOUDVFARONVVOGREDT DKVGGGFPRASCPVPEIGHPLHDLE PFSAPQRINDSSCSSGO DPVALRINKCPAPALLCPH 120 3432 NCLLLQAKGFFIGEIBLQGULTDTERHLLASKFLGGLPETAKSO LNVHMYCAAPEAKEETYKSLMQKGQMLARCPKSAFTNILDDI NNLKEWSSVETKLMER (RY \LEGANLA) MERHISL\OPPTIN WITOAROTIANVASRPSLILDTVLFQIDEHKVFANEVUSRIKSGII ELDKATTHLKYFSOKQUVULINLISVOSYRHOVQRIVERGR SLDDARKRAKOPHEAWSKLMEHLESSKSLDSELEIANDPDKIK TOLAQKKEF FORSGIGAKHAVYDTYTHRTTGRILKATALDADIKLD DMLSELRDKWDTICGKSVERQKKLERA\LLFSGOFTDALQALID WITYSPGIARDQPVHGDIDLWALIDNIKAFQKELGKRTSSVQ ALKKSARELIESSRDDSSWKVQMGELSTREFVCVALSISKQTR LEAALGQAEEFHSVHALLENLARREGTLTRIFGVLDEDBALTI LIDCHEPMKKLEERKAELKANTTMGDTVLAICTEDSITTIKH ITTIRARPEKULAWAKOHQORLASALAGJIAKQELLEALLANLQ WARTTLTDKOKEVITOGEISTENATATMGTVLAICTEDSITTIKH VTKTYKRRAADPSSLQSHIFVLDKORAGKREPPASSLTYSGOT QIETKHPRVALUSKYKQOWLALLERRIKLINALDERLEEPA NEPDELWRKKYMRWMHKKSRWMPFRRIDKODGKITTOGEFID GILSSKPTSSLEBSAVALDIFDEDDGY 1DYSVAALLEBLEELEPA NEPDELWRKYMRWMHKKSRWMPFRRIDKODGKITTOGEFID GILSSKPTSSLEBSAVALDIFDEDDGY 1DYSVAALLEBLEELEPA NEPDELWRKYMRWMHKKSRWMPFRRIDKODGKITTOGEFID GILSSKPTSLEBSAVALDIFDEDDGY 1DYSVAALLEBLEELEPA NEPDELWRKYMRWMHKKSRWMPFRRIDKODGKITTOGEFID GILSSKPTSLEBSAVADIFDEDDGY 1DYSVAALLEBLEELEPA ARVETOPADSKKTPSRFOSRAGSKAGSRASSRRGABSDFIDISE GOSQOLKIVRILRSTVUNVEUGGWMALDEFLVKNDFORAKORT NMEIRKEIT LADGASQOMALFERGARSRSTAKSSRASPITCKAA ECSSPTVOSRAGRTTOGGSKAGSRSSRSASSRRGABSDFIDISE TOSVCSDWETVYDTTRIPTERSLEFGVILGKORFORSPOLKSAN SCAAQAASFQVPATTTRKLHEITENVGRWUTTSKRSFTCKAA ARVETOPADSKKTPSRFOSRAGSKAGSRSSRSARSBABDNISTSVS SQAAQAASFQVPATTTRKLHEITENVGRWUTTSKRSFTCKAA ARVETOPADSKKTPSRFOSRAGSKAGSRSSRSARSSRASSBADIGTTAA ARVETOPADSKKTPSRFOSRAGSKAGSRSSRASSRAGSBADIGTTAA ARVETOPADSKATAGDP 1DYBARAQAOTLVCHTP PMSVLAGHSHTVSDS INSLITSIRDKARACHUTTSRAGATINCD PTMSVLAGHSHTVSDS INSLITSIRDKARACHUTTSRAGATINCH TYAKHTSALLOURYKKAGAUNTATALERVENUTARAGATINCH TYAKHTSALOURYKKATATAGTUARANSCHORGORYKATHTPEREGGIAGOTHAGT TURATARSGII TADLOTTIKTATAGTUARASKLDDISTRAT	1	1	ł	, · · · · · · · · · · · · · · · · · · ·
ONADBLYOTT\RFFREGGLINTENSLSLAAVGNMPPIRITT TOLHROVPEGLIAWTDSVUGSGLWODDELNGVPTPSCOGG FTHYNMREHLEMILGOAGERRADUYVGUVPARGRYVGGFFDT DKVGGGFRRASGTVPPLGPHFLDLPFPSAPGRNVGGFFDT DKVGGGFRRASGTVPPLGPHFLDLPFPSAPGRNVGGFFDT DKVGGGFRRASGTVPPLGPHFLDLPFPSAPGRNVGGFFDT DKVGGGFRRASGTVPPLGPHFLDLPFPSAPGRNVGGFFDT DKVGGGFRRASGTVPPLGPHFLDLPFPSAPGRNVGGFFDT DKVGGGFRRASGTVFGETSDLCOWLTGTENLASKFLGGKGGNLAKCPSAFTNIODI NNLKEKWESVETKLHER, KT\LLESALINLA MEFHRSIL\QPFIN WLITQARGTLANASRFSLLLTUT-KQIDEKKYFARBVGSKERGFI ELDKTGTTHLKYFSQKQDVULIKNLLISVOSRREKVVGRUVGRGR SLDDARKRAKGPHEAWSKLHEWLESSKSLDSBLEIANDPDKIK TQLAGKEFGKSLGAKHSVDTTINTGTSLKEKTSLADDNLKLD DMSGERDKWNTICKGSVERGKKLEBA\LLFSARBVGSKERGT GLAGKEFGKSLGAKHSVDTTINTGTSLKEKTSLADDNLKLD LHYKVEPGLABODPVHGDIDLVMNLIDNIKAFOKELGKRTSSVO ALKRSARELLEGSGDSSWVVOWOMGLSTREHGTDALGALID HLYKVEPGLABODPVHGDIDLVMNLIDNIKAFOKELGKRTSSVO ALKRSARELLEGSGDSSWVVOWOMGLSTREHGVLDEDBLATT LIDQKEFEKKLLEERBALLKAATTRGGTVLAALGEDSITTIKH ITII RAFFEEVLAWAKHOQRILASALAGLIAKQELLBALLAWLO WARTTILIDKOKEVITQB IEEVKALIAHQTFMEDMTRKOPDVDK VTKYTKRRADPSSLQSHILVUKRANGAKRFSULFSGSTT QIETKNPRVNLLVSKWQOVMLLALERRKINDALDALBERLEFA NPDPDIWRKKYMMNHKKSRWMPFFRILDKODGKITTGFFID GILSSKFTISLEMSAVADIFDROGGSYIDYYEFVAALHPIKDA YKPITDANKIBBVTRQVAKCAKARFOVEGIGNKKYRFIJENDA YKPITDANKIBBVTRQVAKCAKARFOVEGIGNKKYRFIJENDA YKPITDANKIBBVTRQVAKCAKARFOVEGIGNKKYRFIJENDA YKPITDANKIBBVTRQVAKCAKARFOVEGIGNKKYRFIJENDA YKPITDANKIBBVTRQVAKCAKARFOVEGIGNKKYRFIJENDA YKPITDANKIBBVTRQVAKCAKARFOVEGIGNKKYRFIJENDA YKPITDANKIBGRYTQGSKAKARSRAGSRAGSRAGSRAGSRAGSRAGSTSTSTAVSSULSAA RUNTOGADSKKTPSRFOSRAGSRAGSRAGSRAGSRAGSRAGSRAGSTSTSTAVS SQAAQAASFQVPATTTYKILHPLTRNYGKMUTNSKMSTPCKAA ECSPFVPSBAGFTTOGSKAKLFGVILGSVILKHTARSLAINFKDP PINSULAGHSTYDDTHTPTAGSFRSTAKPSKIFTPGKSPASK LDKSSKR 1QSVSSNSTATGTTTFTRAGGFRSTAKPSKIFTPGKSPASK YGLGSSBALGGGGTTAGAAQAATLVOTEP PINSULAGHSTAVOTEP PINSULAGHSTAVDALGGGMRAATLABAGSCHCAGTTALACHAGNGT TAATAGSGIAGGAGPETLUSAKGEGGNRAACHTHAATGTALGRAUCH RATAGASGIAGTATTSLAGATGTALGATTHATTATAGASGTATALGTALGRAUCH RATAGASGIAGTOTIVKKSALDDLISSTATTATALGTAGASTKVUKAGA ALQVCTDSTYKRELI ECARAVTEKVSLVLARAQAGSCRCOZ TAATAVS		1		
TQLHROYPOGIUNWTISPUGGGLKMODELANGHREPPSCOPF FTHYNWREEHLERMIGAGGERBADVYGVUPDARGMYVGGFPTD DKVGGGFRPRASGPVPPLGPHFLMDLPFPSAPQRNDSSCSSQSG DPVALRINGERBASGLCPH 120 3432 NCLLLQAKGFREISEDLQGULTDTERHLLASKFLGGLPETAKEQ LNVHMYCARPEAKEETYKSLMQKSQQMLARCPKSAETNIDQDI NNLKEKKSSVETKLERRYKY, LLEGANLA, MEFHNSI, VQPFIN WLTQARGTIANVASRPSLILDTVLFQIDEHKVFANEVNSHREQII ELDKTSTHLKYFSQKQDVLI, INKLLISVOSRMENSHREQII ELDKARTHKYFSQKQDVLI, INKLLISVOSRMENSHREQII ELDKARTHKYFSQKQDVLI, INKLLISVOSRMENSHREQII DMLSERJDKWDTTCKSVERQNKLEEA, LLFSGCFTDALQALID MLSTRJDKWDTTCKSVERQNKLEEA, LLFSGCFTDALQALID MLSTRJDKWDTTCKSVERQNKLEEA, LLFSGCFTDALQALID MLSTRJDKWDTTCKSVERQNKLEEA, LLFSGCFTDALQALID MLSTRJDKWDTTCKSVERQNKLEEA, LLFSGCFTDALQALID MLSTRJDKWDTTCKSVERQNKLEEA, LLFSGCFTDALQALID MLSTRJDKWDTTCKSVERQNKLEEA, LLFSGCFTDALQALID MLSTRJDKWDTTCKSVERQNKLEEA, LLFSGCFTDALQALID MLSTRJDKWSTTCKSVERQNKLEEA, LLFSGCFTDALQALID MLSTRJDKWSTTCKSVERQNKLEEA, LLFSGCFTDALQALID LEAALRQAEEFHSVVHALLENLARRASTTRFIGVLDEDBALIT LIDCHKEPKKLEERKAELKARTTMGGTVLALGTDSTTTTKIH ITTIRARFEEVLAMAKORQORLASALAGLIAKQELLEALLAMLQ WARTTLTDKUSCHIPOSTORY TORGETTORTTKY VTKTYKRRAADPSSLQSHIPVLDKGRAGKKFPRASSLTYSGSGT QIETKHFPKNLUSKKQQVULLALERSRKLNDALDELEELEEFA NFDPDIWRKYMRWNHKKSRWMDFFRIDKOOGKITTGSFTID GILSSKFPTSELEEKSAVADIFORDDGYTTYPSVAALLEBLEELEEFA NFDPDIWRKYMRWNHKKSRWMDFFRIDKOOGKITTGSFTID GILSSKFPTSELEESAVALDETORDDGYTTYPSVAALLEBKLEELEEFA NREIREKEILADGASQOMAAFPERGRRSPSSAGSSAGSPSNGTSSDFTISS SQAAQAASFQVPATTTFKLHELTRINGKWUTTSKNGSTPTCKAA ECSSPFVPSAGROFTQGSKLERGVALGSTERAAQAATVUFFD DRSGCAGHGCUTTTAA ARVETQFADSKKTPSRFGSRAGSRASGRRSGSASPSONLSTSVS SQAAQAASFQVPATTTFKLHELTRINGKWUTTSKNGSTPTCKAA ECSSPFVPSAGROFTQGSKLERGVALGSTERAAQAATVUFFD DRSGAGHGGLUTPTGTBARQAACTACONLUNDFCCAAGAT TURKHTSALCNACTASSTTANPVAKRHVUSSKLLUGGSNGTAGTTTAAACATATATATATATATATATATATATATATA	1	ļ		
FTYNWREEHLERMLOGAGERRADVYVGVDVPARGNVVGGRFDT DKVGGGFRFRASGVPVPLOPPTLMDLPFPSAPGNDSSCSSQSG DPVALRNCPAPAKLCPH 120 3432 NCLLIGAKSPFIGEIEDLGOMITTTERHLLASKPLGGLPETAKEQ LNVHMSVCAAPEAKESTYKSLMGKGGOMLARCSKSAETNIDGDI NNLKERMESVSTKLINER\KT\KLEBEALNIA\MEFINSV\OPPIN WLTQARGTINVASRPSLILDTVLFQTDERHNENSHREGII ELBKTSTHLKYFSGKGDVVLIKNILLISVQSRBSKKVQKLVERGR SLDDARKRAKOPHRAMSKIMBWLESSESKBELEIANDPIKKL TQLAGHKEPGKSLGAKHSVYDTTURTGRSLKERTSLADDILKLD DMLSELRDKWITICGKSVERGNKLERA\LLFSGFTDALQALID WLYRVSPGLASDGPVHGDIDLVNNLIDHKARPGKELGKRTSSVQ ALKRSARELIEGSRDDSSWVKVQMGSLSTRMETVCALISKQTR LEAALRQAGEFHSVVHALLELALBARGTTRRHGVULDDEDALRT LIDGHKEPKIKLEEKRAELINKATTMCDTVLAICHDDSTTTIKH ITITRAFESTLVARMKHQORALSALAGIRRHSVAFSGFT ALKRSARELIEGSRDDSSWVKVQMGSLSTRMETVCALISKQTR WASTTLTDKDKEVIPGE EEVKALIABHGTFNEEMTRKQPDVIK VTKTYKRRAADPSSLGSHTPULDKRGARRFPASSLYPSGSGT QIETKAPRVNLLVSKWQQVMLLALEERRKLADADLDELBELEFPA NPFDDIWRKKYMRWMNHKKSRVMDFFRRIDKODGKITTREPIN GIJSSKFPTSRLEMSAVADIFDRGGGYTDYYSFVAALHRIKDA YKPITDADKIEDEVTRQVAKCKCAKRFQVEGIGDNKFRFIGNG FGDSQLRLVVLILESTWWRVGGGWMALDELBLEEFPAN NEHREKFFILADGASGGNAAFRPRGRSRSSSRASPRSTSVS SQAQAASPOVPATTTPKLLHPLTNYGGGMALDESPLVMDPCRAKGRT NMELREKFFILADGASGGNAAFRPGRSRSSSRASPRSTSVS SQAQAASPOVPATTTPKLLHPLTNYGGGMKALDGLITTAA ARVNTOPADSKKTPSRFDGSKKLHPGYLINSKMSTPCKAA ECSDFPVPBARGTFIQGSKLRLPGYLISGKGPHGSEDSITTTAA ARVNTOPADSKKTPSRFDGSRAGKAGSRASRSRSRSDASDFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPFQKKSPASK LDKSSKR FUNDSTALLHPLTNYGGGMALANGALTAPANNPEPVS 1PAGISSEGGAQBPILVSAKPHGGSSPSKYANSTANL VKTIKALDGDFSEDNINKCRLATAFLIELEVRUTAFASNPEPVS 1PAGISSEGGAQBPILVSAKPHGGSSPSVLISAATIOHID VTKYKHTSALCHACRTASSTVAHFVQARMKSVLISHPOPSTRYSPSV 1PAGISSEGSQAQBFILVSAKPHGGSSSPSVLISAATIOHID PTWSVLAGHSHTVXSSIKSLITSTRDKAPCGGEGTSIDCHIDAD AAGNAKTGDLPAFGECVGTASKALCGLTERAAQAAVIVOTPD PTWSVLAGHSHTVXSKALTATDGISVALAQEQLTSVVQEIGHLID LATAARGEAAQLGHDSFEDNINKTAARAGGAGGARAKTYNTORTICAAGAMSKTOTACT TAATAVSGIIADDTTIMFATAGTUAARANSKTDAGLGAANKTOTACT TAATAVSGIIADDTTIMFATAGTUAARANSKTPADIRENILKTA KALVEDTYKLISSAGMAKTAGAATSPORTICAARAKSVULGAA SLGSDDETGVVVLINAIKDVARALSGGLAFKGAARSKPVDDDS VQLKGAAKWWTNNTSLLKT				
DKYGGFRPRASGPYPTLGPFILMDLPPPSAPQRNDSSCSSQSG DPYALENRCPAPARLCPH 6028 120 3432 NCLLIQAKGFHGEIEDLQQWLTDTERHLLASKPLGGLPETAKEQ LNYHMSVCAAFEAKESTYKSLMQKGQKHAARCEKSAFTINQDI NNLEKWESYSTKLINER, KUT, KLEEALHALAMEFINSL\QDPIN WLTQABQTINVASRPSLILDTVLFQIDEHKYFANEVNSHREQII ELBKTSTHLKKYSKQKQVVLIKULLISVGSKGVVCVENERG SLDDABKRAKQFHEANSKLMSWLEESEKSLDSELEITANDPDKIK TQLAQHKEFOKSLGAKHSVYDTTRRTGRSLKEKTSLADDNIKLD DMLSELREKWDTICGKSVERQNKLEEA\LLFSGGFTDAQALID WLYKVEFQLAEDQPVHGDIDLVNNLIDHKAFOKSLGKTSSVQ ALKRSARELI EGSENDSSWVCVOMGSLSTRRETVCALSISKQTR LEAALRQAEEFHSVVIALLEWLARAGOTLRFHGVUEDDALRT LIDGHKEFMKKIEEKRBELNKATVMGOTLAGHEDDSTATT KHW TTIRRAPPERVLAWAKQHQGLASALAGILAKQELLABLAWLQ NAETTLTDKDKSVTYPGSIESVKALLAEHGTPSSETTKHW TTITRARPERVLAWAKQHQGLASALAGILAKQELLEBLALAWLQ NAETTLTDKDKSVTYPGSIESVKALLAEHGTPSEMTRKQPDVX VTKTYKRRAAPPSSLQSHIPVLDKGRAGKKFFPASSLYPSGSQT QIETKMPRVNLUSVKQQVWLLALERRKKINDALDRLEBLERERA NFPPDTWKKKIMEKKRAEHKSZWMDFFRE INDEDQDGKITRGFFID GILSSKFPTSSLEWSAVADIFDRDGGGYIDVYFEVAALHDNKDA YKPITDADIK SDEVTQVAKKCKCARFPQCGIGNNYKPFIGNQ FODSQQLRLVFILBSTVMVRVGCGWMALDEELVKNDPCRAKGFFI NMELREKET LLADGASGGMAAFPPDGRESREGASPKNSTSSVS SQAQAASPQVPATTTPKILHPLTRNYKKPWLTNSKMSTPCKAA ECSDFPVPSABGTFIGGSKLRLGGYLJSKKMFHSGEDSLLITTAA ARVETQFADSKKTPSKPGSRAGSKAGSKASKSKSSSBGADSDFDISE IQSVCSDVSTVPQTHRPTFRAGSRESTAKPSKLPTPQKKSPASK LDKSSKX 1MPGGSSRLLAGCWTHRNFVSDLSYFDCIESVMENKYLGESM TOLKKHTSALCHACRTASSETARPVAKHFYQGSKEVLGEMDISTAL VKTIKALDGDFSENNIKGETATAFLIELEVNITAFASNPFYS IPAGISSEGSQAGPFILVSAKPHYGGSREVLISHINDT PMSVLAGHSTYNSDSKSTTSTBAAQAAYLVGIPP PMSVLAGHSTYNSSKSKTSTSDGCTISTAAQAAAYLVGIPP PMSVLAGHSTYNSSKSTSTVSGREDTSTGGTRTCTALBAALAHNSKDT PPMSVLAGHSTYNSSKSTSTVSGREDTSTGGTRTCTALBAAGAATLAGIFPERK TPUPQTTTVYKYSTALAVAGGMTKSTVTNEELGGLASGOTSTPPEKS TPUPQTTTVYKYSTALAVAGGMTKSTVTNEELGGLASGOTSPPEKS TPUPQTTVYKYSKALAVAGGMTKSTVTNEELGGLASGOTSPPEKS TPUPQTTVYKYSKALAVAGGMTKSTVINGELGGLASKFYDGLIDID LATARRGEAQLGHKGTQLASYPEPLILAAVGVASKILDHQOM TVLDQYKTLASSAGSUGATDDLAGAGNACHDLAGANKTOQACI TATAVSGILADUTSHARATSFELKGAGAFFYKRITALARAKVAGGRTSQCIS SCHOOLDTWILMEAASSVGLVGMWAALSGLISATKGAASKFYDDDSM YQLKGAAKWYNNTNTSL	1			
DPWALENRCPAPAKLCPH NCLLQAKGFHGEIEDLQQWLTDTERHLLASKPLGGLPSTAKEQ LNYHMSVCAAFBAKESTYKSLIMQKGQQMLARCPKSAPTNIDQDI NNLKERWESVSTKLIMER\KT\KLERAKGTQKHARCPKSAPTNIDQDI NNLKERWESVSTKLIMER\KT\KLERALKILA\MEFINS\DQPIN WLTQARQTINVASRPSLILDTVIFQTDERHKLASKWINGHERQII ELBKTSTHLKYFSQKDVVLIKHLLISVQSRWBKVVQKIJVERGR SLDDARKRAKQFHEMWSKIMBULESESEKSBELEIANDPUKIK TQLAQHKEFQOKSLGAKHSVYDTTNRTGRSLKEKTSLADNIKLD DMLSELRDKWDTITQGSSVERGNIKLERALLESGEFTDALOALID HLYRVEPQLAEDQPVHGDIDLVMNLIDHKAFQKELGKRTSVO ALKRSARBLIBGSRDDSWVKVQMQSLSTRWETVCALSISKQTR LEBALKQABEFHSVVHALLERLARAGTIRHRHVULPDBDALRT LIDDHKEFMKKLEEKRAELINKATTMODTVLAICHPDSITTIKHN ITIIRAFESULAMARQHQALASALAGHTRHRVULPDBDALRT LIDDHKEFMKKLEEKRAELINKATTMODTVLAICHPDSITTIKHN VKTYKTKRAADPSSLQSHIPVIDKRGAKGREFASSLYFSGSGT QIETKMPKVNLLVSKKQQVWLLALBERRKINDADLDELEELBEFA NEPDPINKKKYMRWMHKKSKSWMDFFRALOGDGKITRQEPID GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYEFVAALHPNKDA YKPITDANKIEDEVTRQVAKKKCARFQVURGIGDINKTRPHLGNQ FGDSQLRLVURILESTVAWVGGGWMALDEPLKVNDPGRAKGRT NMELREKFILADGASGGMAAFRERGRSRSSSKASPRSTSVS SQAQAASQVAYDTTPKLHEPLTHNYGGGMKALDGEFLVKNDPGRAKGRT NMELREKFILADGASGGMAAFRERGRSRSSSKASPRSTSTVS SQAQAASDVPATTTPKLHEPLTHNYGGGMKALDGEFLVKNDPGRAKGRT NMELREKFILADGASGGMAAFRERGRSRSSSKASPRSTSPSSKASPSSKASPRSTSVS SQAQAASDVPATTTPKLHEPLTRHYGGGMKALDGALTVEKPLGNS CCSDFPVPSBARGTFIQGSKLRLPGYLJSGKGFHSGEBGILTTTAA ARVNTOFADSKKTPSKRGSRAGSKAGSRASSRSGSDASDFDIS IQSVCSDVSTVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR FONSQCHGULPDIQFARRANQAICMACQNUDPGSSPSQULSAA TIVAKHTSALCNACRIASSKTANPVAKHFYQGSRKVNSTANL VKTIKALDGBYSEDNINKGRTATAFLIKENSAVPLAFAANNTANL VKTIKALDGBYSEDNINKGRTATAFLIKENSAVPLAFAANNTANL VKTIKALDGBYSEDNINKGRTATAFLIKARSALGHUKAYNTANTARSANPEPVS TPAQISSEGSQAQBFILVSAKPTUDGSSPSQULSAA TIVAKHTSALCHACRIASSTYDLEGGGLASQMTSST TRAGTSSTLLTSRICHARAGTHARATARVSGTHABATTARASARPHVS TRADGTSSTLLTSRICHARAGTHARATARVSGTINGR TRIDEGASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP HATAARGBAAQGIHKSTQLASYFPFLILAAVGRAFTHATARANST TRADGTSTRTLETKGRAGASTYDKULJAALGALAGGGRAFTPOTALBERNILKTA KALVEDTKILLSGAGAATFOTALBARNSETPADHRENILKTA KALVEDTKILLSGAGAATFOTALBARNSETPADHRENILKTA KALVEDTKURSARATEGG	Į.			·-
A	1	1		DKVGGGFRPRASGPVPPLGPHFLMDLPFPSAPQRNDSSCSSQSG
LINVIMISUCA PER AKE ET YKS LINGKOGOMILAR CHRSAETINIODI NINLKEKWES VETKLINER (KT KIREALINLA) MEFHINSL \ ODP IN WILTORGOTINVASR PSILILDTUR 20 IDEHKVFANEVURSHEEDI I ELDKTSTHIKYFSOKODVULIKILISVOSRUEKVORLUERGR SLDDARKRAKOFHERWSKLMENLESSEKSLDSELSIANDPOKIK TOLAQHKEFOKSLGAKHSVYDTTRITGRSLKEKTSLADDNIKLD DMLSELRDEKUPTI GORSVERQMILESEL HESOGOTIDAJALID DMLSELRDEKUPTI GORSVERQMILESEL KESOGOTIDAJALID DMLSELRDEKUPTI GORSVERQMILESEKSLDSELSIANDPOKIK TOLAQHKEFOKSLGAKHSVYDTTRITGRSLKEKTSLADDNIKLD DMLSELRDEKUPTOR GORSVERQMILESEKSLDSELSIANDPOKIKLD WLYRVEPQLAEDQPVHGDIDLVMILIDNHKAPQKELGKRTSSVQ ALKKSARELI EBSKDDSSWIKVQMQELSTRWETVALSISKOTT LEPALROAGEFHSVUHALLEWALRAEGTIRFHKOVLPDDEDALRT LIDDHKEFMKKLSEKRAELINKATTMGDTVLAICHPOSITTIKHW ITTIRAR FEEVLAMKACHQORLSALAIKOFLAKSLALIAMIC WAETTLTDKDKEVITOPLISEVALILAHOTTIKHW ITTIRAR FEEVLAMKACHQORLSALAIKAGOTLAKOELISHADHTO WAETTLTDKDKEVITOPLISEVALILAKOELISHALIAMIC WAETTLTDKDKEVITOPLISEVALILAKOELISHALIAMIC WAETTLTDKDKEVITOPLISEVALILAKOELISHALIAMIC WAETTLTDKDKEVITOPLISEVALILAKOHLAKOELISHATIKA WAETTLTDKDKEVITOPLISEVALILAKOELISHAMICA WAETTLTDKDKEVITOPLISEVALILAKOHLAKOELISHAMICA WAETTLTDKDKEVITOPLISEVALILAKOELISHAMICA WAETTLTDKDKEVITOPLISEVALILAKOHLAKOELISHA WAETTLTDKDKEVITOPLISEVALILAKOELISHAMICA WAETTLTDKDKEVITOPLISEVALILAKOELISHAMICA WAETTLTDKDKEVITOPLISEVALILAKOELISHAMICA WAETTLADAISEVALILAGUMALAKAELISHAMICA WAETTLADAISEVALILAGUMALAKAELISHAMICA WAETTLADAISEVALILAGUMALAKAELISHAMICA WAETTLADAISEVALILAGUMALAKAELISHAMICA WAETTLADAISEVALILAGUMALAKAELISHAMICA WAETTLADAISEVALILAGUMALAKAELISHAMICA WAETTLADAISEVALILAGUMALAKAELISHAMICA WAETTLADAISEVALILAGUMALAKAELISHAMICA WAETTLADAISEVALILAGUMALAKAELISHAMICA WAETTLADAISEVALILAGUMALAKAELISHAMICANAENILAHAAAAAAALVUGITOPLORAGAAAAAAAALVUGITOPLORAGAAAAAAAAAULUGITOPLORAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	į.	1	}	DPVALRNRCPAPAKLCPH
LINVIMISUCA PER AKE ET YKS LINGKOGOMILAR CHRSAETINIODI NINLKEKWES VETKLINER (KT KIREALINLA) MEFHINSL \ ODP IN WILTORGOTINVASR PSILILDTUR 20 IDEHKVFANEVURSHEEDI I ELDKTSTHIKYFSOKODVULIKILISVOSRUEKVORLUERGR SLODARKRAKOFHERWEKLMELEESEKSLDSELE IANDPOKIK TOLAQHKEFOKSLGAKHSVYDTTRITGRSLKEKTSLADDNIKLD DMLSELEDEKWOTI GUSVERQMILEES LIKSGOFTELADALIKLD DMLSELEDEKWOTI GUSVERQMILEES LIKSGOFTELADALIKLD DMLSELEDEKWOTI GUSVERQMILEES LIKSGOFTELADALIK WILYRVEPQLAEDQPVHGDIDLVMILIDNIKAPQKELGKRTSSVQ ALKKSARELI EBSKDDSSWIKVQMQELSTRWETVALSISKOTT LEAALROAEEFHSVUHALLEWALRAEGTIRFHKOVLPDEDALRT LIDDHKEFMKKLEKRRELIKATTMGDTVLAICHPOSTTTIKHW ITTIRAR FEEVLAMKOHOQRILSALAIKKOELIKALDAHLO NAETTLTDLOKEVITORE ISEVKALTAGHTUR TIKKVELEDBEALRT LIDDHKEFMKKLEKRRELIKATTMGDTVLAICHPOSTTTIKHW ITTIRAR FEEVLAMKOHOQRILSALAIKKOELIKALDAHLO NAETTLTDLOKEVITORE SUPPLIKATIONED LIKOPOSTATIKHW ITTIRAR FEEVLAMKOHOQRILSALAIKKOELAKOELIKAPOLOK NAETTLTDLOKEVITORE SUPPLIKATORUT VITKYARRAADPSSLQSHI PVLDKGARGKKTPASSLYPSGOT OISTKYBRVNLLVSKMQOVWLLALEKRKINDALDRLEEUREPA NFDPDLWRKKYMMINKKSRWIDFFRRIDKODGKTTROEFIJD GILSSKKFYSILENGSWAOSALATRODISTVE FVALAHLANDAL YKPITDADKIEDEVTROYAKCKCAKRFOVEOIGIDNKYKFFIGNO FGDSQQLRLVRILRSTUMVEVGGGWABEFUWNDE FORAGGT NMELREKFILADGASGOMAAFRPGGRRSRPSSROASPNRSTSVS SQAAQAASDQVDATTTFKILHELTINVGKEWLITNSKMSTECKAA ECSSPPVPBSAETTIGGSKLARLFOYLSKKOFHSGEDSGLITTAA ARVSTOFADSKKTPSRTGGSRAGSKAGSRASSRGSBASDFOISS IOSNCSSDVETVPOTHRPTPRAGSRPSTAKPSKIPTPORKSFASK LDKSSKR INDFGSSRILIRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGSCVGLASKALGGLTERAAQAAVLVGIPD PNSQAGHGGLIVPPIGFARANDAIQNACQNLVDPGSSPSQVLSAA TIVAKHTSALCAACRIASSKTANDVARHCYGSAKEVANSTANL VKTIKALDGDFSEDNRNKCLIATADLIEAVENLTAFASNPSFVS IFAGISSEGSQAGEPILVSAKPMLESSSYLITRTABLAINPKDD PTWSVLAGHSHTYSDSIKSLITSIRKHPOGSAKEVANSTANL VKTIKALDGDFSEDNRNKCLIATADLIEAVENLTAFASNPSFYS IFAGISSEGSQAGEPILVSAKPMLESSSYLITRTABLAINFKDD PTMSVLAGHSHTYNDSIKSLITSITRATAKOPAGRECTYSIDGINRC IRDDOTTVINGTKASSELOPOLAGAOASAATTOLAEVEVALGAANTAGACI TAATAVSGIIADLOTTIMFATAGGTLARANSKLDEGTPPPENE TYDYOTTVIKSKASIANTAGEGGN PKAOHTHDAITERAQLAK EAVDDIMYTLNEASSEVGIPOLAGAO	6028	120	3432	NCLLLQAKGFHGEIEDLQQWLTDTERHLLASKPLGGLPETAKEO
NNILEEKMESVETKLINER\TN\TLEEALNIA\MEFINSI\QDPIN WLTQARQTLIVASRPSLILDTVLPQIDEHKVPANEWSHREQII ELDKTCTHIKKYPSQKQDVVLIKNILISVQSRWEKVVQRIVERGR SLDDARKRAKQPHBAWSKLMEMILESSKSLDSELEIANDPDKIK TQLAQMKEPQKSLGAKHSVPOTTHRTEKEKKTSLLADPDKIKL DMLSELRDKWDTIGGKSVERQMKLEEA\LLPSGQFTDALQALID DMLSELRDKWDTIGGKSVERQMKLEEA\LLPSGQFTDALQALID MLYRVEPQLAEDQPVHGDIDLVMNLIDNHKAPQKELGKRTSSVQ ALKKSARBLIEGSKDDSSWVKVQWGLISTWETVCALSISKQTR LEAALRQAEEFHSVVHALLEMLAEAEQTLEFHGVUPDDEDALHT LIDGHKEFMKLEEKRKAELKATTMGTUALGHPDSTTIT KHW ITTIRAPFEVLAWAKQHQQNLASALAGLIAKQELLBALLANIQ WAETTLITUKGKEVIPQEIEEVKALIAEHQTMEEMTRKQPDVDK VTKTYKRRAADPSSLGSHIPVLDKGRAGKREFPASSLYPSGSGT QIETKMPRVNLUVSKWQQVWLLALERRRKLNDALDRLEELREFA NFPDFUMRKKYMRWMIKKSRVMDFFINDODGKITTGGFID GILSSKPPTSRLEMSAVADIFDRDDGVYIDVYEFVAALHDNKDA YKPITDADKIEDEVTRQVAKCKCAKRFQVEGIGDNKYRFFLGWP GGDSQQLRLVRILBSTTMVRUGGGWMALDEFLVKDDPCRAKGRT NMELREKFILADGASQGMAAFFRGRSRSSRSGSPRRSTSVS SQAQAQAASQDVATTTRYKJHPLTNVGKPWLTNSKMSTSTYS SQAQAQAASQDVAATTTRYKJHPLTNVGKPWLTNSKMSTPCKAA ECSDFPVPSBABGTPIQGSKLRLPGYLGGKGFHGGEDSGLITTAA ARVRTQFADSKKTPSRPGSSRAGSKAGSRRSGSDSDFDISE IQSVCSDVETVPQTHRFTPRAGSRFSTARFSKIPTPQKKSPASK LDKSSKR IMPGGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAGGCVGIASKALCGLTEAAQAAVLUGIPD PNSQAGHQGLVDPIQFARANQAIQMACQNLYDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKHRVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAFLIEAVENLTAFASNPEFVS IPAQISSEGSQAQPB ILVSAKPMLESSYLLFRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPQGPECDYSIDGINGC IRDIEQASLAAVSQSLATROLSVEAQEQLTSVVQEIGHLIDP LATARRGESGOAQPB ILVSAKPMLESSYLLFRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPQGPECDYSIDGINGC IRDIEQASLAAVSQSLATROLSVEAQEQLTSVVQEIGHLIDP LATARRGESGQAQPB ILVSAKPMLESSYLLIFARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPQORECDYSIDGINGC IRDIEQASLAAVSQSLATROLSVEAQEGNKTQTGACI TAATAVSGIIADLOTTIMFATAGTLAARNSLDETGFPPPKS TFVDYQTTVVKYSKALAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAPCGGMAAATAFPEELGFOIRTKVQDLGHGCIFLVVKAGA ALQVCPTDSYTRELIE ECARAPTEEVSLVSLVLSALQAGNKGTQACI TAATAVSGIIADLOTTIMFATAGTLAARNSLDETGFARETABLETIECIKQ ELTVYQS KDVPEKTSS PEESEINTKTGTAATAKAVAAGNSCCGG	1		1	
MILTOAROTINVASRPSILTLOTULFOIDEHKVPANRYNSHREQII ELDKTGTHIKYPSQKQDVVLIKNILISVQSRWEKVVQRIVERGR SLDDAKRAKQFHRAWSKLMSWILDTESSKSLDSELEIANDEDKIK TQLAQKKEFQKSLGAKHSVYDTTRETGRSIKEKTSLADDHIKLD DMISGIRDBKWDTIGGSVSPRQNKLEGH, LPSGQFTDALQALID MILSVERPOLARDOPVHGDIDLVMILIDNHKAFQKSLGKRTSSVO ALKRSARELIEGSRDDSSWKVOMQSISTRETVETVCALSISKQTE LEAALRQABEFHSVWHALLEWLARAGTIRFHGVLPDDEDALRT LIDDHKEFMKKLEKRRELNKATTMGDTVLAICHDGSTTITKHW ITTIRRAFEBVLAWAKQHQQRIASALAIKQELIKALLAMLQ WAETTLIDDKSVIPOSIESVKALIABHQTFMESHTRKQPDVIK VTKTYKRAADPSSLQAHIFVLDKGRAKFPASSLIVPSGSGT QIETKNPRVNLLVSKWQQVWLLALERRRKLNDALDRLEELREFA NFPPDIWRKKYMRWNNKKSRWDFFRR IDKDQDKKTRGEFID GIJSSKFPTSRLEMSAVDSIFFRDGDGVINYVEFVAALHENKDA YKPITDADKIEDEVTRQVAKCKCAKRFQVSQIOKKTRGEFID GIJSSKFPTSRLEMSAVDSIFFRDGDGVINYVEFVAALHENKDA YKPITDADKIEDEVTRQVAKCKCAKRFQVSQIOKKTRGEFIG DGSQGLIKVRILSTUMVRVGGGWALLDEFLVKNDFCRAKGHT NMELREKFILADGASQGMAAFRPGGRSRSSRSGRAFSTSTAFSKSPIAN SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA ECSDFPVPSARGTTIQGSKLRLFQVLSSKGFHSGBDSGLITTAA ARVNTQFADSKKTPSRTGSRAGSKAGSRASSRFGSBADDFDISE USVCSDVSTVVPGTHRFTPRAGSRFSTARPSKIPTPQKSFASK LDKSSKR IMPGGSSRLLRGCWHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPARGECVGIASKALGGLTEAAAQAAYLVGIPD DNSQAGHQGLVDPTQFFARNQAICWACQNLVDFGSSPGVUSASKAL LJKSSKR TVAKHTSALCAACRIAGSSTANDVARPVGARENVSTAAL VKTIKALDGDFSEDNRKKCRIATAPLIEAVENLTAFASNPSFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINNKUD PTWSVLAGHSHTVSDSIKSLTTSRDRAPQGRECCYSTDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVQBIGHLIDP TATARRGERAAQGIKKGPLASYFFELILAAVGVASKILDHQOM TVLDQTKTLABSALQMIXYAKEGGONPKAQHTHDAITEAAQLMK EAVDDIMVILNEAASEVGLOGMVDAILATRAGNSLDGGTPPPPKG TFVDYQTTVKYSKALAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGGMAAATAEPEELGFQIRTRVQDLGHGIFLVDKAG ALQVCPTDTSYTKREIL ERARAFTEEXVSLVLSALQAGNKTGTQGIT TATATAVSGIIADLDTTIMFATAGTLNABNSETFADHENILKTA KALUEDTSKLLUSGAASTPDLAAGAASAATITOLAEVYKLIGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKWWITNYSLLKTVKAVEDERTRGTTAALEATITECLIV			1	1 1212
ELDKTGTHLKYFSQKQDVVLIKNLLISVQSRMEKVVQRLVERGR SLDDARKRAKQPHEAWSKLMBULESEKSLDSELEIANDPDKIK TQLAQKKEPQKSLGAKHSVYDTINGTGRSLKEKTSLADDNIKLD DMLSELBDKWDTICGKSVERQNKLEEA\LLFSGGTTDALQALID WLYSVERPOLAEDDPVHGDIDLVNNLIDNKKAPQKSLGKTSSVQ ALKRSARELIEGSRDDSSWVKVQMQSLSTRMETVCALSISKQTR LEAALRQAEEFHSVVHALLEWLARASQTLRFHGVLPDDEDALRT LIDCHKSFMKKLEERRAELNKATTMODTVLAICHPDSITTIKHW ITIIRARFEVLAWAKQHQQRLASALAGIJARQELLBALLAWLQ WASTILTDKDKSVIPGEIEEWKALABGTLRFHGVLYDAKUN VTKTYKRRAADPSSLQSHIPVLDKGRAGKKRFPASSLYPSGGT QIETKMPRVNLVSKWQQVWLLALERRRKLMDALDRLEBLREFA NFDPDIWRKKYMRWNHKKSRVWDFFRRIDKDQDGKITNGEFTA GILSSKFPTSRLEMSAVADIFDRGGGYIDVYBFVAALHDNKDA YKPITDADKIEDEVTRQWAKCKAKFQVVGQIGDNKYRFIGNG FGDSQQLRLVRILRSTVMVRVGGGWALDEFLVWNDPCRAKGRT NMELREKFILADGASQGWAAFRPRGRSRBSSRGSDNRSTSVS SQAQAASPQVPATITPKIHBLTHRYGKPWITNSKWSTCKAA ECSDFPVPSABGTPTQGSKLRLPGYLSGKGFHGEDSGLITTAA ARVSTQADSKKYTSBROSRAGSKASSRASGRASBRASDAFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR IMPGGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPARGECUGIASKALGGITERAAQAAYLVGIPD PNSQAGHOGLVDP IQFARANQALUAPGASSPQVLSAA TIVAKHTSALCNACRIASSKTANFVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDMRNCRIATAPLIEAVEBLITAFASNPEFVS IPAQISSEGSQAPETLUNARPMESSYLIRTARISLAINFKDP PTWSVLAGHSHTYSDSIKSLTSTRDKAPQORCDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVAAQGKLOPGGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANFVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDMRNCRIATAPLIEAVEBLITAFASNPEFVS IPAGISSEGSQAPETLUNARPMESSYLIRTARISLAINFKDP PTWSVLAGHSHTYVSDIKSLTSTRDKAPQORCDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVAAQGKLOPGGSSPGQUISRC TATARREBAQGIGKSTOLASSKTANFENGETPEPKS TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGLDTTUTLABSALOMIXAREGGGRPKAQHTHDAITTBAQLMK EAVDDINVTLINEASEVGLUGGWUALBAMSKEDETPEPKS TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAPQGOMAARTAEPEEIGFGTRTRVQLLGHCIFLVQKAG\ ALGVCPTDSYTKREILECARAVTEKVSLVLSALQAGNKGTQACI TATARVSGIIADDTTIMFATAGTLARMSEFTFADHERNILKTA KALVEDTYDSCYTDSTTREILECARAVTEKVSLVLSALQAGNKGTQACI TATARVSGIIADDTTIMFATAGTLANKSETFADHERNILKTA KALVEDTYGKYDYSKTSSPEESIRTKYGLTWANTARALBARGCROZ BLGYCPGSKVYDVTSLLKTVKAVEDEATRGTRALBATIECIKQ	1			, , , , , , , , , , , , , , , , , , , ,
SLDDARKRAKOPHEAMSKLUMENLESEKSLDSELEIANDPDKIK TQLAQHKEFQKSLGAKHSVYDTTNRTGRSLKEKTSLADDNIKLD DMISELRDKWDTICGKSVERQNIKLERA\LLPSGGFTDALQALD WLYKVEFQLAEDQFVHGDIDLVNNLIDNIKARQKELGKRTSSVQ ALKRSARELIGESGNDSSWKVKONGSTRWETVCALSISKQTR LEAALRQAEEFHSVVHALLEWLAEAEQTLRFHGVLPDDEDALRT LIDCHKEFFMKKLEEKRAELMKATTMCDTVLALGHDSITTIKHW ITITRAFEEVLAMAKQHQCRLASALAGLIAKQELLERLIAWLQ WAAETTLTDKOKEVIPGEIEBEVKALIAEHGTPMEEMTRKQPDVDK VTKTYKRRAADPSSLQSHIPVLDKGRAGKKRFPASSLYPSGSOT QIETKWPRVNLLVSKWQQVWLLALERRRKLNDALDRLEELREFA NFDPDIWRKKYNRWMNHKKSRVMDFFRRIDKDODGKITRGEFID GILSSKFPTSRLEMSAVADIFBRGYIDVYSEVYAALHDNKDA YKPITDADKIEDEVTRQVAKCKCAKRFQVEQIGDNKYRFFLGWQ FGDSQGLRLVRILRSTVWVRGGGWMALDEFLVKNDCKAKGT NMELREFFILDAGASQCMAAFPRFGRSSRPSSRGASPRSTSTSVS SQAQAASSPQVPATTTPKILHPLTRNYGKPWLTNKNGSTPCKAA ECSDFPVPSARGFTPLGGSKRLEVYLSGKGFHSGEDSCLITTAA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRFTPRAGSRFSTAKPSKITPPQRKSPASK LDKSSKR 6029 1 3533 IMPGGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTDLPAGGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHQGLVDP IQFARAMQALQMAQCMLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANFVAKRHYGSAKEVANSTANL VKTIKALDGDFSGDNRNKCRIATBLIAVUSAKEVANSTANL VKTIKALDGDFSDRNNKCRIATBLIAVUSAKEVANSTANL VKTIKALDGDFSGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSTRNKAPGGRCDYSIDGIINC IRDIGASLANVSGSLARTDDISYBAQCILTVOSAGK TUDGASLANVSGSLARTDDISYBAQCILTVOSAGK TYDDYGTTVVKYSKAIAVTAQEMMTKSVTURBELGGLASQMTSD YGHLAFQGGMAAATAPEEIGGFQTRTRVQDLHGCIFLVQKAG ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADDLTTHFATAGTLAARMSETFADHERNILKTA KALVEDTKLLISCAASTPOKLAGASAATTTOLLAEVVKLGRA SLGSDDETOVVLINAIKUNKALAGDLSAATRGAARAKFAUVLGKTURVAGSCICK GLGSDEDTOVVLINAIKUNKALAGDLSAATRGAASKFVDDPSM YQLKGAAKWWINVTSLIKKVKAVEDEATRGLARALBERIECKQ SLGSDDETOVVLINAIKUNKALAGDLISATRGAASKFVDDPSM YQLKGAAKWWINVTSLIKKVKAVEDEATRGTRALBATIECIKQ ELTVYGGKDVPERTSSPESIRTKGITMATALBATIECIKQ ELTVYGGKDVPERTSSPESIRTKGITMATALBATIECIKQ ELTVYGGKDVPERTSSPESIRTKGITMATALBATIECIKQ		1		· = ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~
TOLAQHKEFQKSLGAKHSVVDTINRTGRSLKEKTSLADDNILKLD DMLSELRDKWDTICGKSVERQNKLEBA\LLFSGQFTDALQALID WLYKVEFQLAEDQPVHGDIDLVNHLIDNIKAFQKELGKRTSSVQ ALKRSARELIEGSRDDSSWVKVOMQSLSTREFUTVCALSISKQTR LEAALRQAEFHSVVHALLEKLAEVITRFUTVALSISKQTR LIDQHKEFMKKLEKRAELNKATTMGDTULAICHPDEIGLET LIDQHKEFMKKLEKRAELNKATTMGDTULAICHPDEIGLTIKH ITIIRAFFEVLAWAKCHQORLASALAGLIAKGELBALLAHQ WAETTLTDKDKEVIPGE LEEVKALLAEHGTTMEEMTRKQPVDK VTKTYKRRAADPSSLQSHIFVLDNGRAGKRKPASSLYPSGSGT QIETKMPRVALLVSKWQVWLLALBERRKLDDALDRLEELREFA NFDFDIWRKKYMRWMNHKKSRVMDFFRIDKDQDGKITRQEFID GILSSKFPTSRLEMSAVADIFDRDGDGYIDVJFBVAALHBNKDA YKPITDADKIEDEVTRYQVAKCKCAKFPQVEQIGDNKVFFLGNG FGDSQQLRLVRILRSTVWVRVGGGWMALDEFLVKNDPCRAKGRT NMELREKFILADGASQGMAAFPRERSFSSGRASPRSTSVS SQAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA ECSDFPVPSABGTPJQGSKLRLPQYLSGKGPHSGEDGSLITTAA ARVNTOFPADSKKTPSFGSRAGSKASSRASSRRSGBADFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR 6029 1 3533 IMPGGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALGGLTBAAQQAYLVGIPD PNSQAGGGLVDP IQPARANQAIQAMQONLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDMRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQPETLVSAKPMLESSSVLIRTARSLAINFKDP PTWSVLAGHSHTVSDSIKSLTSIRDKAPGQBECDYSIDGINRC IRDIEQASLANVSIGSLARTDDIESQLEQLTSTVDGEIGHLIDP LATRARGEAAQLAHTHDASTRAAQAAYLVGISHR EAVDDINTINERASEVGLVGGWALDEGLEGTPEPKS TFVDYQTTVVKYSKALAVTAQEMMTKSVTNPEELGGLASQMTED YGHLAFQGGMAAATAPEEGIGTQIRTRVQDLGHGTPEPKS TFVDYQTTVVKYSKALAVTAQEMMTKSVTNPEELGGLASQMTED YGHLAFQGGMAAATAPEEGIGTQIRTRVQDLGHGCTPEPKS TFVDYQTTVVKYSKALAVTAQEMMTKSVTNPEELGGLASQMTED YGHLAFQGGMAAATAPEEGIGTQIRTRVQDLGHGCTPEPKS TFVDYQTTVVKYSKALAVTAQEMMTKSVTNPEELGGLASQMTED YGHLAFQGGMAAATAPEEGIGTQIRTRVQLLGHGCIFLVQKAG ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGII ADLDTTINFATAGTLAAMSSETFADHRENILKTA KALVEDTYKLLVSGAAATPOLKLAGASAATTTOLLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVWTNVTSLLKTVKAVEDEATRGTRALBATIECIKQ ELITVYGSKDYPETSSPEESIRTRYKGITMAATALBATIECIKQ ELITVFQSKDYPETSSPEESIRTRYKGITMATALBATIECIKQ) · · · · ·
DMLSELRDKWDTICKSVERQNKLEEA\LLPSGGFTDALQALID WLYRVEPQLAEDQPVHGDIDLVMNLIDNHKAFQKELGKRTSSVQ ALKKSARELIEGSRDDSSWXVQMQELSTRWETVCALSISKQTR LEAALRQAEEFHSVVHALLEWLAEAEQTLRPHGVLPDBDEDLTT LIDQHKEFMKLEKERAELINKTODTVLAICHDSITTIKH ITIIRAFEEVLAWAKQHQQRLASALAGLIAKQELLEALLAWLQ WAETTLTDKDKEVIPQE IEEVKALLAEHQTTMEBMTRKQPDVDK VTKKTYKRRAADPSLQSHIPVLAGKAGARKRFPASSLYPSGSGT QIETKNPRVNLLVSKWQQWLLALERRRKINDALDRLBELREFA NFDFDIWRKKYMRWNHKKSRVMDFTRRIDKDQDGKITRQEFID GILSSKFPTSRLEMSAVADIFDRDDGGYIDYYEFVAALHENNDA YKPITDADKIEDBVTRQVAKCKCARFGVEGIGDNKYRFPLGNG FGDSQGLRLVRILRSTVMWVGMALDEFLVKNDPCRAKGRT NMELREKFILADGASQGMAAFFPRGRRSPSSRGASPNRSTSVS SQAAQAASPQVPATTTPKILHELTNTVSKWFMITNSKMSTPCKAA ECSDFPVPSAEGFTJGGSKLIRGVENTINKNSTPCKAA BCSDFPVPSAEGFTJGGSKLIRGVENTINKNSTPCKAA ARVRTQFADEKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHPPTRAGSRPSTAKPSKIFTPQRKSPASK LDKSSKR 6029 1 3533 IMPGGSSRLURGCWTHPNEVSDLSYFDCIESVMENNSKVLGEM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLUGIFD PNSQAGHGGLVDPIGPARANQAICMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHVQSAKEVANSTANL VKTIKALDGGDFSEDNNKCRIATAFLIERVFNUTAFASNEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGGRECUTSIODINEC IRDIEGASLAAVSGSLATRDDISVEALGQGLTSVVQEIGHLIDP LATAARGEAAQLCHKGTOLASYFEELILAAVGVASKILDBQQM TVLDQTKTLABSALQMLYAAKEGGENPKAQHTHDAITEAAQLMK EAVDDINVTLINEAASSVGLIVGGMVDAIAEAMSKLDEGTPPEPRIG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAPQGGMAAATAPEEELGFTRETVODLGHGCT FLVXXAG ALQVCPTDSYTKRELIECARAVTEKUSLVLSALQAGNKGTQACI TAATAVSGIIADDLTTIMPATAGTLNARNSETFADHRENILKTA KALVEGTRELVSGASATPFOKLAGASSATTIOLAEVVLLGAA SLGSDDPETQVLINAKDVALALBGLISATKGAASKRUDLAEVUDDSM YQLKGAAKVWITNVTSLLKTVAVEDEATRGTRALEATHECIKQ ELTVYGSKDVPEKTSSPEESIEMTKGITMATAKAVAAGASSCRGE ELTVPGSKDVPEKTSSPEESIEMTKGITMATAKAVAAGASCRGE	1		Į.	1 - ,
MLYRVEPOLAEDOPVHGDI DLVMNLIDNHKAFGKELGKRTSSVQ ALKRSARELIEGSRDDSSWKVQWGLSTRWETVCALSISKQTR LEAALRQAEEFHSVVHALLEWLAEAGTLRFHGVLEDDBDALRT LIDCHKEFMKKLEEKRAELNKATTMGDTVLAICHPDSITTIKW ITI IRARFEEVLAWAKQHQQRLASALAGLIAKQELLBALLAWLQ WAETTLTDKDKEVIPGE IEBYKALIAEHQTFMEEMTRKQPDVDK VTKTYKRRAADPSSLQSHIPVLDKGRAGARKFFASSLYPSGSGT QIETKRPRVALLUSKKQQWULLALERRKKIDADARLBELREPA NFDFDIWRKKYMRWMHKKSRVMDFFRIDKDQGKITRQEFID GILSSKFFTSRLEMSAVADIFDRDDGGYIDYYFEVAALHBYNDA YKPITDADKKEDBEVTRQVAKCKAKRFQVEQIGDNKKFFLGKQ FGDSQQLRLVRILRSTVWRVGGGWMALDEFLVXNDPCRAKGRT NMELREKFILADGASQGWAAFRPGRRSRFSRGASFNSTSTSY SQAAQASPQVPATTTPKILHPLTINYGKPWLTMSKMSTPCKAA ECSDFPVPSABGTPIQGSKLRLPGYLGKGHGGEDSGLITTAA ARVRTQFADSKKTFSRFSRGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRFTFRAGSRFSTRAKSKIPTPGRKSPASK LDKSSKR LDKSSKR LDKSSKR LDKSSKR TIPGGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHGGLVDPIQFARANQAIQWACQNLVDRGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANYAKHFVGSSPSVLSAA TIVAKHTSALCNACRIASSKTANYAKHFVGSSPSVLSAA TIVAKHTSALCNACRIASSKTANYAKHFVGSAKVANSTANL VKTIKALDGDFSEDNENKCRIATAPLIEAVENLTAFASNPEFVS IPAGISSEGSQAGEPILVSAKFMLESSSYLLRTARSLAINFKDP PTWSVLAGHSHTVSDSIKSLITERAKPAGGRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP LATAARGEAAQLCHKGTGLASYFEPLILAYGVASKILDHQQOM TVLLOQTTTLABSGLOMLYAAKGGGNPKAOHTHDAITEAAQLMK EAVDDIMVTINEAASEVGLUGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNEELIGGLAGMTSD YGHLAFQGGWMAATABPEELIGCIKTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTINAENSETFADHRENILKTA KALVEDTYLLVSGAASTPDKLAQAQASSAATITQLAEVVULGAA SLGSDPETTOVULINAIKDVAKALSGLISATKGAASKPVDDPSM YGLKGAAKVWUTNVTSLLKTVAKVEGLAATRGTRALEATIECIKQ ELITVPQSKDVPEKTSSPEESIRWEGETMARAVARAGASCRGB	i	1	1	
ALKRSARBLIEGSRDDSSWWKVOMQSLSTRWETVCALSISKOTR LEAALGAEFHSVVHALLEWLARAEQTLRFHGVLPDDEDALRT LIDOHKREFMKKLEEKRAELMKATTMODTULAICHDSITTIKHW ITIIRARPEEVLAMAKCHQORLASALAGLIAKQELLEALLAMIQ WAETTLTDKDKEVIPQBIEEVKALIAHQTFMEEMTRKOPDVDK VTKTYKRRAADPSSLQSHIPVLDKGRAGKRRFFASSLYPSGSOT QIETKNPRVNLLVSKWQQVWLLALERRKINDALDRLEELREFA NPDPDIVRKKYMRMMINKKSKVMDFFRRIDKDDGKITRGEFID GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYEFVAALHPNKDA YKPITDADKIEDEVTRQVAKCKCAKEQVQGIGDNKYRFFLONQ FGDSQOLRLURILSTTWUKVGGWMALDEFLYWNDPCAKGRT NMELREKFILADGASQOMAAFRPRGRSRFSSRGASPNRSTSVS SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA ECSDFPVPSARGTTIQGSKLELPGYLSGKGFHSGEDSGLITTAA ARVRTQFADSKKTPSRPGSRSRSSRAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR IMPGGSSRLERGCWTHPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR TMPGGSSRLERGCWTHPNEPVSDLSYTDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGISKALGGLTEAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANFVAKRHVOGSAKRVANSTANL VKTIKALDGDPSEDNRNKCRIATAPLIEAVENNITAFASNEPVS IPAQISSEGSQARPILVSAKPMLESSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQCCDYSIDGINRC IRDIEQASLAAVSGSLATRDDISVEALQECLTSVVQEIGHLIDP IATAARGEAQLGHKGTQLASYFFPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLMEAASEVGLUGWUDAIAEAMSKLDEGTPPEPKG TPVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGGMAAATAEPEETGTRTEDLIGKGTFLVQKAGA ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATTAGTLAHARNSETFADHERIILKTA KALVEDTKLLUSGASSTPDKLAQAQASSAATTQLAEVVKLGAA SLGSDDETQVVLINAIKQBASTARDISTATQLAERVVKLGAA SLGSDDEPTQVVLINAIKQBASTARDISTATCLAERVUKLGAA SLGSDDEPTQVVLINAIKQBASTARDTARLEATIECIKQ ELITVPQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRGB		· ·		DMLSELRDKWDTICGKSVERQNKLEEA\LLFSGQFTDALQALID
LEAALRQAEEFHSVUHALLEWLARASCTRFHGVLEDDEDALRT LIDGHKEFMKKLEKRAELMKATTMODTURAICHPDSITTIKHW HTITRAFFEEVLAWAKGHQOPALSALAGILAKQELLEALLAWLQ WASTILTDKUKEVIPQBIBEVKALIABHQTFMSEMTRKQPDVDK VTKTYKRRADPSSLQSHIPVLDKGRAGRKEFPASSLYPSGSOT QIETKNPRVNLLVSKMQQWWLLALERRKKINDALDRLEELREFA NPDFDIWRKKYMRWMNIKKSRVMDFFRRIDKDDGGKITRQEFID GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYBFVAALHPNKDA YKPITDADKIEDEVTRQVAKCKCAKBFQVEQIGDNEYRFFLGMQ FGDSQQLRLVRILBESTTMVRUGGGWWALDEFLVKNDPCRAKGRT NMELREKFILADGASQGMAAFRPRGRRSPSSRGASPRSTSVS SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA ECSDFPVPSARGTIQGSKLRLEGYLSGKGFHSGEDSGLITTAA ARVRTQPADSKKTSRPGSRAGSKAGSRASSRGSDASPDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR 6029 1 3533 IMPGGSSRLEGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHGGLVDPIQFARANQALQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCHACRIASSTANFPVARHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAPASNPEPVS IPAQISSEGSQASPILVSAKPMLESSYLIRTARSLAINPKDP PTWSVLACHSHTVSDSIKSLITSIRDKAPGQRECDYSIGDINC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQBIGHLIDP LATAARGEAQLGHKGTQLASYFPPLILAAVGVASRILDHQQOM TVLDQTKTLABSALQMLYAARGGGGNPKAQHTHDATTEAAQUMK EAVDDIWTLNEAASEVGLVGGWDDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKALAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFGGQMAAATAEPEEIGFOIRTRVQDLGHGGIFLVQKAG\ ALQVCPTDSYYKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNABNSETFADHRENILKTA KALVEDTTKLLVSGASSTPDKLAQAQASSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKWMVTNVTSLIKTVKAUYDBEATRGTRALEATIECIKQ ELITVPQSKUVPEKYSSPEESIRMTKGITMATAKAVAAGNSCCGB	ļ	1		WLYRVEPQLAEDQPVHGDIDLVMNLIDNHKAFQKELGKRTSSVQ
LIDQHKEFMKKLEEKRAELNKATTMGDTVLAICHDDSITTIKHW ITIIRARPEEVLAWAKCHQORLASALAGIIAKQELLEALLANLQ WAPETTLTDKOKEVIPQEIEEVKALIAEHGTFMEMTRKQPDVDK VTKTYKRRAADPSSLQSHIPVLDKGRAGRKRFPASSLYPSGSOT QIETKNPRVILLVSKWQOWHLALERRKINDALDKEELREFA NPDEDIWRKKYMRWINKKSKSWUDFFRRIDKDDGBKITRGEFID GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYEFVAALHPNKDA YKPITDADKIEDEVTRQVAKCKCAKERQVEQIGDNKYRFFLGNQ FGDSQOLRLURILESTTWURGGWMALDEFLYWNDDCRAKGRT NMELREKFILADGASQGMAAFRPRGRRSRSSRGASPNRSTSVS SQAAQAASPQVPATTTPKILHPLTRNYGKWUTNSKWSTPCKAA ECSDPVPSABGTPIQGSKLEQYJSKGMFHSGEDSGLITTMA ARVRTQPADSKKTPSRGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRFTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR 6029 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALGITEAAAQAAYLVGIFD PNSQAGHGGLUDPIQFARAMQAIQMAQQNLUVDFGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDPSEDNRNKCRIATAPLIEAVENNITAFASNPERVS IPAQISSEGSQAQPBILUSAKAPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTOLASYFEPLILAAVGAASKILDHQQM TVLDQTKTLABSALQHKGTOLASYFEPLILAAVGAASKILDHQQM TVLDQTKTLABSALQHKGTOLASYFEPLILAWGANSKILDHQQM TVLDQTKTLABSALQHKGTOLASYFEPLILAWGANSKILDHQQM TVLDQTKTLABSALQHKGTOLASYFEPLILAWGANSKILDHQCMT TVLDQTKTVLARSALQHKGTOLASYFEPLILAWGANSKILDHQCOM TVLDQTKTLABSALQHKGTOLASYFEPLILAWGANSKILDHGQTFPEPKG TFVDYQTTVVKYSKALAVTAQEMMTKSVTTPBELGGLASQMTSD YGHLAFGQGMAAATASPEEIGFGIRTKVQDLGGGFFLVQKAG ALQVCPTDSYTKRELI ECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGII ADLDTTIMFATAGTLARANSETFADHRENILKTA KALVEDTTKLLVSGAASTPDKLAQAASSAATITOLAEVVKLGAA SLGSDDFTQVVLINAIKDUTALKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKWUVTNVTSLLKTVKAVEDBATRGTRALBATIECIKQ ELTVPQSKOVPEKTSSPEESIRMTKGITMATAKAVAAGNSCCRG				ALKRSARELIEGSRDDSSWVKVQMQELSTRWETVCALSISKQTR
LIDQHKEFMKKLEEKRAELNKATTMGDTVLAICHDDSITTIKHW ITIIRARPEEVLAWAKCHQORLASALAGIIAKQELLEALLANLQ WAPETTLTDKOKEVIPQEIEEVKALIAEHGTFMEMTRKQPDVDK VTKTYKRRAADPSSLQSHIPVLDKGRAGRKRFPASSLYPSGSOT QIETKNPRVILLVSKWQOWHLALERRKINDALDKEELREFA NPDEDIWRKKYMRWINKKSKSWUDFFRRIDKDDGBKITRGEFID GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYEFVAALHPNKDA YKPITDADKIEDEVTRQVAKCKCAKERQVEQIGDNKYRFFLGNQ FGDSQOLRLURILESTTWURGGWMALDEFLYWNDDCRAKGRT NMELREKFILADGASQGMAAFRPRGRRSRSSRGASPNRSTSVS SQAAQAASPQVPATTTPKILHPLTRNYGKWUTNSKWSTPCKAA ECSDPVPSABGTPIQGSKLEQYJSKGMFHSGEDSGLITTMA ARVRTQPADSKKTPSRGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRFTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR 6029 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALGITEAAAQAAYLVGIFD PNSQAGHGGLUDPIQFARAMQAIQMAQQNLUVDFGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDPSEDNRNKCRIATAPLIEAVENNITAFASNPERVS IPAQISSEGSQAQPBILUSAKAPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTOLASYFEPLILAAVGAASKILDHQQM TVLDQTKTLABSALQHKGTOLASYFEPLILAAVGAASKILDHQQM TVLDQTKTLABSALQHKGTOLASYFEPLILAWGANSKILDHQQM TVLDQTKTLABSALQHKGTOLASYFEPLILAWGANSKILDHQQM TVLDQTKTLABSALQHKGTOLASYFEPLILAWGANSKILDHQCMT TVLDQTKTVLARSALQHKGTOLASYFEPLILAWGANSKILDHQCOM TVLDQTKTLABSALQHKGTOLASYFEPLILAWGANSKILDHGQTFPEPKG TFVDYQTTVVKYSKALAVTAQEMMTKSVTTPBELGGLASQMTSD YGHLAFGQGMAAATASPEEIGFGIRTKVQDLGGGFFLVQKAG ALQVCPTDSYTKRELI ECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGII ADLDTTIMFATAGTLARANSETFADHRENILKTA KALVEDTTKLLVSGAASTPDKLAQAASSAATITOLAEVVKLGAA SLGSDDFTQVVLINAIKDUTALKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKWUVTNVTSLLKTVKAVEDBATRGTRALBATIECIKQ ELTVPQSKOVPEKTSSPEESIRMTKGITMATAKAVAAGNSCCRG				
ITIIRARPEEVLAWAKQHQQRLASALAGLIAKQELLEALIANLQ WAETTITDKKREVJPQEIEEVKALIAEHQTFMEEMTRKQDPVDK VTKYTKRRAADPSSLQSHI PVILDKGRAGRKRPPASSLYPSGSOT QIETKNPRVNLLVSKWQQVWLLALERRRKLNDALDRLEELREPA NFDFDIWRKKYMRWNHKKSRVMDFFRRIDKDQDGKITRQEFID GILSSKFFTSKLEMSAVADIFDRDDGGYIDYYEFVAALHPINKDA YKPITDADKIEDEVTRQVAKCKCARFFQVEQIGDNKYRFFLONQ FGDSQQLRLVRILRSTVMVRVGGWMALDEFLVKNDPCRAKGRT NMELREKFILADGASQGMAAFRPRGRRSPSSRGASPNRSTSVS SQAQAQASPQVPATTIPKILHELTRNYGKPWLTINSKMSTPCKAA ECSDFPVPSABGTPIQGSKLRLPGYLSGKGFHSGEDSGLITTAA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGBDASDFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR LDKSSKR AGISONAKTGDLPARGECVGIASKALCGLTEAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATHDDISVEALQEDLTSVVQEIGHLIDP LATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLABSALQMLVAAKSGGONPKAQHTHDAITEAAQLMK EAVDDINVTLNEBASEVGLVGGMVDAIAEBMSKLDEGTPPEPRG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAPPEELIGCARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNABNSETFADHRENILKTA KALVEDTTKLLVSGAASTPDKLAQAAQSSAATITQLAEVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTTALEATIECIKQ ELTVPQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGASCRQB			1	· · · · · · · · · · · · · · · · · · ·
WAETTLITDKDKEVIPQEIEEVKALLAEHQTFMEEMTRKQPDUDK VTKTYKRRAADPSSLQSHIPVLDKGRAGKRFPASSLYPSGSGT QIETKNPEVNLLVSKWQQVWLLALERRRKLNDALDRLEELREFA NFDFDIWRKKYMRWMNHKKSRVMDFFRRIDKODGKITTQEFID GILSSKFFTSRLEMSAVADIFDRODGYIDYYEFVAALHPNKDA YKPITDADKIEDEVTRQVAKCKCARRFQVEQIGDNKYRFICNO FGDSQQLRLVRILRSTVMVRVGGGWMALDEFLVKNDPCRAKGRT NMELREKFILADGASQGMAAFRFBGRSRPSSRGASPNRSTSVS SQAQAASPQVPATTIP KILHPLTNNYGKPWITNSKMSTPCKAA ECSDFPVPSABGTPIQGSKLRLPGYLSGKGFHSGEDSGLITTAA ARVKTQFADSKKTPSRPGSRAGSKASSRASSRRGBDASDFDISE IQSVCSDVETVPYTRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR FOOSSELLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHGGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPPQISSESGAQEPILVSAKFMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIGGINRC IRDIEQASLAAVSQSLATRODISVEALQEQLTSVVQEIGHLIDP TATAARGERAQIGHKGTQLASYFEPLILLAAVGVASKILDHQQQM TVLDQTKTLABSALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVCLVGGUVDAIAEAMSKLDEGTPPEFRG TFVDYQTTVVKYSKALAVTAQEMMTKSVTNYBELIGGLASQMTSD YGHLAFQQCMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTERUSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNTRUSPTFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKFVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTTALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGKSCRQE	1			
VTKTYKRRAADPSSLQSHIPVLDKGRAGRKRFPASSLYPSGSQT QIETKNPRVNLLVSKWQQVWLLLALERRRKLNDALDRLEELBEFA NPDFDIMKRKYMRWHMKKSRVMDFFREIDKDQDGKITRQEFID GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYBFVAALHPNKDA YKPITDADKIEDBVTRQVAKCKCAKRPQVEGIGDNKYRFFLGNQ FGDSQQLRLVRILRSTVMVRVGGGWMALDEFLVKNDPCRAKGRT NMBLREKFILADGASQGMAAFBPRGRSRPSSRGASPNRSTSVS SQAQAASPQVPATTTPKLLHPLTRNYGKPWLTNSKMSTPCKAA ECSDFPVPSABGTPIQGSKLRLPGYLSGKGFHSGEDSGLITTAA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHQGLIVDPIQFARANQAICMACQNLUDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNINKCRIATAPLIEAVENLTAFASNPBEVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGGRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALGQCLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESSLQMLYAAKEGGRPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKATAVTAQEMMTKSVTNPEBLGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECCARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIJADLGTATMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKEVDDPSM YQLKGAAKWWYNTNYTSLLKTVKAVEDEATRGTALEATIECIKQ BLTVPQSKDVPEKTSSPESIRNTKGITMATAKAVAAGNSCRQB	į		1	
QIETKNPRVNLLVSKWQQVWLLALERRRKLNDALDRLEELREFA NFDFDIWRKKYWRWNHKKSRVWDFFRRIDKODGKITRGEFID GILSSKFPTSRLEMSAVADIFDRDGOGYIDYVSFVAALHPINKDA YKPITDADKIEDEVTRQVAKCKCAKRFQVEQIGDNKYRFFLGNQ FGDSQQLRLVRILRSTVMVWCGGWMALDEFLVKNDPCRAKGRT NMELREKFILADGASQGMAAFRPRGRRSRPSSRGASPNRSTSVS SQAAQAASPQVDAATTPKILHPLTRNYGKPWLTMSKMSTPCKAA ECSDFPVPSABGTPIQGSKURLPGYLSGKGFHSGEDSGLITTAA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR 6029 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALGGLTBAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTAMPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNENKCRIATAPLIEAVENLTHAFASNPEPVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGGRECDYSIGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGPRCDHTHDAITEAAQLMK EAVDDIMVTLNEBASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVPYQTTVVVKYSKALTAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVISALQAGNKGTQACI TAATAVGGIIADLDTIJMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAQSSAATITQLAEVVKLGAA SLGSDPETQVVLINAIKDVAKALSDLISATKGAASKFVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVPQSKDVPERTSSPESIRMTKGITMATAKAVAAGNSCRQB				1
NPDFDIWRKKYMRWMNHKKSRVMDFFRRIDKDQDGKITRQEFID GILSSKFFTSRLEMSAVADITDRDGDGYIDYYBFVAALHPNKDA YKPITDADKIEDEVTRQVAKCKCARFQVEQIGDNKKFFLGNQ FGDSQQLRIVRILRSTVMVRVGGGWMALDEFLVKNDPCRAKGRT NMELREKFILADGASQGMAAFRPRGRSRPSSRGASPNRSTSVS SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA ECSDFPVPSABGGTPIQGSKLRLPGYLSGKGFHSGEDSGLITTAA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRFTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR 6029 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPBFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQRQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKLLDHQQQM TVLDQTKTLABSALQMLYAAKEGGENPKAQHTHDAITEAAQLMK EAVDDIMVTLNEASSCULVGGMUDAIAEAMSKLDGTPPEPERG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGGMAAATAEPEEIGFOIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHENIILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKFVDDPSM YQLKGAAKVMVTNVTSLIKTVKAVEDEATRGTRALEATIECIKQ ELTVPQSKDVPERTSSPEESIRMTKGITMATAKAVAAGNSCROB				<u> </u>
GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYEFVAALHPNKDA YKPITDADKIEDBVTRQVAKCKCARRFQUEQIGDNKYRFFLGNQ FGDSQQLRLVRILRSTVMVRVGGGMMALDEFLVKNDPCRAKGRT NMELREKFILADGASQCMAAFRPRGRSRPSSRGASPNRSTSVS SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA ECSDFPVBSABGTPIQGSKLRLPGYLSGKGFHSGEDSGLITTAA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVBTVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR LDKSSKR IMPGGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRLATAPLIEAVENLTAFASNPBFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLTTSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIABAMSKLDEGTPPEFKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGGMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKFVDDPSM YQLKGAAKVMVTNVTSLLKKTVKAVEDEATRGTRALEATIECIKQ ELTVPQSKDVPERTSSPEESIRMTKGITMATAKAVAAGNSCRQE	1			T =
YKPITDADKIEDEVTRQVAKCKCAKRFQVEQIGDNKYRFFIGNQ FGDSQQLRLVRILRSTVMVRVGGGMMALDEFLVKNDPCRAKGRT NMELREKFILADGASQGMAAFRPRGRRSRPSSRGASPNRSTSVS SQAAQASSPQVPATTTPKILHPLTRNYGKPMLTNSKMSTPCKAA ECSDFPVPSABGTPIQGSKLRLFGYLSGKGFHSGEDSGLITTAA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR 6029 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQATQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFFASNPBFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPBPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLCHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITOLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVALBDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVALBDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVALBGLISATTGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVALBGLISATTGAASKPVDDPSM			1	
FGDSQQLRLVRILRSTVMVRVGGGMMALDEFLVKNDPCRAKGRT NMELREKFILADGASQGMAAFRPRGRSRPSSRGASPNRSTSVS SQAAQASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA ECSPFPVPSARGTPTQGSKLRLPGYLSGKGFHSGEDSGLTTTAA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR LDKSSKR IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGKGTQLASYFEPLILAAVGVASKILDHQQM TVLDQTKTLABSALOMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKATAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVKLGAA SLGSDDPTQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNYTSLLKTVKAVEDEBATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE				GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYEFVAALHPNKDA
NMELREKFILADGASQGMAAFRPRGRRSRPSSRGASPNRSTSVS SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA ECSDFPVPSARGTPIQGSKLRLPGYLSGKGFHSGEDSGLITTAA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRPTPRAGSRRSTAKPSKIPTPQRKSPASK LDKSSKR 6029 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCTESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITTSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP LATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKALAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAPPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVYKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNYTSLLKTVKAVSDEBATRGTALBATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE			·	YKPITDADKIEDEVTRQVAKCKCAKRFQVEQIGDNKYRFFLGNQ
SQAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA ECSDPPVPSABGTPIQQSKLRIPGYLSGKGFHSGEDSGLITTAA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR 6029 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVYSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP LATAARGEAAQIGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNERASEVGLVGGWVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGGIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMYTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE	1	-		FGDSQQLRLVRILRSTVMVRVGGGWMALDEFLVKNDPCRAKGRT
SQAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA ECSDPPVPSABGTPIQQSKLRIPGYLSGKGFHSGEDSGLITTAA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR 6029 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVYSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP LATAARGEAAQIGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNERASEVGLVGGWVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGGIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMYTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE	l		ſ	NMELREKFILADGASQGMAAFRPRGRRSRPSSRGASPNRSTSVS
ECSDFPVPSABGTPIQGSKLRLPGYLSGKGPHSGEDSGLITTAA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNYTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE	1			
ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPARGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP LATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTTALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE	Į	1		1 -
IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR 6029 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP LATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKEVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE	1			
LDKSSKR IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE	1	,		1
IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMYTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE	1		1	1 - 2 - 1 - 2 - 1 - 2 - 1 - 1 - 2 - 1 - 1
AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE			<u> </u>	
PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLXAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE	6029	1	3533	1 -
TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLXAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQB	1			
VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPBFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQB	1			PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA
IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQB			1	TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL
IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQB	1		1	VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQB		1	Į.	IPAOISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQB	1	1		
IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE				•
TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE				
EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE		1		
TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE			1	
YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE	İ			
ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE		İ		
TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE			1	
TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE	l			ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI
KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE	1	1		Yes
SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE	1			
YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE	İ			
ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE				
	1			
DATATANDSKVAAADIMITACAAASLUEDAAATKADKIGIEC	1			
	L		<u> </u>	DATUTUM DOVIVA SPRINTINCV Ó VOLUEDA ODE A VITA PRESIDENCE

0.00	1817-1		
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	1	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
Ī		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA
	•		EAMKGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRAK
1		•	PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
			VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA
1 .			SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV
ł			KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
			LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6030	3	1777	FPGRGSPALQLEVLICLGLMGLERALNVLAPIFYRNIVNLLTEN
			APWNSLAWTVTSYVFLKFLQGGGTGSTGFVSNLRTFLWIRVQQF
l			TSRRVELLIFSHLHELSLRWHLGRRTGEVLRIADRGTSSVTGLL
1		1	SYLVFNVIPTLADIIIGIIYFSMFFNAWFGLIVFLCMSLYLTLT
1			IVVTEWRTKFRRAMNTQENATRARAVDSLLNFETVKYYNAESYB
			VERYREAIIKYQGLEWKSSASLVLLNQTQNLVIGLGLLAGSLLC
1			AYFVTEQKLQVGDYVLFGTYIIQLYMPLNWFGTYYRMIQTNFID
1			MENMFDLLKK\ETEVKDLPGAGPFRFQKGRIEFENVHFSYADGR
	:		ETLQDVSFTVMPGQTLALVGPSGAGKSTILRLLFRFYDISSGCI
		•	RIDGQDISQVTQALFRFSHWELCPKDTVLFNDTIADNIRYGRVT
			AGNDEVEAAAQAAGIHDAIMAFPEGYRTQVGERGLKLSGGEKQR
1			VAIARTILKAPGIILLDEATSALDTSNERAIQASLAKVCANRTT
			IVVAHRLSTVVNADQILVIKDGCIVERGRHEALLSRGGVYADMW
1			QLQQGQEETSEDTKPQTMER
6031	160	1694	LRMSENLDKSNVNEAGKSKSNDSEEGLEDAVEGADEALQKAIKS
1			DSSSPQRVQRPHSSPPRFVTVEELLETARGVTNMALAHEIVVNG
1			DFQIKPVELPENSLKKRVKEIVHKAFWDCLSVQLSEDPPAYDHA
			IKLVGBIKETLLSFLLPGHTRLRNQITEVLDLDLIKQEAENGAL
1	,		DISKLAEFIIGMMGTLCAPARDEEVKKLKDIKEIVPLFREIFSV
ŀ			LDLMKVDMANFAISSIRPHLMQQSVEYERKKFQEILERQPNSLD
	. '		FVTQWLEEASEDLMTQKYKHALPVGGMAAGSGDMPRLSPVAVON
			YAYLKLLKWDHLQRPFPETVLMDQSRFHELQLQ\REQLTILGAV
			LLVTFSMAAPGISSQADFAEKLKMIVKILLTDMHLPSFHLKDVL
1	,		TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDP
1	,		IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELEEVAI
6032	39	2415	KFARLVNYNKMVFCPYYDAILSKILVRS
0032]	2413	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
:			SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
			YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
i 1			QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
[PIGSSAGLLALSSALGGOSHLPIKDEKKHHDNDHQRDRDSIKSS
] . [SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK
	,		SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
]	ľ		ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
			NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
			MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAYGRSPVVGFD
]	Į		PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL
	Ī		IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
]	1		DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
	ł		SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
1			AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
	ŀ	į	W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V
	ļ		EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
	Ī		W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\
			RATVYBVIY
6033	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
	1		SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
}			YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
ŀ			QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
			PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS
			SVSPSASFRGAEKHRNSADYSSESKKOKTEEKEIAARYDSDGEK
			SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
			ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
]		Ì	NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAYGRSPVVGFD
1			PHHHMRVPAIPPNLTGIPGGKPAYSPHVSADGQMQPVPFPPDAL
			IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
1			DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
			SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
1			AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
1			W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V
ì			EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
			W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\
Į.			RATVYEVIY
6034	2683	714	ESGRRRLKRRRSPCPGTAGGPGETNPGPGACPRGPREEAAAAM
5552		1	EIAPQEAPPVPGADGDIEEAPAEAGSPSPASPPADGRLKAAAKR
			VTFPSDEDIVSGAVEPKDPWRHAQNVTVDEVIGAYKQACQKLNC
}	Ì		ROIPKLLROLOEFTDLGHRLDCLDLKGEKLDYKTCEALEEVFKR
			LOFKVVDLEQTNLDEDGASALFDMIEYYESATHLNISFNKHIGT
			RGWQAAAHMMRKTSCLQYL\DARNTPLLDHSAPFVARALRIRSS
1			LAVLHLENASLSGRPLMLLATALKMNMNLRELYL\ADNKLNGLQ
j .			DSAQLGNLLKFNCSLQILDLRNNHVLDSGLAYICEGLKEQRKGL
1	ĺ		VTL\VLWNNOLTHTGMAFLGMTLPHTQSLETLNLGHNPIGNEGV
	!		RHLKNGLISNRSVLRLGLASTKLTCEGAVAVAEFIAESPRLLRL
1	1	1	DLRENEIKTGGLMALSLALKVNHSLLRLDLDREPKKEAVKSFIE
		ĺ	TQKALLAEIQNGCKRNLVLAREREEKEQPPQLSASMPETTATEP
			QPDDEPAAGVQNGAPSPAPSPDSDSDSDSDSDGEEEEEEGERDET
1	Į.		PSGAIDTRDTGSSEPOPPPEPPRSGPPLPNGLKPEFALALPPEP
1			PPGPEVKGGSCGLEHELSCSKNEKELEELLLEASQESGQETL
6025		404	SVTYLGIILHKNTGALPADPVQLISQTPTPSTKQQLLSFLGMVG
6035	19	404	YFYLWIPGFAILTKPLCKLTKENLADAIDPKSFSHSSFRSLKTA
	1	i i	IF I I WIFGE ALL I REACKED I REAL MADAL DE ROS SIEST ROSKIA
			TENDOTE, AT DISCORD STUTAR VOCCOMPTITOCICALIN
6006	1745	356	LENASTLALPDSSQPF\SLHTARVQGCVVEILTQGLGPLPV
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKBKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKBKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL
			LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK
6036	17 4 5	1919	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK
			LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKFVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR
			LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKFVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG
			LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKPPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKFVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI
			LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKPPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL
			LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKPPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA
			LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWREMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS
			LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKBKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRFFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSSSSSSSSSTLDNSRRLPIFSRLSISDD
			LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKBKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPSPQDSLSDQEGYLS SSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH
6037	2936	1919	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKBKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRFFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSSSSSSSSSTLDNSRRLPIFSRLSISDD
6037	2936	1919	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPILSADDILLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGYPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG
6037	2936	1919	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKBKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRFFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS
6037	2936	1919	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPILSADDILLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGYPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG
6037	2936	1919	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPILSADDILGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSSSSSSDSPTLDNSRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK
6037	2936	1919	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSHSGSDSPTLDNSRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK
6037	2936	1919	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSHSGSDSPTLDNSRRIPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCEICD VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL
6037	2936	1919	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRILLYCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCEICD VHVNSETQLKQHISSRRHKDRAAGKPPKKYSPYNKLQKTAHPL GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAAVAVSSPFSLRTAP AATLFQTSALPPALLRPAPGPIRTAHTPVLFAPY
6037	2936	1919	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKPPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRILLYCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCEICD VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAAVAVSSPFSLRTAP AATLFQTSALPPALLRPAPGPIRTAHTPVLFAPY LDEYEARLTLANLDDFEEDNEDDDENRVNQEEKAAKITELINKL
6037	2936	1919	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKBKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRFFTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPSPQDSLSDQEGYLS SSSSHSGSDSPTLDNSRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCEICD VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL GVKLVFSKEPSKPLAPRILPRPLAAAAAAAAVAVSSPFSLRTAP AATLFQTSALPPALLRPAPGPIRTAHTPVLFAPY LDEYEARLTLANLDDFEEDNEDDDENRVNQEEKAAKITELINKL NFLDEAEKDLATVNSNPFDDPDAAELNPFGDPDSEEPITETASP
6037	2936	1919	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAENIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKBKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCEICD VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAVAVSSPFSLRTAP AATLFQTSALPPALLRPAPGPIRTAHTPVLFAPY LDEYEARLTLANLDDFEEDNEDDDENRVNQEEKAAKITELINKL NFLDEAEKDLATVNSNPFDDPDAAELNPFGDPDSEEPITETASP RKTEDSFYNNSYNPFKEVQTPQYLNPFDEPEAFVTIKDSPPQST
6037	2936	1919	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV DIDWPIAEQRVLRYGYFGKBKLKEIKLLVCNIDGCLTNGHIYVS GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL MEKGLINFMPKNRNLAVNIGEKK WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRFFTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPSPQDSLSDQEGYLS SSSSHSGSDSPTLDNSRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCEICD VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL GVKLVFSKEPSKPLAPRILPRPLAAAAAAAAVAVSSPFSLRTAP AATLFQTSALPPALLRPAPGPIRTAHTPVLFAPY LDEYEARLTLANLDDFEEDNEDDDENRVNQEEKAAKITELINKL NFLDEAEKDLATVNSNPFDDPDAAELNPFGDPDSEEPITETASP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	M-Termenter W. Thursday, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	Doquence		\=possible nucleotide insertion)
			PKPSPIPSPVLGRKPNASQSLLVWCKEVTKNYRGVKITNFTTSW
j			RNGLSFCAILHHFRPDLIDYKSLNPQDIKENNKKAYDGFASIGI
ł	i		SRLLEPSDMVLLAIPDKLTVMTYLYQIRAHFSGQELNVVQIEEN
			SSKSTYKVGNYETDTNSSVDQEKFYAELSDLKREPELQQPISGA
			VDFLSQDDSVFVNDSGVGESESEHQTPDDHLSPSTASPYCRRTK
ļ	l .	1	SDTEPQKSQQSSGRTSGSDDPGICSNTDSTQAQVLLGKKRLLKA
			ETLELSDLYVSDKKKDMSPPFICEETDEQKLQTLDIGSNLEKEK
			LENSRSLECRSDPESPIKKTSLSPTSKLGYSYSRDLDLAKKKHA
1			SLRQTESDPDADRTTLNHADHSSKIVQHRLLSRQEELKERARVL
			LEQARRDAALKAGNKHNTNTAAPFCNRQLSDQQDEERRRQLRER
			ARQLIAEARSGGKMSELPSYGERAAEKLKERSKASGDENDNIEI
1 1			DTNEEIPEGFVVGGGDELTNLENDLDTPEQNSKLVDLKLKKLLE
			VQPQVANSPSSAAQKAVTESSEQDMKSGTEDLRTERLQKTTERF
1 1		•	RNPVVFSKDSTVRKTQLQSFSQYIENRPEMKRQRSIQEDTKKGN
			EEKAAITETQRKPSEDEVLNKGFKDS\SQYVVGELAALENEOKO
.			IDTRAALVEKRLRYLMDTGRNTEEEEAMMQEWFMLVNKKNALIR
			RMNQLSLLEKEHDLERRYELLNRELRAMLAIEDWQKTEAQKRRE
1 1	·		QLLLDELVALVNKRDALVRDLDAQEKQAEEEDEHLERTLEQNKG
	-		KMAKKEEKCVLQ
6040	475	1052	PTALMTAPSCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLM
			LSSNQITMVINVSVEVVNTLYEDIQYMQVPVADSPNSRLCDFFD
1			PIADHIHSVEMKQGR\TLLHCAAGVSRSAALCLAYLMKYHAMSL
			LDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPV
			GMIPDIYEKEVRLMIPL
6041	2	3886	TEKDEKTAHNLENVLIHFWERLSEICVAKISEPEADVESVLGVS
1 1			NLLQVLQKPKGSLKSSKKKNGKVRFADEILESNKENEKCVSSEG
			EKIECWELTTEPSLTHNSSGLLSPLRKKPLEDLVCKLADISINY
1 1			VNERKSEQHLRFLSTLLDSFSSSRVFKMLLGDEKQSIVQAKPLE
1			IAKLVQKNPAVQFLYQKLIGWLNEDQRKDFGFLVDILYSALRCC
1 1			DNDMERKKVLDDLTKVDLKWNSLLKIJEKACPSSDKHALVTPWL
1 1			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ
1 1	. 1		HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEAESSDSSVSFIC
	·		DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI
		•	CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL
1			DINSLOVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWEK
		•	MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIKTLPSHLCT
1	j		SALLSKMVLIALRKETVLENNELEKIIAELLYSLQWCEELDNPP
1 .1			IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW
	.		SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP
1 .1	ľ		FLSKEEKKEFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ
1 1			TKSIDDGELLHGILKIIISWKKEHEDIFLFSCNLSEASPEVLGV
1			NIEIIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL
		•	YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK
1 1			EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY
1			ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP
			VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEEPALSPPAALMS
1 1		ł	LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI
			LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAB
]]		.	TAVEVPNKDPKTFFTBELQLSIRETTMLPYHIPHLACSVYHMTL
1 .			KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQBISSVQT
1			STQLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS
1 1	}		IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN
			VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY
6042	1306	252	KWFTSSNKSTCSLCRETFF
	2300	253	MAELAPASPSDIKASVSNGDTTLLCSRRQSCGMNEVRQVSLTYP
			GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY
			GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE
	İ		LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV
	ļ	ļ	QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS
		1	PDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTIDLVAFL
<u> </u>		<u>-</u>	GYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLK

650	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ	l .	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	bequence		ILADAAAEGVPVRGARNQLRMYLTMAVAAAQPMLMYWLTFHLVR
	465		LCLFFFFPCATPVLPLPSLISAL/CLSHLSVSSWFCPCQPPLPC
6043	403	599	1 · · · · · · · · · · · · · · · · · · ·
			PLPPLQNKTAKGSLSTEQSERG
6044	793	412	KLEMWNFTLISKVKISREVTMIASKFGIGQQVRHSLLGYLGVVV
1			DIDPVYSLSEPSPDELAVNDELRAAPWYHVVMEDDNGLPVHTYL
Į.	1		AEAQLSSELQDEHP\EQPSMDELAQTIRKQLQAPRLRN
6045	155	2299	SPLPQVAAMNYLRRRLSDSNFMANLPNGYMTDLQRPQPPPPPPG
			AHSPGATPGPGTATAERSSGVAPAASPAAPSPGSSGGGGFFSSL
	}		SNAVKOTTAAAAATFSEOVGGGSGGAGRGGAASRVLLVIDEPHT
İ			DWAKYFKGKKIHGEIDIKVEQAEFSDLNLVAHANGGFSVDMEVL
ì	Ì	i	
1			RNGVKVVRSLKPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPS
			VNSLHSVYNFCDKPWVFAQMVRLHKKLGTEEFPLIDQTFYPNHK
1			EMLSS\TTYPVVVKMGHGTLWGWGKVKVDNQHDFQDIASVVALT
Ī			KTYATAEPFIDAKYDVRVQKIGQNYKAYMRTSVSGNWKTNTGSA
1		1	MLEQIAMSDRYKLWVDTCSEIFGGLDICAVEALHGKDGRDHIIE
i			VVGSSMPLIGDHQDEDKQLIVELVVNKMAQALPRQRQRDASPGR
1			GSHGQTPSPGALPLGRQTSQQPAGPPAQQRPPPQGGPPQPGPGP
	1		QRQGPPLQQRPPPQGQQHLSGLGPPAGSPLPQRLPSPTSAPQQP
1		!	ASQAAPPTOGOGROSRPVAGGPGAPPAARPPASPSPQRQAGPPQ
	1	!	ATROTSVSGPAPPKASGAPPGGOOROGPPOKPPGPAGPTROASO
		i	AGPVPRTGPPTTOOPRPSGPGPAGRPKPOLAOKPSODVPPPATA
Į			
j		1	AAGGPPHPQLNKSQSLTNAFNLPEPAPPRPSLSQDEVKAETIRS
			LRKSFASLFSD
6046	212	1075	EGLTGPCERVPFLLGRGPPHGATRAGHRRAVRWAGPESLPPLPR
			SLIMDSPRAGTHQGPLDAETEVGADRCTSTAYQEQRPQVEQVGK
			QAPLSPGLPAMGGPGPGPCEDPAGAGGAGGGSEPLVTVTVQCA
1			FTVALRARRGADLSSLRALLGQALPHQ\AQLGQLSYLAPGEDGH
ĺ		{	WVPIPEEESLQRAWQDAAACPRGLQLQCRGAGGRPVLYQVVAQH
	ļ.		SYSAQGPEDLGFRQGDTVDVLCEVDQAWLEGHCDGRIGIFPKCF
i]	VVPAGPRMSGAPGRLPRSQQGDQP
6047	49	1405	PVLVTSLRMREADTLRPPQLMEVSADIISTVEFNHTGELLATGD
	**		KGGRVVIFQREPESKNAPHSQGEYDVYSTFQSHEPEFDYLKSLE
		1	IEEKINKIKWLPOONAAHSLLSTNDKTIKLWKITERDKRPEGYN
1) ·	{ ·	LKDEEGKLKDLSTVTSLQVPVLKPMDLMVEVSPRRIFANGHTYH
	-		1 · · · · · · · · · · · · · · · · · · ·
1			INSISVNSDCETYMSADDLRINLWHLAITDRSFTP\NIVDIKPA
l			NMEDLTEVITASEFHPHHCNLFVYSSSKGSLRLCDMRAAALCDK
			HSKLFEEPEDPSNRSFFSEIIS\SVSDVKFSHSDRYMLTR\DYL
		,	TVKVWDL\NMEARPIETYQVHDYLRSKLCSLYENDCIFDKFECA
1.			WNGSDSVIMTGA\YNNFFRMFDRNTKRDVTL\EASRESSKPRAV
1			LKPRRVCVGGKRRRDDISVDSLDFTKKILHTAWHPAENIIAIAA
	1		TNNLYIFQDKVNSDMH
6048	1	3194	GIRTPKFCDSPTSDLEMRNGRGRGKRMRPNSNTPVNETATASDS
1	1		KGTSNSSKTRAGANSKGRRGSQNSSEHRPPASSTSEDVKASPSS
1		1	ANKRKNKPLSDMELNSSSEDSKGSKRVRTNSMGSATGPLPGTKV
1			EPTVLDRNCPSPVLIDCPHPNCNKKYKHINGLKYHQAHAHTDDD
1		}	SKPEADGDSEYGEEPILHADLGSCNG\ASVSQK\GSLSPARSAT
1			PKVRLVEPHSPSPSSKFSTKGLCKKKLSGEGDTDLGALSNDGSD
1			
Į			DGPSVMDETSNDAFDSLERKCMEKEKCKKPSSLKPEKIPSKSLK
1			SARPI/APLAIPPQQIYTFQTATFTAASPGSSSGLTATVAQAMP
1			NSPQLKPIQPKPTVMGEPFTVNPALTPAKDKKKKKKKKKKKESSKE
1			LESPLTPGKVCRAEEGKSPFRESSGNGMKMEGLLNGSSDPHQSR
l			LASIKAEADKIYSFTDNAPSPSIGGSSRLENTTPTQPLTPLHVV
i			TQNGAEASSVKTNSPAYSDISDAGEDGEGKVDSVKSKDAEQLVK
1	1		EGAKKTLFPPQPQSKDSPYYQGFESYYSPSYAQSSPGALNPSSQ
Ī			AGVESQALKTKRDEEPESIEGKVKNDICEEKKPELSSSSQQPSV
1			IQQRPNMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ
1			YEEOOKRQSLEQOORGVDKKAEMGLKEREAALKEEWKQKPSIPP
1			TLTKAPSLTDLVKSGPGKAKEPGADPAKSVIIPKLDDSSKLPGQ
1			
1			APEGLKVKLSDASHLSKEASEAKTGAECGRQAEMDPILWYRQEA
L	<u> </u>	L	EPRMWTYVYPAKYSDIKSEDERWKEERDRKLKEERSRSKDSVPK

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	Graduic Acid, F=Phenylaianine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
· I	to first		L=Leucine, M=Methionine, N=Asparagine,
Ì		amino acid	P=Proline, Q=Glutamine, R=Arginine,
ľ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
			EDGKESTSSDCKLPTSEESRLGSKEPRPSVHVPVSSPLTQHQSY
}		1	IPYMHGYSYSQSYDPNHPSYRSMPAVMMQNYPGSYLPSSYSFSP
ı		i	VCCAICCOEDADA DA COOMINION DO COMPANA DA COM
			YGSKVSGGEDADKARASPSVTCKSSSESKALDILQQHASHYKSK
•		1	SPTISDKTSQERDRGGCGVVGGGGSCSSVGGASGGERSVDRPRT
		1	SPSQRLMSTHHHHHHLGYSLLPAQYNLPYAAGLSSTAIVASQQG
			STPSLYPPPRR
6049	215	1089	AMTGVFDRRVPSIRSGDFQAPFQTSAAMHHPSQESPTLPESSAT
Ì	İ	1	DSDYYSPTGGAPHGYCSPTSASYG\KALNPYQYQYHGVNGSAGS
		1	YPAKAYADYSYASSYHQYGGAYNRVPSATNQPEKEVTEPEVRMV
			NGKPKKVRKPRTIYSSFQLAALQRRFQKTQYLALPERAELAASL
	1	1	CLTOTOVKINEONYPCYTYKINKYGTWPDTHORGCOPHASL
	1	İ	GLTQTQVKIWFQNKRSKIKKIMKNGEMPPEHSPSSSDPMACNSP
	1		QSPAVWEPQGSSRSLSHHPHAHPPTSNQSPASSYLENSASWYTS
F 5550	 		AASSINSHLPPPGSLQHPLALASGTLY
6050	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
I		İ	PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
			RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW
1		ļ	DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY
			YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR
			RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
			ENET TENDENT THE DAME TO COME COME CONTROL OF THE CONTROL OF THE COME CONTROL OF THE COME CONTROL OF THE COME CONTROL OF THE CONTRO
			FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
	Ì		FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
			PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6051	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
1			PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
			RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW
i l			DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY
			YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR
1			RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
			RESERVED LEED A DEPARTMENT OF THE PROPERTY OF
			FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
			FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
			PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6052	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
1 1	, j	· ·	PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
1 • •	·	•	RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW
			DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY
1 . 1	1		YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKERBEDLR
]		•	RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
			FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
1	'	ı	PVI CCCVI NA CROCMETIDIONER PROPERTICIONES PROPERTI
	:		FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
6053			PSAATLINIRNARKHFEKLERVDGPKQCLLMR
0023	201	1704	KGTEMNKSRWQSRRRHGRRSHQQNPWFRLRDSEDRSDSRAAQPA
1	ŀ		HDSGHGDDESPSTSSGTAGTSSVPELPGFYFDPEKKRYFRLLPG
[ľ		HNNCNPLTKESIRQKEMESKRLRLLQEEDRRKKIARMGFNASSM
	1		LRKSQLGFLNVTNYCHLAHELRLSCMERKKVQIRSMDPSALASD
1	.		RFNLILADTNSDRLFTVNDVTVGGSKYGIINLQSLKTPTLKVFM
j	İ		HENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLAETPGCATLL
į į			PASLFVNSHPAGIDRPG\MLCSFRIPGAWSCAWSLNIQANNCFS
į į	į		TGLSRRVLLTNVVTGHRQSFGTNSDVLAQQFALMAPLLFNGCRS
1 1	ł		GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILQDEQYLMASD
]			MAGKIKLWDLRTTKCVRQYBGHVNEYAYLPLHVHEEEGILVAVG
.	ļ		QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG
			APGLLMAVGQDLYCYSYS
6054	1	1054	PPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH
1	1		KQSSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY
			VTTGTVDDWGDGTEVVNDDOTOGT VDFAAVSSAREVERITKEDY
		{	VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV
			DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH
			GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK
1			LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF
			VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPE
f			FKVLEDAWTVVSLD/TSKVSAQFEHTVLITSRGAQILTKLPHEA
			The state of the s

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
ſ	sequence	bequeince	\=possible nucleotide insertion)
6055	421	2364	PPYFLLSFLAWWLYGQSDRTETDISQSAGPPPGTLQCSALHHDP
0033	121	2301	GCANCSRFCRDCSPPACQCHTHVFPGNALNGVQPPBLSRTLALI
1			SSREPPRKKKKSOTETGKERERTSFLTQGGKRFELQHGLAGICM
i			TLLITGDSIVSAEAVWDHVTMANRELAFKAGDVIKVLDASNKDW
	ĺ		WWGOIDDEEGWFPASFVRLWVNHEDEVEEGPSDVQNGHLDPNSD
ł			CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKDICEGYLKQC
			RKRRDMFSDEQLKVIFGNIEDIYRFQMGFVRDLEKQYNNDDPHL
[SEIGPCFLEHODGFWIYSEYCNNHLDACMELSKLMKDSRYQHFF
			EACRLLOOMIDIA\IDGFLLTPVQKICKYPLQLAELLKYTAQDH
1			SDYRYVAAALAVMRNVTQQINERKRRLENIDKIAQWQASVLDWE
			GEDILDRSSELIYTGEMAWIYQP\YGRNQQRVFFLFDHQMVLCK
1			KDLIRRDILYYKGRIDMDKYEVVDIEDGRDDDFNVSMKNAFKLH
			NKETEEIHLFFAKKLEEKIRWLRAFREERKMVQEDEKIGFEISE
		1	NOKRQAAMTVRKVPKQKGVNSARSVPPSYPPPQDPLNHGQYLVP
-	Í		\DG1AQSQVFEFTEPKRSQSPFWQNFSRLTPFKK
6056	43	3358	SGGRGPVRVRSEQLSPSAEQVSQISQISLGRRPLSSLPPPPSRA
		,	LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRPSMEEFREFNK
			YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDIDNLLIPAPIQQ
ļ			MVTGQSGLFTQYNIQKKAMTVKEFRQLANSGKYCTPRYLDYEDL
İ			ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDVVE
			EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFGEP
1			KSWYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRHKMTLISPSV
1			LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNFAT
			VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQGKD
			IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSKRP
	ļ	•	KADEEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNTEA
]	SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDDKA
1			YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPESCS
		1	SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKVPS
		İ	IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVLSI
l			EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHCAI
	,		CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEMCF
			IYSEENIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPSH
			EICDGWLCARCKRNAWTAECCLCNLRGGALKQTKNNKWAHVMCA
			VAVPEVRFTNVPERTQIDVGRIPLQRLKLKCIFCRHRVKRVSGA
		1	CIQCSYGRCPASFHVTCAHAAGVL\MEPDDWPYVVNITCFRHKV
		1	NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFYEV
1			MFDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVVQVKWPDGKLYG
	,		AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF
		1	VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF
	<u> </u>	 	LSGTY
6057	1	853	FVARLKEQEGEGGLGPRKEKGRARGRBRRRKMQLTRCCFVFLVQ
			GSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKS RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFG
			WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR
		1	TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR
Ī			
6050	ļ		LVQKVCPDYNYHSDTPYYPSG
6058	1	986	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR
i			VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR
]			PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL
		1	
			PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGBP
COE0	1	3660	SREAGPWASLNCTLDPSASTP QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT
6059	2	3650	QQDFESLADLTDHRAHKCPGDGDDDPQLSWVASSPSSKDVASSP QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH
	1		SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS
			RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK
1			EHLAKSEKEAKKDDFMCDYCEDTFSQTEELEKHVLTRHPQLSEK
L	L	L	PUTITION DEVOUVED TANGED IN STATE OF THE STA

CDA	Dradiated	Description of the second	13-1-2 and gogment
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of -	S=Serine, T=Threonine, V=Valine,
1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			ADLQCIHCPEVFVDENTLLAHIHQAHANQKHKCPMCPE\QFSSV
			\EGVYCHLDSHRQPDSSNHSVSPDPVLGSVASMSSATPDSSASV
1			BRGSTPDSTLKPLRGQKKMRDDGQGWTKVVYSCPYCSKRDFNSL
İ			AVLEIHLKTIHADKPQQSHTCQICLDSMPTLYNLNEHVRKLHKN
			HAYPVMQFGNISAFHCNYCPEMFADINSLQEHIRVSHCGPNANP
ľ		<u> </u>	SDGNNAFFCNQCSMGFLTESSLTEHIQ\Q\AHCSVGSAKLESPV
	·		VQPTQSFMEVYSCPYCTNSPIFGSILKLTKHIKENHKNIPLAHS
ł		İ	KKSKAEQSPVSSDVEVSSPKRQRLSASANSISNGEYPCNQCDLK
ļ			FSNFESFQTHLKLHLELLLRKQACPQCKEDFDSQESLLQHLTVH
1		İ	YMTTSTHYVCESCDKQFSSVDD\LQKH\LLDMPHPLCCTHCT\L
i			CQEVFDS\KVSI\QVHLAVKHSNEKKMYRCTACNWDFRKEADLQ
		1	VHVKHSHLGNPAKAHKCIFCGETFSTEVBLQCHITTHSKKYNCK
	1		FCSKAFHAIILLEKHLREKHCVFDAATENGTANGVPPMATKKAB
			PADLQGMLLKNPEAPNSHEASEDDVDASEPMYGCDICGAAYTME
			VLLQNHRLRDHNIRPGEDDGSRKKAEFIKGSHKCNVCSRTFFSE NGLREHLQTHRGPAKHYMCPICGERFPSLLTLTEHKVTHSKSLD
		i	TGTCRICKMPLQSEEEFIEHCQMHPDLRNSLTGFRCVVCMQTVT
1			STLELKIHGTFHMQKLAGSSAASSPNGOGLOKLYKCALCLKEFR
			SKQDLVKLDVNGLPYGLCAGCMARSANGQVGGLAPPEPADRPCA
1			GLRCPECSVKFESAEDLESHMQVDHRDLTPETSGPRKGTQTSPV
		Ì	PRKKTYQCIKCQMTFENEREIQIHVANHMIEEGINHECKLCNQM
			FDSPAKLLCHLIEHSFEGMGGTFKCPVCFTVFVQANKLQQHIFA
	İ		VHGQEDKIYDCSQCPQKFFFQTELQNHTMSQHAQ
6060	2145	202	SYEIVGKNKLEVNHSQLKALCKCSLPSRLLPLGENLPLLDRGFR
		302	KEPRSRGSRERDNMLHLHHSCLCFRSWLPAMLAVLLSLAPSASS
]		DISASRPNILLLMADDLGIGDIGCYGNNTMRTPNIDRLAEDGVK
i	ł		LTQHISAASLCTPSRAAFLTGRYPVRSGMVSSIGYRVLQWTGAS
-			-
E .			
1			GGLPTNETTFAKILEEKGYATGLIGKWHLGLNCESASDHCHHPL HHGFDHFYGMPFSLMGDCARWELSEKEVNLEOKLNFLFOVLALV
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV
	· : ·	· -	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA
		· ·	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLGTAQHSDHEFLMHYCERFLHAARWHQRDR
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPPLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD
6061	110	1330	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPPLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ
6061	110	1330	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ
6061	110	1330	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN
6061	110	1330	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHPQTQTEPVDLSINK
6061	110	1330	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS
6061	110	1330	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ
6061	110	1330	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG
6061	110	1330	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSTVLTPGPLVASASGVGGQQFLHILHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY
6061	110	1330	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER,VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHILHPVPPSSPMNLQ SNKLSHVHRIPVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLFNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSTVLTPGPLVASASGVGGQQFLHILHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY
6061	110	1330	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPPLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSTVLTPGPLVASASGVGGQQFLHILHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVTTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLFNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHILHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDLDPVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLGTAQHSDHEFLMHYCERPLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDEDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLGTAQHSDHEFLMHYCERPLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDEDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKCMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYPVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKCMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERPLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDEDDDLPNTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP
6062	71	1079	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQNSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGNVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGNVHRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP
6062	71	1079	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
6062	71	1079	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFFTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDPE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
6062	71	1079	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHILHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRGNRYCRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWARMLGRV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
6062	71	1079	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFFTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDPE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP

SEQ Predicted Deginning No: location location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence Sequence	E= e, top EELP GYYP FEHG INID FRIV
NO: nucleotide location corresponding corresponding to first amino acid residue of amino acid residue of amino acid sequence ne, Codon, /=possible nucleotide deletion, _possible nucleotide deletio	e, top EELP GYYP FEHG INID FRIV
Corresponding corresponding to first amino acid amino acid residue of amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=S (Codon, /=possible nucleotide deletion, \text{\colored}\) Ppossible nucleotide deletion, \text{\colored}\) Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide insertion) \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide insertion) \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide deletion, \text{\colored}\ Ppossible nucleotide insertion) \text{\colored}\ Ppossible nucleotide insertion) \text{\colored}\ Ppossible nucleotide insertion \text{\colored}\ Ppossible nucleotide insertion \text{\colored}\ Ppossible nucleotide insertion \text{\colored}\ Ppossible nucleotide insertion \text{\colored}\ Ppossible nucleotide insertion \text{\colored}\ Ppossible nucleotide insertion \text{\colored}\ Ppossible nucleotide insertion \text{\colored}\ Ppossible nucleotide insertion \text{\colored}\ Ppossible nucleotide insertion \text{\colored}\ Ppossible nucleotide insertion \text{\colored}\ Ppossible nucleotide inser	EELP GYYP FEHG INID FRIV
L=Leucine, M=Methionine, N=Asparagine, p=Proline, Q=Glutamine, R=Arginine, sediue of amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, M=Tryptophan, Y=Tyrosine, X=Unknown, *=S code, M=Tryptophan, Y=Tryptophan, Y=Tyrosine, X=Unknown, *=S code, M=Tryptophan, to first amino acid residue of amino acid residue of amino acid sequence P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=S Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) EEGEDLHFPANEKKGIEQDEQWVVPQVKVEKTRHARQASE INDTTENGIEFPPMLDERGYCCIYCRGNRYCRRVCEPLL YPYCYQGGRVICRVIMPCNWWARMLGRV P=Proline, Q=Glutamine, N=Arginine, S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=S Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) EEGEDLHFPANEKKGIEQDEQWVVPQVKVEKTRHARQASE INDTTENGIEFPPMLDERGYCCIYCRGNRYCRRVCEPLL YPYCYQGGRVICRVIMPCNWWARMLGRV TTSGKRVVYVDGKEEIRKEMMFKLVGKBTFYVGAAKTKAT AISGFAYEYTLBINGKSLKKYMEDRSKTTNTWVLHMDGEN LEKDAMDWCNGKKLETAGEFVDDGTETHFSIGTH\ACYI SSG\RKKEGIIHTLVDNRSIPELAS AEEBAPWAATERRMPGGCSVLLFEQGGSQVVGMGRGLLNY BLYAAARRVLGYDLLEISLHGPQETLDRTVHCOPALIFVAS BKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG FERNENGTHERFTTNANHVYFNODGTKIAAGSSD\FLVKIUDV QQKTRGHDAPVLSLSFDPKDIFLASASCDGSVRWQISI ISWFLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVW ESWSHQFDLSDMFISQYLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGI CDPSGKTISSK KVSSRVEKDVNDLFDGDDMSNAGDFLNDNA SFSKGIINDEDDEDLMMASGRPRQRSHILEDDENSVDIE GSSLLKEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQW GSTPLHLTHRFMVWNSIGIIRCYNDEGDNAIDVEFHDTSI HLSNTLNYTIJADLSHEAILLACESTDELASKLHCLHFSSY EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGV SLAGPVVSMAGHGEQLFIVVHERGTPDCDQCLGVQLLEIL QILHGDPLPLTRKSYLAWIGFSAECTPCVVDESG IVRMLN NTWTPICNTREHCKGKSDHWVVGIHENPQQLRCIPCKGS	EELP GYYP FEHG INID FRIV
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, residue of amino acid sequence Codon, /=possible nucleotide deletion, \	EELP GYYP FEHG INID FRIV
residue of amino acid sequence Codon, /=possible nucleotide deletion, \ -possible nucleotide deletion, \ -possible nucleotide insertion) EEGEDLHFPANEKGIEONEOWVPCVKVEKTRIARQASE INDYTENGIEFDPMLDERGYCCIYCRRGNYCRRVCEPLL YPYCYQGGRVICRVIMPCNWWARMLGRV 6064 913 311 NLPQSLPRPTEHSPPYSLEKMTDLVAVWDVALSDGVHKIE TTSGKRVVVVDGKEEIRKEWMFKLVCKETFYVGAAKTKAT AISGFAYEYTLEINGKSLKKYMEDRSKTTNTWVLHMDGEN LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYI SSG\KRKEGIIHTLIVDNREIPELAS 6065 1153 641 MSVRVARVAWVRGIGASYRRGASSFPVPPPBQAQGVAELLR AEEEAPWAATERRMPGQCSVLLFPQGGSQVVGMGRGLLNY ELYAAARRVLGYDLLELSLHGFQETLDRTVHCCPALFVAS EKLHHLQPSVIENCYAAAGFSVCEPAALVFAGAMEFAEG EDLDDDDPKFINVCEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGGGTKIAAGSSD\FLVKIDV QQKTFRGHDAPVLSISFPPKDIFIASASCDGSVRWOGISI ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVK ESWSHGFDLSDNFISQTLNIVTWSPCGGYLAAGSINGLII ETKCMERVKHEKGYALGLAWHPTCGRISYTDAEGNLGI CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNN SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSTLKEEEDGQGGSINHLPLVTSORPFYDGPMFTPRQK GSTPLHLTHRFWVMNSIGIIRCYNDEQDDMAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKHCLHFSSE EWIIDLPONBDIEAICLGGGWAAAATSALLLRLFTIGGVG SLAGPVVSMAGHGEQLFIVYHRGTGFDGDCLGVQLLELG QILHGDPLPTIRKSYLAWIGFSAEGTPCYVDSBGIVMLU NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	EELP GYYP FEHG INID FRIV
amino acid sequence Codon, /=possible nucleotide deletion, -possible nucleotide insertion -possible nucleotide insertion	EELP GYYP FEHG INID FRIV
amino acid sequence Codon, /=possible nucleotide deletion, -possible nucleotide insertion -possible nucleotide insertion	EELP GYYP FEHG INID FRIV
\=possible nucleotide insertion	GYYP FEHG INID FRIV
EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASE INDYTENGIETDPMLDERGYCCIYCRRGRRYCRRVCEPLL YPYCYQGGRVICRVIMPCNWWARMLGRV NLPQSLPRPTEHSPPYSLEKMTDLVAVWDVALSDGVHKIE TTSGKRVVYVDGKEEIRKEWMFKLVGKETFYVGAAKTKAT AISGFAYEYTLBINGKSLKKYMEDRSKTTNTWVLHMDGEN LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYI SSG\KRKEGIIHTLIVDNREIPEIAS 6065 1153 641 MSVRVARVAWWRGLGASYRRGASSFPVPPPBAQGVAELLR AEEEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNY BLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVAS EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG 6066 68 3470 VKENMPATRKPMRYGHTEGHTBVCFDDSGSFIVTCGSDGE EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISL ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVX ESWSHQFDLSDNFISGTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGI CDPSGKTSSSKVSSRVEKDYNDLPDGDDMSNAGFLNDNM SFSKGIINDDEDDEDLMMASGRPRGRSHILEDDENSVDIS GSSLLKEBEEDGQEGSIHNLPUTSQRPFYDGPMPTPRQE GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNBDIEAICLGQGWAAAATSALLLRLFTIGGVC SLAGPVVSMAGHGEQLFIVVHRGTGFDGDQCLGVQLLEICG GILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSBGIVRMLN NTWTPICNTREHCKGKSDHYWVGIHENPQQLRCIPCKGS	GYYP FEHG INID FRIV
INDYTENGIEFDPMLDERGYCCIYCRGNRYCRRVCEPLL YPYCYQGGRVICRVIMPCNWWWARMLGRV 1153 311 NLPQSLPRPTEHSPPYSLEKMTDLVAVWDVALSDGVHKIE TTSGKRVVVVDGKEEIRKEWMFKLVGKETFYVGAAKTKAT AISGFAYEYTLEINGKSLKKYMEDRSKTTNTWVLHMDGEN LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYI SSG\KRKEGIIHTLIVDNREIPEIAS 6065 1153 641 MSVRVARVAWVRGIGASYRRGASSFPVPPPGAQGVAELLR AEEEAPWAATERRMPGQCSVULFPGQGSQVVGMGRGLLNY BLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVAS EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG EBLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISE ISWFLLQKKNDVINAKSICRLAWQPKSGKLLAIPVEKSY ESWSHQFFLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHERGYAICGLAWHPTCGRISYTDAEGNIGI CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNA SFSKGIINDDEDDEDLMNASGRPRQRSHTLEDDENSVDIS GSSLLKEBEEDGGGSIHNLPLVTSQRPFYDGPMPTPRQK GSTPLHTTHRFWWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIERICLGGGWAAAATSALLLRFTIGGVY SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG OILHGDPLPITRKSYLAMIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQRCIPCKGS	GYYP FEHG INID FRIV
YPYCYQGGRVICRVIMPCNWWARMLGRV 6064 913 311 NLPQSLPRPTEHSPPYSLEKMTDLVAVWDVALSDGVHKIE TTSGKRVVVDCKEEIRKEWMFKLVGKETFYVGAAKTKAT AISGFAYEYTLEINGKSLKKYMEDRSKTTNTWVLHMDGEN LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYI SSG\KRKEGIIHTLIVDNREIPEIAS 6065 1153 641 MSVRVARVAWVRGLGASYRRGASSFPVPPPGAQGVAELLR AEEEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNY BLYAAARRVLGYDLLELSHGPQETLDRTVHCQPAIFVAS EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG 6066 68 3470 VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGL EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASACCDGSVRVWQISL ISWPLLQKCNDVINAKSICRLAMQPKSGKLLAIPVEKSVR ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGI CDPSGKTSSSKVSSRVSRVEKDYNDLPDGDDMSNAGDFLNDN SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEBEEDGGGESIHNLPLVTSQRFFYDGMPTPRQB GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSV EWIIDLPQNEDIERICLGQGWAAAATSALLLEFTIGSV SLAGBVVSMAGGHGEQLFIVYHRGTGFDGDQCLGVQLLEIG QILHGDELPLTRKSYLAMIGFSAEGTPCVVDSBGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQRCIPCKGS	FEHG INID FRIV
S11 NLPQSLPRPTEHSPPYSLEKMTDLVAVWDVALSDGVHKIE	INID FRIV
TTSGKRVVYVDGKEEIRKEWMFKLVGKETFYVGAAKTKAT AISGFAYEYTLEINGKSLKKYMEDRSKTTNTWVLHMDGEN LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYI SSG\KRKEGIIHTLIVDNREIPEIAS 6065 1153 641 MSVRVARVAWVRGLGASYRRGASSFPVPPPGAQGVAELLR AEEEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLINY BLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVAS EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG 6066 68 3470 VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGL EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISL ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVK ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGI CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNP SFSKGIINDDEDDEDLMMASGRPRQRSHILBDDENSVDIS GSSLLKEBEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQF GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSK EWIIDLPQNBDIEAICLGGGWAAAATSALLLRLFTIGGVG SLAGPVVSMAGHGEQLFIVVHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAECTPCYVDSEGIVRMLM NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	INID FRIV
AISGFAYEYTLEINGKSLKKYMEDRSKTTNTWVLHMDGEN LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYI SSG\KRKEGIIHTLIVDNREIPEIAS 6065 1153 641 MSVRVARVAWVRGLGASYRRGASSFPVPPFGAQGVAELLR AEEEAPWAATERMFQCCSVLLFPGQGSQVVGMGRGLLNY BLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVAS EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG 6066 68 3470 VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGD EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISL ISWPLLQKCNDVINAKSICTLAWQPKSGKLLAIPVEKSVK ESWSHQFDLSDNFISQTLNIVTWSPCGQVLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGI CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNP SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQK GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSV EWIIDLPQNBDIEAICLGGGWAAAATSALLIKLFTIGGVC SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	FRIV
LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYI SSG\KRKEGIIHTLIVDNREIPEIAS 6065 1153 641 MSVRVARVAWVRGLGASYRRGASSFPVPPPGAQGVAELLR AEEEAPWAATERMPGQCSVLLFPGQGSQVVGMGRGLLLR BLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVAS EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG 6066 68 3470 VEENMPATRKEMRYGHTEGHTEVCFDDSGSFIVTCGSDGD EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISL ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVK ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNIGII CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNA SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQK GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVC SLAGPVVSMAGHEQLFIVYHRGTGFDGDQCLGVQLLEIG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYI SSG\KRKEGIIHTLIVDNREIPEIAS 6065 1153 641 MSVRVARVAWVRGLGASYRRGASSFPVPPPGAQGVAELLR AEEEAPWAATERMPGQCSVLLFPGQGSQVVGMGRGLLLR BLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVAS EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG 6066 68 3470 VEENMPATRKEMRYGHTEGHTEVCFDDSGSFIVTCGSDGD EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISL ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVK ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNIGII CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNA SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQK GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVC SLAGPVVSMAGHEQLFIVYHRGTGFDGDQCLGVQLLEIG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
SSG\KRKEGIIHTLIVDNREIPEIAS 6065 1153 641 MSVRVARVAWVRGLGASYRRGASSFPVPPPGAQGVAELLR AEEEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNY BLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVAS EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG 6066 68 3470 VKEMMPATRKPMRYGHTEGHTEVCFDDSSFIVTCGSDGD EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISL ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVK ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGII CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNA SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEEEEDGQEGSINNLPLVTSQRPFYDGPMPTPRQK GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGGGWAAAATSALLLRLFTIGGVG SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
6065 1153 641 MSVRVARVAWVRGLGASYRRGASSFPVPPPGAQGVAELLR AEEEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNY BLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVAS EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG 6066 68 3470 VKEMMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGD EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISD ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVK ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGII CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNA SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKBEBEDGQEGSIHNLPUTSQRPFYDGPMPTPRQR GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNBDIEAICLGQGWAAAATSALLLRLFTIGGVC SLAGPVVSMAGHGEQLFIVVHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSBGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
AEEEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNY BLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVAS EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG 6066 68 3470 VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGE EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISD ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVK ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGI CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNA SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQK GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
BLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVAS BKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG 6066 68 3470 VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGD EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISD ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVK ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGI CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNA SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQK GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG 6066 68 3470 VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGD EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISD ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVR ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGI CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNF SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQR GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
6066 68 3470 VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGD EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISE ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVK ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGI CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAAGDFLNDNA SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQK GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	LAAV
6066 68 3470 VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGD EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISE ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVK ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGI CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAAGDFLNDNA SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQK GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
EDLDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHT VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISE ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVR ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGI CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNA SFSKGIINDDEDDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQK GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNBDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	VRIW
VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDV QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISD ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVK ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGI CDPSGKTSSSKYSSRVEKDYNDLFDGDDMSNAGDFLNDNA SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEBEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQK GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISD ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVK ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGII CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNA SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEBEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQKI GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVK ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGI CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNA SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLKEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQK GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLII ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGI CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNA SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKBEBEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQH GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSBGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGL CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNA SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQR GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNA SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQR GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	VWNV
SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQR GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	LENV
SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDIS GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQR GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	VEIP
GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQR GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSI HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSW EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVÇ SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELG QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLN NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLM NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	
NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGS	KKKK
1 1	RGLG
1 1	RFPP
TO THE PROPERTY OF THE PROPERT	
KNGYEYEESTKNQATKEQQELLMKMLALSCKLEREFRCVE	
MTQNAVNLAIKYASRSRKLILAQKLSELAVEKAAELTATQ	
EEEEDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEF	
KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSQGRVNPFF	.VSAS
SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSI	IIKP
LIPKPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSE	TPAI
CPPONTENORPKTGFOMWLEENRSNILSDNPDFSDEADII	
IRFRVLSTEERKVWANKAKGETASEGTEAKKRKVVDESI	
OEEKAKENLNLSKKOKPLDFSTNOKLSAFAFKQE	
	77777 77
6067 858 321 LPWQRLGVLLSRGKMAVTGWLESLRTAQKTALLQDGRRKV	
PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGQWQLEVGI	
GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKI	
SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLS	FA\T
PTAP	
6068 13 1730 GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDS	GEEP
RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAI	
PPFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTS	
FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKPKEQQI	
PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPI	
RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATC	QAFV
FGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQ	YISS
SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDAI	
AAESGSESSSQEATPEKESLAESAAAYTKATARKCLLEKT	
	THE TOTAL
GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMAS	
TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SII	STDDG
DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQI	STDDG RITAM
MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGG	STDDG RITAM
T T	STDDG RITAM EQEAK
	STDDG RITAM EQEAK
	STDDG RITAM EQEAK OTTGS
RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMI	STDDG RITAM RQEAK ROTTGS
IDELLELESEEERSRKIQGLLKSCGKPVEDFIQELLAKLQ	STDDG RITAM RQEAK QTTGS GLQK PDEIN

SEQ	Predicted	Predicted end	I Amino poid gormant contains
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			Q\PGLRQPSPSP\DGQPSAPFQGPGARTASPLTLLALFPGPPER
		1	RPALLCVLSCI
6070	478	858	IRVTVDGEFLHY1FPLQFLDSPBW/RFTETHRGRHF\QVTLTAE
	1		TDCRYVSWRRKKLYLLFAQHRYISRLFSVLIGSDIADKLYALND
			RVYIGKRYHYDIRLPNFYQMSTPEIRRSPLTQHFQNSRRYW
6071	2	1654	HEARTKGNMALARP\VRLFSLVTRLLLAPRRGLTVRSPDEPLPV
			VRIPVALQRQLEQRQSRRRNLPRPVLVRPGPLLVSARRPELNQP
			ARLTLGRWERAPLASQGWKSRRARRDHFSIERAQQEAPAVRKLS
			SKGSFADLGAWKPRVLHALQE\AAPEVVQ\PTTVQSSTIPSLLR
			GRHVVCAAETGSGKTLSYLLPLLQRLLG\HPSLDSLPIPAPRGL
1	ì		VLVPSRELAQQVRAVAQPLGRSLGLLVRDLEGGHGMRRIRLQLS
1		1	RQPSADVLVATPGALWKALKSRLISLEQLSFLVLDEADTLLDES FLELVDYILEKSHIAEGPADLEDPFNPKAQLVLVGATFPEGVGQ
1	1		LLNKVASPDAVTTITSSKLHCIMPHVKQTFLRLKGADKVAELVH
1			ILKHRDRAERTGPSGTVLVFCNSSSTVNWLGYILDDHKIOHLRL
1	1		QGQMPALMRVGIFQSFQKSSRDILLCTDIASRGLDSTGVELVVN
			YDFPPTLQDYIHRAGRVGRVGSEVPGTVISFVTHPWDVSLVQKI
			ELAARRRSLPGLASSVKEPLPOAT
6072	1	742	KMERTEMMPTINSQLEFKSKPFPLVSSSRWLVKRGELTAYVEDT
1			VLFSRRTSKQQVYFFLFNDVLIITKKKSEESYNVNDYSLRDOLL
İ			VESCONEELNSSPGKNSSTMLYSRQSSASHLFTLTVLSNHANEK
İ			VEMLLGAETQSERARWITALGHSSGKPPADRTSLTQVEIVRSFT
1		,	AKQPDELSLQVADVVLI\YQRVSDGWYEGER\LRDGERGWFPME
·			CAKEITCQATIDKNVERMGRLLGLETNV
6073	620	860	PCRRGLARPLSRRPG/SILVHCAVGVSRSATLVLAYLMLYHHLT
			LVEAIKKVKDHRGIIPNRGFLRQLLALDRRLRQGLEA
6074	168	1110	PGARCMATELQCPDSMPCHNQQVNSASTPSPEQLRPGDLILDHA
1.		,	GGNRASRAKVILLTGYAHSSLPAELDSGACGGSSLNSEGNSGSG
			DSSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTIIR
· :			DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE
	,	· ·	GVKFEKGNCGVSIMRSGEAMEQGLRDCCRSIRIGKILIQSDEET QRAKVYYAKFPPDIYRRKVLLMYPILOTG\NTVIEAVKVLIEHG
1 -		• •	VQPSVIILLSLFSTPHGAKSIIQEFPEITILTTEVHPVAPTHFG
· .	1	× *	OKYFGTD
6075	320	1091	PPTCQPQEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSHLLGT
,	, 320	1001	KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV
	'		LRRPQEFVNRTPBTVFIFWGPPSKMOKPOGSLVRVIORAGLVFP
			NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA
		•	VELCDHVHVYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI
			QNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT
6076	1721	107	HPSPTEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGAEV
			KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGAFDPED
			GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD
			HGDYAFDIWGQGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV
			LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPEIQRRDSYYMTS
] }			SQLSTPLQQWRQGEYKCVVQHTASKSKKEIFRWPESPKAQASSV
			PTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEKEEQEERE
1 1			TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD
			AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNA
			GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE
	·		A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\
]			RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL
<u> </u>			EVSYVTDHGPMK
6077	3687	1268	LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ
•			AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR
Į l	1		GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP
j !	ļ		QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN
	İ		EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS
	ļ		PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA
<u></u>			VCGSLIGWRNVTRLLVFSTDAGFHFAGDGKLGGIVLPNDGQCHL

		37 4 4	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
			S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	S=Serine, T=Infectine, v=valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence	_	\=possible nucleotide insertion)
	Bequeinee		ENNMYTMSHYYDYPSIAHLVQKLSENNIQTIFAVTEEFQPVYKE
			LKNLIPKSAVGTLSANSSNVIQLIIDAYNSLSSEVILENGKLSE
Į.	1	1	LKNLIPKSAVGILSANSSNVIQLIIDAINSLSSEVIIBNGKUSE
	j .	1	GVTISYQSY\CKNGVNGTGENGRKCSNISIGDEVQFEISITSNK
1	Į.		CPKKDSDSFKIRPLGFTEEVEVILQYICECECQSEGIPESPKCH
1			EGNGTFECGACRCNEGRVGRHCECSTDEVNSEDIGCFTARKENQ
1	Į.	ŀ	FOKSASNHGRVPSAGQCVCRKRDNTNEIYSGKFCECDNFNCDRS
l		}	NGLI CGGNGVCKCRVCECNPNYTGSACDCSLDTSTCEASNGQIC
[Į.	1	NGLICGGNGVCKCKVCECNFNYIGSACDCSEDISICEASNGQIC
l			NGRGICECGVCKCTDPKFQGQTCEMCQTCLGVCAEHKECVQCRA
			FNKGEKKDTCTQECSYFNITKVESRDKLPQPVQPDPVSHCKEKD
			VDDCWFYFTYSVNGNNEVMVHVVENPECPTGPDIIPIVAGVVAG
1	1	[IVLIGLALLLIWKLLMIIHDRREFAKFEKEKMNAKWDTGENPIY
ļ			i i
Į.			KSAVTTVVNPKYEGK
6078	1426	180	ETEDVMELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILE
1			GSVRNSLWRPVPFKCPTCRKKTFSYWELIPLQVNYSLKGIVEKY
1	1	1	NKIKISPKMPVCKGH\LGQPLNIF\CL\TDMQLDL/CGIC\ATR
1		1	GEHTKHVFCSIEDAYAQERDAFESLFQSFETWRRGDALSRLDTL
1	1		GENTANAL CATEDWINGERDULE SORE ASSET SURVEYEDIN
1			ETSKRKSLQLLTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMK
	1		LAVMQAYDPEINKLNTILQEQRMAFNIABAFKDVSEPIVFLQQM
	1		QEFREKIKVIKETPLPPSNLPASPLMKNFDTSQWEDIKLVDVDK
]	1	1	LSLPQDTGTFISKIPWSFYKLFLLILLLGLVIVFGPTMFLEWSL
Ì	1		FDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIFNE
1	Ł	1	
i	}	1	RFKNFTLVVLNNVAEFVCKYKLL
6079	1586	141	ATARDLGCARRIDRVVMESTPSRGLNRVHLQCRNLQEFLGGLSP
1	1	1	GVLDRLYGHPATCLAVFRELPSLAKNWVMRMLFLEQPLPQAAVA
1		[LWVKKEFSKAQEESTGLLSGLRIWHTQLLPGGLQGLILNPIFRQ
	1	-	NLRIALLGGGKAWSDDTSQLGPDKHARDVPSLDKYAEERWEVVL
	•	1	
l .	}		HFMVGSPSAAVSQDLAQLLSQAGLMKSTEPGEPPCITSAGFQFL
1	1	l .	LLDTPAQLWYFMLQYLQTAQSRGMDLVEILSFLFQLSFSTLGKD
1		1	YSVEGMSDSLLNFLQHLREFGLVFQRKRKSRRYYPT/RALAINL
		l control of the cont	SSGVSGAGGTVHQPGFIV\VETNYRLYAYTESELQIALIALFSE
1		1	MLYPFP\NMVV\ARVTR\ESVQQAIASGITAQQIIHFLRTRAHP
1		1	METALLING THE TOTAL TOTAL TOTAL TOTAL TOTAL COLUMN
ł	·	1	VMLKQTPVLPPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDF
ł	•	1	ELL\LAHAPKLGVLVFB/NTPAKRLMVVTPAGHSDVKRFWKRQK
	* .	1	HSS
6080	1	1199	IETIDHVGEFAMAAQAAGVSRQRAATQGLGSNQNALKYLGQDFK
6080	1	1 1133	TLROQCLDSGVLFKDPEFPACPSALGYKDLGPGSPQTQGIIWKR
1		1	THEORY THE VINE LANCES WHO I VING LODGE THE
1		1	PTELCPSPQFIVGGATRTDICQGGLGDCWLLAAIASLTLNEELL
1			YRVVPRDQDFQENYAGIFHFQPLCPPSP\FWQYGEWVEVVIDDR
1			LPTKNGQLLFLHSEQGNEFWSALLEKAYAKLNGCYEALAGGSTV
Į.			EGFEDFTGGISEFYDLKKPPANLYQIIRKALCAGSLLGCSIDVY
1			SAAEAEAITSQKLVKSHAYSVTGVEEVNFQGHPEKLIRLRNPWG
I	,		
1			EVEWSGAWSDDAPEWNHIDPRRKEELDKKVEDGEFWMSLSDFVR
l	1		QFSRLEICNLSPDSLSSEEVHKWNLVLFNGHWTRGSTAGGCQNY
1.	1 .	1	PGSS
C003		865	EMLPLLLPLPLLWA/GALAQDARFRLEMPESVTVQEGLCIFVHC
6081	3	000	SVFYLEYGWKDSTPAYGHWFREGVSVDQETPVATNNSTQKVQKE
1			
}			TOGRFHLLGDPSRNNCSLSIRDARRRDNGSYFFWVARGRTKFSY
1		1	KYSPLSVYVTALTHRPDILIPEFLKSGHPSNLTCSVPWVCEQGT
!	1		PPIFSWMSAAPTSLGPRTLHSSVLTIIPRPQDHGTNLICQVTFP
1			GAGVTTERTIQLSVSWKSGTVEEVVVLAVGVVAVKILLLCLCLI
1	1 .		
1		<u> </u>	ILSFHKKKAVRAVEVEENVYAVMG
6082	283	1288	EARSPGPTQTRTAPGLAAPGLAQPAALRLLLSRPPSAAMDGDGD
			PESVGQPEEASPEEQPEEASAEEERPEDQQEEEAAAAA\Y\LDE
1			LPEPLLA/LRVLAALPRHE\LVQACR\LVCLRWKELVDGAPLWL
1	1		DECEDITAL DECAMBERS IN TO A CONTROL OF STATE OF
j		ļ	LKCQQEGLVPEGGVEEERDHWQQFYFLSKRRRNLLRNPCGEEDL
1		1	EGWCDVEHGGDGWRVEELPGDSGVEFTHDESVKKYFASSFEWCR
1	1	1	KAQVIDLQAEGYWEELLDTTQPAIVVKDWYSGRSDAGCLYELTV
İ			KLLSEHENVLAEFSSGQVAVPQDSDGGGWMEISHTFTDYGPGVR
1	{		WHO BEILD OD CANTAL DOCA ALLA CANDOCCALIFIED
L			FVRFEHGGQDSVYWKGWFGARVTNSSVWVEP
6083	1865	309	KOWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPAIE

		<u> </u>	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
]	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		<u> </u>	NORTHOLDI CORRUNTANT WRONG TO THE PROPERTY OF
			DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIBEYISKQAKA
			SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR
ı	İ	· ·	FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
1	1		VVSVTASTTQGQQLSEEELERLEEACDMALELNASKHRIYEYVE
1			SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
i			AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
	<u> </u>		RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDBIERKFDKW
	į į		QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
•			ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
1	1		RISKTLORTLOKOSVVYGGKSTIRDRSSGTASSVAFTPLOGLEI
1			VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
6084	1865	309	KQWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPAIE
1			
1			DVQEETQLDLSGDSVKTIAKLWDSKMFABIMMKIEEYISKQAKA
			SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR
ŀ			FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
			VVSVTASTTQGQQLSEEELERLEEACDMALELNASKHRIYEYVE
			SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
			AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
1	j		RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
			QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
			ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
			RISKTLORTLOKOSVVYGGKSTIRDRSSGTASSVAFTPLOGLEI
			VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
6085	2	1456	SGPRSFQGNRAVGRISLGGKRNPEVTLLPGVSSERVRRWRRARV
	_	7.55	GVARVKPGNPWKPSPATQVPR/VPAQVYLPGRGPPLREGEELVM
1			DEEAYVLYHRAQTGAPCLSFDIVRDHLGDNRTELPLTLYLCAGT
			ONE CAN COMPLEMENT DISTRICT TO THE CALCULATION OF T
	<u>-</u>		QAESAQSNRLMMLRMHNLHGTKPPPSEGSDBEEEEEDEEDEEER
			KPQLELAMVPHYGGINRVRVSWLGEEPVAGVWSEKGQVEVFALR
i l			RLLQVVEEPQALAAFLRDEQAQMKPIFSFAGHMGEGFALDWSPR
			VTGRLLTGDCQKNIHLWTPTDGGSWHVDQRPFVGHTRSVEDLQW
1			SPTENTVFASCSADASIRIWDIRAAPSKACMLTTATAHDGDVNV
			ISWSRREPFLLSGGDDGALKIWDLRQFKSGSPVATFKQHVAPVT
; ;		•	SVEWHPQDSGVFAASGADHQITQWDLG/IVERDPEAGDVEADPG
		•	LADLPQQLLFVHQGETELKELHWHPQCPGLLVSTALSGFTIFRT
			ISV
6086	2419	1357	GAATQHGGAMNLLPCNPHGNGLLYAGFNQDHGCFACGMENGFRV
1 1	. [YNTDPLKEKEKQEFLEGGVGHVEMLFRCNYLALVGGGKKPKYPP
] .[NKVMIWDDLKKKTVIBIEFSTEVKAVKLRR\DKIVVVLDSMIKV
	.		FTFTHNP\HQLHVFE\TCYNPKGLCVLCPNSNNSLLAFPGTHTG
			HVQLVDLASTEKPPVDIPAHEGVLSCIALNLQGTRIATASEKGT
1 1			LIRIFDTSSGHLIQELRRGSQAANIYCINFNQDASLICVSSDHG
j i			TVHIFAAEDPKRNKQSSLASASFLPKYFSSKWSFSKFQVPSGSP
1		Į.	CICAFGTEPNAVIAICADGSYYKFLFNPKGECIRDVYAQFLEMT
H-22-1		<u> </u>	DDKL
6087	476	1877	QNSQRTGLPITIFSRSFPLLTGSDLCBNMPCTCTWRNWRQWIRP
]			LVAVIYLVSIVVAVPLCVWELQKLEVGIHTKAWFIAGIFLLLTI
ļ f	1		PISLWVILQHLVHYTQPELQKPIIRILWMVPIYSLDSWIALKYP
]	1		GIAIYVDTCRECYEAYVIYNFMGFLTNYLTNRYPNLVLILEAKD
[-		QQKHFPPLCCCPPWAMGEVLLFRCKLGVLQYTVVRPFTTIVALI
j			CELLGIYDEGNFSFSNAWTYLVIINNMSQLFAMYCLLLFYKVLK
	1		
1	1		EELSPIQPVGKFLCVKLVVFVSFWQAVVIALLVKVGVISEKHTW
			EWQTVEAVATGLQDFIICIEMFLAAIA\HHYTFSYKPYVQEAEE
, ,		ľ	GSCFDSFLAMWDVSDIRDDISEQVRHVGRTVRGHPRKKLFPEDQ
] [ļ		DQNEHTSLLSSSSQDAISIASSMPPSPMGHYQGFGHTVTPQTTP
			TTAKISDEILSDTIGEKKEPSDKSVDS
6088	1684	689	GASGLVRLLQQGHRCLLAPVAPKLVPPVRGVKKGFRAAFRFQKE
•		į	LERQRLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLQENFSLDLL
] }	J	j	KTAFVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF
		ļ	SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE
			QLTLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI
			TQMTGKELFEMWKIINPMGLLVBELKKRNVSAPESRLTRQSG\A
	L		А/ осухтилсачистиливатилите

Seg				
NO: nucleotide	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cortesponding to first amino acid amino acid residue of amino acid Sequence Sequence	1	1		
to first amino acid residue of amino acid sequence sequence 8-Serine, T=Threonine, V=Valine, w=Trytopian, Y=Tyrosine, X=Unknown, Y=Stop Codon, /=possible nucleotide deletion, _>possible nucleotid	NO:			
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence PTALPIYOUNDERAL BERGISTURE TRAINESSTISSERELARISTERS TRAINESSTISSERELARISTERS TRAINESSTISSERELARISTERS TRAINESSTISSERELARISTERS TRAINESSTISSERELARISTERS TRAINESSTISSERELARISTERS TRAINESSTISSERELARISTERS TRAINESSTISSERELARISTERS TRAINESSTISSERELARISTERS TRAINESSTISSERELARISTERS TRAINESSTISSERELARISTERSITERSITERSITERS TRAINESSTISSERELARISTERSITERSITERSITERS TRAINESSTISSERELARISTERSITERSITERSITERSITERS TRAINESSTISSERELARISTERSITERSITERSITERSITERS TRAINESSTISSERELARISTERSITERSITERSITERS TRAINESSTISSERELARISTERSITERSITERSITERSITERSITERS TRAINESSTISSERELARISTERSITERSITERSITERSITERSITERS TRAINESSTISSERELARISTERSITERSITERSITERSITERSITERSITERSITE				
amino acid residue of amino acid sequence Sequence Sequence PATTYPOCHON, /=possible nucleotide deletion, \possible nucleo				
residue of amino acid sequence	1		4	
amino acid sequence	1			
Sequence N-possible mucleotide insertion PRADEPTY-WOLVENGENIARENSITAS	Ī			
PRAIDLY PULL YORK LIABSONE TWAN ARE SARAN VALERLY OF TENRIPMYS KINCH LIABANS 1738 3 3054 TRIGIT SISTERICALIAN SCHIKKING SISTEMAN ARE THE STREET OF THE STRE			sequence	
TENDERHMYSKYRETURARKSITAS 3 3054 TELGIGSTITSSERGLALARGHEGHSWTGSRAGARTGADAG PERELDILPAGGMERICALARGHEGHSWTGSRAGARTGADAG PERELDILPAGGMERICALARGHEGHSWTGSRAGARTGADAG PERELDILPAGGMERICALARGHEGHSWTGSRAGARTGADAG PERELDILPAGGMERICALARGHEGHSWTGSRAGARTGADAG PERELDILPAGGMERICALARGHEGHSWTGSRAGARTGADAG PERELDILPAGGMERICALARGHEGHSWTGSRAGARTGADAG QAKMAT POLSEYKHTULQDPOLARGHEGHSWTGSTAGATAGTE QAKMAT POLSEYKHTULQDPOLARGHEGHSWTGSTAGATAGTE QAKMAT POLSEYKHTULQDPOLARGHESHDEKKHKERIKALAGKDD KOLDPURLISERSLIDMYSEVLDVI.SDVDASYHTODHILPRVUTVG DOSAGKTSVLENI JAQAAT PERGGSRAMTSSDVYKTI.SGDHUPARVUTVG ROLPPURLISERSLIDMYSEVLDVI.SDVDASYHTODHILPRVUTVG DOSAGKTSVLENI JAQAAT PERGGSRAMTSSDVYKTI.SGAMA LAVANDSORIQUIT DEGVIDNYTSGADADTYSCHT ESTAMA DAVALLICLODASVDARBSI VYDLVSQMDHUGRT I FVITKVDI. ARKYNASDSRIQUIT DEGVIDNYTSGADADTYSCHT ESTAMA DAVALLICLODASVDARBSI VYDLVSQMDHUGRT I FVITKVDI. ARKYNASDSRIQUIT DEGVIDNYTSGADADTYSCHT ESTAMA DAVALLICLODASVDARBSI VYDLVSQMDHUGRT I FVITKVDI. ARKYNASDSRIQUIT DEGVIDNYTSGADATAGTAGATAGAT PROBESTATRATAGATAGATAGATAGATAGATAGAT PROBESTATRATAGATAGATAGATAGATAGATAGATAGATAGATAG		sequence		
TRILIJEGSTISSERLICHARAGHTGISSWTGSHAGAHTGALD PERILIDIPAGGAWELRRANACEVOGILMEISGSLOPLOX LIHINGIST YHSHHPTILKIQRPOLRTSFQOPSSLITSLIPLIKUKER PIKKYGVOPRINWARDALTATILLIKURVILLIGANGCHTAKTUPD QKKMMTPOLSSYKWIVDJUWEIDEYIDPEKTRKADESGSUKHPER VSDKEKIODLOGELLHTOLKYGRILERILEKRHKELRILVLIGANG KIEPPEKIRKSILDIMYSSVLONISYTYDASYTUDOHLPRVVVVS DOSAGKTSYLEMIAQARITPRGGGEMMTRS SVKVILSEGPHVAV LADPDRIVESLINMISSULOHSYDVINSTYDASYTUDOHLPRVVVVS DOSAGKTSYLEMIAQARITPRGGGEMMTRS SVKVILSEGPHVAV LEKOSREPOLITERILARISTSULOHSYDVANOTYTISLIANSSULOHLPR WVDWAL LEKOSREPOLITERILARISTSULOHORSYDVANITSEGRAPHVAVI LEKOSREPOLITERILARISTSULOKSONDHERRITYUTKVDL ARKAVASPBRIQQITERILARISTSULOKOHPRRAVVVTKIGASSPSTAT REYERPPONSKLIKTSHLANDARISTYRILSIANSCHWINWES VSQQADSPRATRINLETSHKNYTYRILSIADSCHWINWES VSQQADSPRATRINLETSHKNYTYRILRILARISTYLTHANGING THYTTUTILIKONTOKOLPHKAVEVANETILOBEPSRYMTEPKOK ENDOPPAKAKEN STRINLETSHKNYTPINITYTYRILARISTYTYRIKLE SSRCVEUDPSLIKTOTHKOYTOKOLPHKAVEVANETILOBEPSRYMTEPKOK KENTOROCUMBERSIADSHANDERAGISTYTYRIKLE SSRCVEUDPSLIKTOTHKOYTOKOLPHKAVEVANETILOBEPSRYMTEPKOK KENTOROCUMBERSIADSHANDERAGISTYTYRIKLE SSRCVEUDPSLIKTOTHKOYTOKOLPHKAVEVANETILOBEPSRYMTEPKOK KENTOROCUMBERSIADSHANDERAGISTYTYRIKLE SSRCVEUDPSLIKTOTHKOYTOKOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOYTOKOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOYTOKOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOYTOKOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOYTOKOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOYTOKOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOHOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOHOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOHOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOHOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOHOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOHOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOHOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOHOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOHOLPHAVENSTALITYRINLE PURCHAGE PUPPPBARAVENSTALITYRINLEPHANOLOHOLPHAVENSTALITYRINLE DEBLOCHOLPHAVENSTALITYRINLEPHANOLOHOLPHAVENSTALITYRINLE LARGOCALLARISTICATION ON THE TOTHKOHOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOHOLPHAVENSTALITYRINLE SSRCVEUDPSLIKTOTHKOHOLPHAVENSTA				
PERRIADIPAGGWELERAAVACEVOOSLAWISSGIT KISLIPÜG LILIVSISI YIHHIPÜLKIQEPULTSFOORSIITALLIKAKUF PIKYGYOPERNEMPARLATILLIKARVILLIGSAVGGOTTAKTEPI QAKKMI POLISEVSKI VEDIVWEL DEVI PERKIRKALPSSEDLVK LAPPPKI VEBLELLIKOPETSGIS PERTAPRATORSISSINKER VEDKEKIDOLOBELLIKOPETSGIS PERTAPRATORSISSINKER VEDKEKIDOLOBELLIKOPETSGIS PERTAPRATORSISSINKER VEDKEKIDOLOBELLIKOPETSGIS PERTAPRATORSISSINKER VEDKEKIDOLOBELLIKOPETSGIS PERTAPRATORSISSINKER VEDKEKIDOLOBELLIKOPETSGIS PERTAPRATORSISSINKER LAPVAGGOLOBEVALDARI LARGELELIKORKOVALISSIVAL PERTAPATORSISSINKER LEVISSER POLITIKER LARGEN VALVAGOROPHI PERVAVUL DASAKTISTIKA PARTAPATA LAPVASORELOBUL DASAKTIVAL VALVAGADEPHERILISE LARVA DENALILLICOSSIDARSIVITU. VASQADEPHERITY PILIPISA PARTA DENALILLICOSSIDARSIVITU. VASQADEPHERITY PILIPISA PARTAPA PERSER PONSKLIATORILARIO VITERILISIA SIDCETHIMVESS VALGADEPHERITE PILIPISA PARTAPA VALGEDPARATORIA PARTAPATA PERSER PONSKLIATORILARIO VITERILISIA SIDCETHIMVESS VALGEDPARATORIA PARTAPATA PERSER PONSKLIATORILARIO VITERILISIA PARTAPATARA PERSER PONSKLIATORILARIO VITERILISIA PARTAPATARA PERSER PONSKLIATORILARIO VITERILISIA PARTAPATARA PERSER PARTAPATARA PERSER PARTAPATARA PARTAPATARA PARTAPATARA PERSER PARTAPATARA PARTAPATARA PARTAPATARA PERSER PARTAPATARA PARTAPATARA PARTAPATARA PARTAPATARA PERSER PARTAPATARA PARTAPATARA PARTAPATARA PARTAPATARA PERSER PARTAPATARA PARTAPATARA PARTAPATARA PARTAPATARA PARTAPATARA PERSER PARTAPATARA PARTAPA				
LIHLWISEST YHSHHPPILKLQRPQLKTSFQOPSITMLLYKKLYSP PIKKYQYOPRINPRABLATHLILKAYLILGSAVGGYTAKTIPP QKKMMIDOLGSYKWIVDIVWEIDEYIDFKIRKALDSGSDKHPK VADRENIOLGSELLHTOLKYGRILEKTEKSKERERISIAVLOVAU LAPPPOKIVESLLKOPTSGAS DESTAFRATORSSSOKHPK VSDKENIOLGSELLHTOLKYGRILEKTEKSKERERISIAVLOVAU ROI PETBELKRSILDMISSTAUDHISVAVOLDHIPRAVVAVU DQSAGKTSTULEMIAQARI TPROSCEMMITESPVKVTLSEGPHAVA LIFKDSSREPDLTEERDLAALRIE ELPARKHVELGTUSPETIA LIMYKGRGLQBWINDLDGVATYTYSCHAADPUSETT FEISCAMD DPNAITLCIQOSSVDARSIVTDLVSQMDPHGRRTIPVITYVOL ARKWASPSRIQDIIBGKLPPHRALOYTAVTOKKASSISIEDI RRYSEBPPONSALLKTSHLKARQVTTRILSLANSOCTWANTESE VSQQADSFKATRENISTEKNINT PERIRELDREHEFEGANDETLD BYISLSQVTPEHNEBILGQSLMERVSTRVIENITHAPAGYMMS TENTIVUTIKKGNOTHOKOLDRINAVEWARTIQGEFERAMETLD BYISLSQVTPEHNEBILGQSLMERVSTRVIENITHAPAGYMMS TENTIVUTIKKGNOTHOKOLDRINAVEWARTIQGEFERAMETLD BYISLSQVTPEHNEBILGQSLMERVSTRVIENITHAPAGYMMS KRITORSQCUHRETRRELEGRALGKORESHAVLASDELTITUKKNIN KRRTORSQCUHRETRRELEGRALGKORESHAVLASDELTITUKKNIN SKOVEUPPSLIKOTHOVYRRRIPETARLENMINGOLYKKRULNY KRIVEDPSADDEKKKLKLINGRKVOLAEDLKAVERICGRENDAYTE BYDSELECHDOVUPPRIQBRIALITATURGQLINTEVRELEGRUDAFET ALHOBE 6090 194 1560 PUPYPARGRAVLEGAS/ASPPLATIQTVVPLQHCKIPFLYQASIL FELLEPFREDEKKKLLINGRKVOLAEDLKAVERICGRENDAYTE LIATOMSLCRSLHHIPRITYSFINLLYFILIFETTY LIATOMSLCRSLHHIPRITYSFINLLY	6089	3	3054	
PIKYGYOPRINFWARLATILLKIRYLILGSAVGGGTYAKTYPO QKKMIPDLGSYRVI VDIVWEIDEVIDPRETRADGSEDILVE LAPPPRIVEGELLIKDPETGGS PERTAPRATORGSEDILVE LAPPPRIVEGELLIKDPETGGS PERTAPRATORGSEDILVE VEDKENIDOLGBELHITOLKORI LERGEKERKERE RIVULGKER VEDKENIDOLGBELHITOLKORI LERGEKERKERE RIVULGKER KGIPPIESEJRKSLIDMYSSYLDVLSDYDAS SYTODHLPRYVVTLSEGPHIVA LEKNSSREPLIKEREDLAALERIE ELRMRINVEGGHIVA LEKNSSREPLIKEREDLAALERIE ELRMRINVEGGHIVA LEKNSSREPLIKEREDLAALERIE ELRMRINVEGGHIVA LEKNSSREPLOTISCHARIUS PROVINTUTISGAADDYKETIFSISKAMI DENAILLCIQOSVADARSI VITUSVONGOPHORRITIVULKVOL AEKNVASPSRIQQIIEGKLEFMKALGYRAVVTKINSSSELT IVULKVOL AEKNVASPSRIQQIIEGKLEFMKALGYRAVVTKINSSSELT REYSEBEPFONSKLIKETMIKANJOVAGNOPHORRITIVULKVOL BERINDAD PRANILLCIQOSVAPRINISCHEMINISCHEMINGE VEQQADSFKATRINLETEMINIY FRURELDEELEKAANKEIT BYSTYTUJUKLKONTOKOLDHKAVEVAMETLOBEFSRIMTEPSK VEQQADSFKATRINLETEMINIY FRURELDEELEKAANKEIT EVISENGE HEDDIFELKERAVESI KIKHMEVSTIVI ENITYLPAAGTIMISG TENTTUJUKLKONTOKOLDHKAVEVAMETLOBEFSRIMTEPSK SIDKOQMBALIYFMEBILOGILKERSTIVITUSTIVILARENSI TENTTUJUKLKONTOKOLDHKAVEVAMETLOBEFSRIMTEPSK SIDKOQMBALIYFMEBILOGILKERSHAVILASDITTURKNILE SERGVEUDPSLIKDTHEQVYRRIFIKTALMHONLCRGFYYYGMI FOLGBELECHOUVYRRIFIKATALMHONLCRGFYYTYMI ROSCURBETREBEKMILKTATAVIROQUITURURURURURURURURURURURURURURURURURURU				
QRIXMITEDLISTYMINDELDEVIDERIRKALPSSEDSLY LAPPDFKVERSILLKOPPTSGES PETAFRATNORSSENDRIPK VSDREKIOLOGELLHFOLKYOR LERILEKREKELRILVLOK KGI PPTESLARS, LIMTSSEULDUSSYDAS YNTOOHLPRVVAUD DOSAGKTSTULMIAQALI PPROSCEMMTES SVEVILSEGEHUM, LEKNSSREPLLTEBLRAKHSES SVEVILSEGEHUM, LEKNSSREPLLTEBLRAKHSES SVEVILSEGEHUM, LEKNSSREPLLTEBLRAKHSES SVEVILSEGEHUM, LEKNSSREPLLTEBLRAKHSES SVEVILSEGEHUM, LEKNSSREPLLTEBLRAKHSES SVEVILSEGEHUM, LEKNSSREPLLTESHLAKHSE LEHRRKHVERGESSES LEI LAVKOROLORWILVOLOGUTUNTYTSOMADDYKSTITSIEKAM, DPNALILICIDOS VORDARSES VITULOS VORDHORMET IPULTKVOL ARKIVAS PSRIQUILDEKLEPPKKALAYFRAVVTOKKINSSES LEI REYSESEF PONSKLLKTSHLKAROVTTRALSLAVSOLOTHINVESS VSQQADSFRATRENSETSKOMT PELRELDRIBELFEGAKNE ILD EVISLSQVIP KHREBILGQLING VANKTLUGER SPRITE PKOK HEIDI FOLKKERVKESS I KRHEMMDPABOSLAV LQHRALEDDSI TENTIVOLIKKONTIKOLENKAVEVANSTLUGER SPRITE PKOK HEIDI FOLKKERVKESS I KRHEMMDPABOSLAV LQHRALEDDSI SSKOVODPSIL KNHEROLORIKUSTRALBALDSILAV LQHRALEDDSI SSKOVODPSIL KNHEROLORIKUSTRALBALDSILAV LQHRALEDDSI SSKOVODPSIL KNHEROLORIKUSTRALBALDSILAV LQHRALEDDSI SSKOVODPSIL KNHEROLORIKUSTRALBALDSILAV LQHRALEDDSI SSKOVODPSIL KNHEROLORIKUSTRALBALDSILAV LQHRALEDDSI SSKOVODPSIL KNHEROLORIKUSTRALBALDSILAV LQHRALEDDSI SSKOVODPSIL KNHEROLORIKUSTRALBALDSILAV LQHRALEDDSI SSKOVODPSIL KNHEROLORIKUSTRALBALDSILAV LQHRALEDDSI SSKOVODPSIL KNHEROLORIKUSTRALBALDSILAV LQHRALBADSI SKOVODPSILAV LANGKAR KNUHEROLORIKUSTRALBALDSILAV LQHRALBADSI SSKOVODPSILAV LANGKAR KNUHEROLORIKUSTRALBALDSILAV LQHRALBADSI LTATRITUS LANGKAR PARTISLEPHAMBANGANGA SSEPELATIVATIVA LANGKAR SAYVAPVEVER YKNITIYA DIKAKSSOLILABUSTISLIPLITATIVAL LEGAVI VVQLVSIMSSEKHHOTISLAL LLEGAVI VUSUKSAVSKAR LANGKARSPALLATRISLIPLITATIVAL LEGAVI VVQLVSIMSSEKHHOTISLAL LLEGAVI PARABANI LANGKAR SSKONSAVORANDA PARABANI LANGKAR LANGKAR KVENCOLILADER PARABANI LANGKAR LANGKAR LANGKAR KVENCOLILADER PARABANI LANGKAR LANGK	1			
LADDPIKIYBELGILKDFTISGS PERTAPADRGS SENKIFER VSDREKIDOLGELHIPTOLKYDR LIERLEKERKELRELVLOKDO KGI PPIESIARSIJIMYSEVIJOVI LEVIJASYSTYDOHLPYVIVO DOSAGKTSVILMINOAR I FPROSGRMMTES PVOVITI.SEGPHIVA LEKOSREPDIJTKERDIJALRHEI ILLEWRKIVKECCTVS PERTIS LINVKSPGLORMVIVOL PQVITNIT TSGMAD PTVITSGAD PTVITA DENAITILCI DOS VDARRS I VTDLU SQMDPHGRRTI FVIJTKVOLL ARKAVAS PSR LQQII EGKLEPHHALDI FAVVTGKONS SSI EAI REYSEBEPONS KLIKTSHLERGLYTARVYTGKONS SSI EAI REYSEBEPONS KLIKTSHLERGLYTARVYTGKONS SSI EAI REYSEBEPONS KLIKTSHLERGLYTARVYTGKONS SSI EAI REYSEBEPONS KLIKTSHLERGLYTARVYTGKONS SSI EAI REYSEBEPONS KLIKTSHLERGLY TAVOTGKONS SSI EAI REYSEBEPONS KLIKTSHLERGLY TAVOTGKONS SSI EAI REYSEBEPONS KLIKTSHLERGLY TAVOTGKONS SSI EAI REYSEBEPONS KLIKTSHLERGLY TAVOTGKONS SSI EAI REYSEBEPONS KLIKTSHLERGLY TAVOTKOKONS SSI EAI REYSEBEPONS KLIKTSHLERGLY TAVOTKOKONS SSI EAI REYSEBEPONS KLIKTSHLERGLY TAVOTKOKONS SSI EAI REYSEBEPONS KLIKTSHLERGLY TAVOTKOKONS SI EAI REYSEBEPONS KLIKTSHLERGLY SHEKTON TAVOTKOKONS SI EAI REYSEBEPONS KLIKTSHLERGLY SHEKTON TO THE TORTH TO THE TORTH TO THE TORTH TO THE TORTH TO THE TORTH TO THE TORTH TO THE TORTH TO THE TORTH TO THE TORTH TO THE TORTH TORTH TO THE TORTH TO THE TORTH TO THE TORTH TO	ľ			
VSDKEKIDOLOBELHITOLKYOR LIERLEREKKELKILL/KORD KGI PITBISINSLIDMYSEUNJASYNTODHLIPRUVUVG DOSAGKTSVLEMIAOARI TEPRGGGEMMITES DYKUTLSEOPHIVA LEKOSSEEPJLIVKERDLAALIKEEL ELEMREKUGCTVSPETIS LINVIGGEGORWILVERBOLAALIKEEL ELEMREKUGCTVSPETIS LINVIGGEGORWILVERBOLAALIKEEL ELEMREKUGCTVSPETIS LINVIGGEGORWILVERBOLAALIKEEL ELEMREKUTYOKANSSISTEAI REYEEBFYONSKLIKTSNIKARIQVITERUSJAVSOCHWINGES VEQQADSFKATERINETETBUKNYPELRELDRIFERRANDELD BUTSLSQVIPRHWEELLQOSLBERVSTHVIERILTERAGVINSS TENTIVDIKLKONTENOLPHKALOFTAVETVISTANSSISTEAI REYEEBFYONSKLIKTSNIKARIQVITERUSJAVSOCHWINGES TENTIVOIKLKONTENOLPHKALOFTAVETVISTANSSISTEAI REYEEBFYONSKLIKTSNIKARIQVITERUSJAVSOCHWINGES TENTIVOIKLKONTENOLPHKALOFTAVETVISTANSSISTEAI REYEEBFYONSKLIKTSNIKARIQVITERUSJAVSOCHWINGE TENTIVOIKLKONTENOLPHKALOFTAVISTANSSISTEAI REYEEBFYONSKLIKTSNIKARIQVITERUSJAVSOCHWINGE TENTIVOIKLKONTENOLPHALOGENERYPTVISTANSSISTEAI REYEEBFYONSKLIKTSNIKARIQVITERUSJAVSOCHWALEDRSI SORQMADALITYMEELQOSLBERVSTHVIERITIAAGOTHNISS TENTIVOIKLKONTENOLPHALOGENERYPTVISTANSSISTEAI REYEEBFYONSKLIKTSNIKARIQVITERUSJAVSOCHWALEDRSI SORQMADALITYMEELQOSLBERVSTHVIERITIAAGOTHNISS TENTIVOIKLKONTENOLPHALOGENERYPTVISTANSSISTANSIALITERUSJAVANA KARVILEDPABOGEKKIKLITSKRIVALOFBALISSUTTURNILE SORVENDESLECHOVLEWILTYKTUWEP SERPESHTSLERIHLI PEDERBARDEKKIKLITSKRIVALOFBALISTANILATERUSJAVAN KEVILEDPABOGEKKIKLITSKRIVALOFBALISTANILATERUSJAVAN KEVILEDPABOGEKKIKLITSKRIVALOFBALISTANILATERUSJAVAN PARTASISTANILATERUSJAVAN				1 ~ 1
KGIPPIRSLRKSLIMUSSEVLOVLSDVADASYNTODHLEPVUVVO DOSAGKTSVLENTAQARI FPROGGGMMTRS DVATULSEGPHUVA LFKDSSREPDLTKERDLALRHEI ELRMRKNVKGCCTVSPETIS LRVKGRGLQRMVLVDLPQUINTVTSGMAPDTKETIFSISKAYMQ DPNAITLCIQOGSVDARRSIVTDLVSQMDPHCRRTIFVLTKVDL AEKAVASPERIQQIIEGKLFFMKALGYFAVVTGKSNSSSIEAT REYEBEPCNSKLLKTSNLKANGVTKINSLAVSDCFMEMVRES VEQQADSFKATENLETBKRNYPPLERBLDRREIFEKARNSILD EVISLSQVTPKHWEBILQOSLERKVSTHVLENTSUTSDCFMEMVRES VEQQADSFKATENLETBKRNYPPLERBLEFEKARNSILD EVISLSQVTPKHWEBILQOSLERKVSTHVLENTLYDAQTNNSG ETDITPVTUDIKLKONTDKOLPNKAVEVAMETIQBESFARTMETKEK ENDIFFKLKERAVKERSIKKHKNNPAEDLSETTYNKTLE SUKQMDATATYPHERALQAKLKOTENAATENMYGPD\MKKRLIVA KNRTQGCCHMETTENLEKNIKNDFAEDLSETTYNKTLE SUKQMDATATYPHERALQAKLKOTENAATENMYGPD\MKKRLIVA KNRTQGCCHMETTENLEKNIKKNDFAEDLSETTYNKTLE SUKQMDATATYPHERALQAKLKOTENAATENMYGPD\MKKRLIVA KNRTQGCCHMETTENLEKNIKKNDFAEDLSETTYNKTLE SUKGWSUPPABDGEKKIKLLTKORKQULABLIKKVRSIGEKLDAFTE FVOSELECHDVVLFWRIQWTRHFLICTAANICALCRGFYYYORH FVDSELECHDVVLFWRIQWTRHFLICTAANICALCRGFYYYORH FVDSELECHDVVLFWRIQWTRHFLICTAANICALCRGFYYYORH FVDSELECHDVVLFWRIQWTRHFLICTAANICALCRGFYYYORH FVDSELECHDVVLFWRIQWTRHFLICTAANICALCRGFYYYORH FVDSELECHDVVLFWRIQWTRHFLICTAANICALCRGFYYYORH FVDSELECHDVVLFWRIQWTRHFLICTAANICALCRGFYYYORH FVDSELECHDVVLFWRIQWTRHFLICTAANICALCRGFYYYORH FVDSELECHDVVLFWRIQWTRHFLICTAANICALCRGFYYYORH FVDSELECHDVVLFWRIQWTRHFLICTAANICALCRGFYYYORH FVDSELECHDVVLFWRIQWTRHFLICTAANICALCRGFYYORH FVDSELECHDVVLFWRIQWTRHFLICTAANICALCRGFYYORH FVDSELECHDVVLFWRIGWTRHFLICTAANICALCRGFYYORH FVDSELECHDVVLFWRIGWTRHFLICTAANICALCRGFYYORH FVDSELECHDVVLFWRIGWTRHFLICTAANICALCRGFYYTHFLICTAANICALCRGFYTHIOPHOPHOPHOPHOPHOPHOPHOPHOPHOPHOPHOPHOPHO	į			l I
DOSAGKTSVLEMIAOAR I FPRGSGEMMTRSPYKVTLSEOPHHVA LEKOSREPDIATEREDLAAR, ERE I ELMREKNECTVS PETIS LINVKGPOLORWIJNDL POUTNYTSGMAPDYKETIPS I SKAYMO DPNAILLCIOOS VOARES I TUDLVSQMOMPERTYPJTKYDL ARKNVASS FRIQQIIEGKLFPMKALGYFAVYTGKGNSSES I EAI RYSEBEP FONSKLIKTSNLRARGYTTRANISLAVODCHWINGES VEQQADS FRATRENETERWINGYP FALRELDREELFERARMSILD BY ISLSGVYPKHWEBILQOSLMERVSTHVIENITLARGATINSG TENTTUD I KLOWITOKOLOP KNAVEVAMETLOGESSER MATEKEK BIDDI FPKLKEAVKERS I KRHKNIDFARDSLEVI QHNALEDRSI SOKQOMDAI TYMERALQALKOTENALEMIA KOTSEHPAYLASDE I TYTKINLE SEGVEUPS LIKDTHROYVERHELKIALNIKGREST TYMENLE SEGVEUPS LIKDTHROYVERHELKIALNIKGREFYTYORM FVDSELECKDVVLFWI LORMALTANTIRQOLTNTEVRELEKIN KNETQEGCVHMETKINLEKMILKOTENIELHKAVERSTYTYMKILE SEGVEUPS LIKDTHROYVERHELKIALNIKGREFYTYORM FVDSELECKDVVLFWI LORMALTANTIRQOLTNTEVRELEKIN KNETQEGCVHMETKINLEKMILKOTENIELKKVRE TOOKALASTILTERTY FUDSELECKDVVLFWI LORMALTANTIRQOLTNTEVRELEKIN KRYLEPPRADEGKKI KLUTOKRVOLAHEKUN KRYLEPPRADEGKA KANATAN KURKOLAHEKUN KRYLEPPRADEGKA KANATAN KURKOLAHEKUN KRYLEPPRADEGKA KANATAN KURKOLAHEKUN KRYLEPPRADEGKA KANATAN KURKOLAHEKUN KRYLEPPRADEGKA KANATAN KURKOLAHEKUN KRYLEPPRADEGKA KANATAN KURKOLAHEKUN KRYLEPPRADEGKA KANATAN KURKOLAHEKUN KRYLEPPRADEGKAN KANATAN KURKOLAHEKUN KRY	-			
LFKDSSREPDLTKERDLAALRHEI ELRMEKKWYKEGCTSPETIS LIAWKGPGLGRWILDDLGGWITVTUSGMAPDYKETISTSKAYM DPNATILCIQOSSUDARRSIVTDLVSGMDPHGRRTIFYUTKVOLL REKKWASPSRIQQIIEGKLFPMKALGYFAVVTGKOMSESIEAI REYEEBFPGNSKLKKYSMLKAHGYTRTVINLSKAUSDCYMGWRES VEQQADSFRATEFRIETEMKNNY PRIRELDENELFSKANSILD BVISLSGVYTKHWEEILQGSLEWRSTHVINENTYLPAAGYNNSG TENTIVDIKLKGWTDKQLDHKAVEVAMETLQBEFSFRMTEYKKK EHDDIFPKK.KEAVKESSI KRIKHMOPEABSLEVIQHNALBERSI SDKQMDAAITFMERALQARLKDTENAISBLTVTQHNALBERSI SDKQMDAAITFMERALQARLKDTENAISBLTVTQHNALBERSI SDKQMDAAITFMERALQARLKDTENAISBLTVTQHNALBERSI SDKQWDAAITFMERALQARLKDTENAISBLTVTQHNALBERSI SDKQWDAAITFMERALQARLKDTENAISBLTVTQHNALBERSI SDKQWDAAITFMERALQARLKDTENAISBLTVTQHNALBERSI SDKQWDAAITFMERALQARLKDTENAISBLTTVTRNLE SGUEVDPSLIKDTWHGVYTRHFLKTALMHCNLCRBGFYYTQRI FUDSELECROVVLPHRIQBKALATVANTLABETTTVRNLE SGUEVDPSLIKDTWHGVYTRHFLKTALMHCNLCRBGFYYTQRI FUDSELECROVVLPHRIQBKALATVANTLABETTTVRNLE SGUEVDPSLIKDTWHGVYTRHFLKTALMHCNLCRBGFYYTQRI FUDSELECROVVLPHRIQBKALATVANTLABETTVRNLE SGUEVDPSLIKDTWHGVYTRHFLKTALMHCNLCRBGFYYTQRI FUDSELECROVVLPHRIQBKLAITVANTLABETSTVRNLE SGUEVDPSLIKTBURLATURTURTHURT FUDSELECROVVLPHRIQBKLATVANTLABETSTVRNLE SGUEVDPSLIKTBURLATURTHURTURTHURTHURTH	Ì			1
INVERDELIGRMULUDLEGUTITUTSGMAPDTKETTESTEKATMO DDNAILICTOOSSUNABRSITUTULUSGMORTSTEVITYUTUL AEKNVASPSRIQQIIEGKLFPMKALGYFAVVTGKONSSESIEAI REYSEBEFFONSKLIKTSMLKAHQVTTRAILSLAVSDCFMMVRES VEQQADSFRATTEFBLETEMKINYPRIKELDELDRELFFKAKNISLL BYJSLSQYTPKHWEBILQQSLMBRVSTHVIENTLIPAQTNINGS TENTTUTUIKLKOWTOKQLORIKAVEVAWETULGBEFSKAMUSLL BYJSLSQYTPKHWEBILQQSLMBRVSTHVIENTLIPAQTNINGS SISKQOWDAALTYPMERALQARIKOTEMAIENWOSPOWALEDRSI SISKQOWDAALTYPMERALQARIKOTEMAIENWOSPOWALEDRSI SISKQOWDAALTYPMERALQARIKOTEMAIENWOSPOWAKENLYM KNRTQEQCVHNETKNBLEKMLKCHERHPAYLASDSITTVRINLE SRGVEVDPSLIKDTMHQVYRRHPLKTALAHCHCRGFFYYYORH FYDBELECKIDVULFWRI QRMLAITANTLICQUINTEVRRLEKNV KEVLEDPFABDGEKKIKLITGKRVQLAEDLKKVRSIGEKLDAFTE FYDBELECKIDVULFWRI QRMLAITANTLICQUINTEVRRLEKNV KEVLEDPFABDGEKKIKLLTGKRVQLAEDLKKVRSIGEKLDAFTE FYDBELECKIDVULFWRI QRMLAITANTLICQUINTEVRRLEKNV KEVLEDPFABDGEKKIKLLTGKRVQLAECKLOPETSLENDY LYATOMSLECKSLIHLHFTSTYINLLAF PROSSONOB CMARTPCP/FHACCLSPSLIRESVEJEMUNJEVDAABLE P\RKTSLFPHMASHGPREAVSGLAKSRDVLITTE VARAGSSTODS CMARTPCP/FHACCLSPSLIRESVEJEMUNJEVDAABLE P\RKTSLFPHMASHGPREAVSGLAKSRDVLITTE NEWGSTODDS CMARTPCP/FHACCLSPSLIRESVEJENSTHAUDFNWRMKEVLVSSML SAYYVAFVOWFVKNITHYDDKWRSCELFILVSITSTVILMGHLI PASYCOLLHKAAAHLGGWOXUPPALGSNULGHPHTECMWPQGY LVKHSKMYVKAYAGHYNUA PSDUSHFREFFFFSPRILILILL LEGAUIVYQLYSLMSSEKHHOTISLAILLFSNYYAFFKLLADRL VIGKAYSYSASPORDLDHFPS SSETFEMBEREILRRQIRLLGGLLDDYKTLHGNAPAPGTPAASG WQPPTYHISGRAFSARYPRSRRGYSSHDFPSFRIKLIADRL VIGKAYSYSASPORDLDHFPS SSETFEMBEREILRRQIRLLGGLLDDYKTLHGNAPAPGTPAASG WQPPTYHISGRAFSARYPRSRRGYSSHOPSWKXYSLVINRPPG PEDDFAAHAVRLHGARGGQPPVPQCHVLERQVOLSQGONVVIK VKPRYBLANDHTDQPVDSSVGGPAPAPSGARGSPPAADAGSVASCAPQ LIGDRYNDAHTDQPVDSSVGGPAPASSSGORPARGASSSSSSSSPROARRALSPRVARASHSCHACGGGPT TIKFRKINYKWVAASSKSPVLKRTRANSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTRNSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTRNSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTRNSTSLPGDKKSGTSPAATAKSHLSLR RRUSLSSSLVLANRPPORAGGGKAPQCGSKAPGSSASSSSSSSSSSSSSSSSSSSSSSSSSSPRAARRALSPRVARKSSPSCASSSSSSSSSSPPARATSSRFORGCCPY HIDPBVK AVCTEPVBGTCKKTTGTCPSSHTVKRTVKTRASSPSSAGASSSCAA SSSS		,		
DPNAILCIQOSSUARRSIVTDLVSQMDPHGRATIPULTVUDL AEKNVASPSRIQQIIEGKLPPMKALGYFAVYTGKGNSSESIEAI REYSEBEPPONSKLKYSMLKAHQVTYRNISLAUSDCPMMWYRES VEQQADSFKATEFRIETEMKINYP FALRELDENELFSKANSILL BYJSLSGYTPKHWEEILQGSLENKEVSTHYLENTLPAAGTNINSS TENTIVDIKLKQWTDKQLSMRKVSTHYLENTLPAAGTNINSS TENTIVDIKLKQWTDKQLSMRKVSTHYLENTLPAAGTNINSS TENTIVDIKLKQWTDKQLSMRKVSTHYLENTLLPAAGTNINSS TENTIVDIKLKQWTDKQLSMRKVSTHYLENTLYLBAAGTNINSS TENTIVDIKLKQWTDKQLSMRKVSTHYLENTLYLBAAGTNINSS SDKQQWDAAITYPMERALQARLKDTENAITHANTLRQQLYNTEKHEKNY KWRTQEQCUHNETKREEKMLKCMEEHRAPLASDEITFVRKNLE SRGWEVDPSELKCNDVLIFWRIQRMLAITANTLRQQLYNTEKRLEKNY KWYLEDPEABDGKKIKLLIGKKCNEEHRAPLASDEITFVRKNLE SRGWEVDPSELKCNDVLIFWRIQRMLAITANTLRQQLYNTEKRLEKNY KWYLEDPEABDGKKIKLLIGKKCNEEHRAPLASDEITFVRKNLE PUFPPARGAVELOAS/ASPPLATOTVVPLQHCKIPELPYQASIL FELQLFFCQLIALPHYINIVKTWWYPPSHPDSHTSLMPHLID FRILMVTTIVLIGRRFIGSIVKEASQRGKVSIFRSILEPLURALER PRATSLEJHRHASMAGGREKKUSLAKSRDYLLTIRK, KROSSTQDS CMARTPCP/PHACCLSSEILSEWETLKMDFWMMKEVLVSSML SAYYVAFVPWFWINTHYDKRWSCELFLLVSISTSVILMGHLI PASYCDLIKKRAAHLGKGVVDPALCSNUPMTESCMPQGV LVKHSKAVVKANGHYNVA TPSDVSHFRPHFPFSKPLRIINILLL PASYCDLIKKRAAHLGKGVVDPALCSNUPMTSECMPQGV LVKHSKAVVKANGHYNVA TPSDVSHFRPHFPFSKPLRIINILLL LEGAVUVYQLYSLMSSEKHQTISLALLIFSNUPFKLRENDE SSRTEMEEKELIKRQIRLLGGLLDDYKTHGNAPAGTPAASG WOPPTYHSGRAFSARYBRYSRRGVSSHHGPSWRKKYSLVNRPPG PSDDPADHAVRPLHGARGGGPPVQOHVLERQVQLSGGNVVIK VKPPSKSGRASASGARGARSLEFFEDTFWARGYGSSTGNOTIK VKPPSKSGRASASGARGARSLEFFEDTFWARGYGSHSVASCAPQ LLGGRRYDAGHTDQPVPSGSVGCPARPAGGPRQAREASIVVTCR TIKKFKKNINKWVAASSKSPRVARRALSPRVAARAVCCASAGMAN KVENGULLADPPPKRRTPASSGYGGAPPSSASSSS SFRNGSEAGSHDHASQLSPVLSRSPSGD NRAVSHASDLKPLGGE TPLSAYKVKSRTKLTIRRRSTSTSLPGOKKKYKRASSPSASSSS SFRNGSEAGSHDHASQLSPVLSRSPSGD NRAVSHASHLFKER RKLSLSKSINLARRFYNASGTSTSLPGOKKRYKRASSPSASSSS SFRNGSEAGSHDHASQLSPVLSRSPSGD NRAVSHRSLKFRUGGVLY KVSANKLSKTSGOPSDAGSRPLLKTGLDPAGSCGSALBARAVQ GELAITRAGARGREKEREVGWYTHRFGCRRGEECFYIHDPEKV AVCTFFVRGTKKTTGTCFPSSHVYSKRMPVCSTYLGICSNSN CYPSHVVYSKRABEVCSFPSKAGKMPVCSTYLGICSNSN CYPSHVVYSKRABCVSDFTKGYGVPLGKGCKKKHTLLCPDPARG A				
ARKNVASPERIOQLISEKLFPMKALGYTAVVTKGKRSSESTEAT REYEBEPFONSKLIKTSMLKAHQVTTRNISLAVSDCFMKMVRES VEQQADSFRATTEFNLETEKRNNYPRIRELDRNELFEKAKNEILD EVISLSGVTPKHWEBILQOSLWBRVSTHVIENYILPAQTYNNSG TENTTVDILKOWTDKQLGNKAVEVAMETLQBEFSRFMTEYEKK EHDDIFPKLKRAVKERSIKRHKMNDFAEDSLRVIQHALEDRSI SDKQQMDAILYPMERALQARIKDTENAILENWYGPD\WKKRHLYW KNRTQEGCVHNETKNELEMMLKCHERHPAYLASDSITTVRKNLE SRGWEVDPSLINDTMGVYRHPHLKTALHANCHCRGFYYYORH FVDSELECNDVVLPWRIQRMLAITANTLRQQLTNTEWRELEKNV KRYLEDFABGEKKIKLITGKRVQLAEDLKKVRRIQEKUAAFIE SALHQEK FVFYBARGAVLEQAS/ASPPLATQTVVPLQHCKIPELPQASIL FFLQLFFCQLIALFVHINIKTVWWYPPSHPPSHTSLNFHLID FFLLMVTTIVLGRRFIGSIVKEASQRKVSLFRSILLPITRFTV LTATGMSELGSLIHLHFTSYFINLL/FPLSWVHISVPABLE P\RKTSLFHHMASMGPREAVSGLAKSDVLLTHE\RGSSTQDS CMARTPCP/FHACCLSPSLIRSEVEFLKWDYMMKMSVLVSSML SAYVAPVEVWEVENTHYTDKRMSCELFLLVSISTSVILMQHLL PASYCDLLHKAAAHLGGWKVDPALGSNVLGHFWTEGWMPQGV LVKHSKAVYKANGHYNVALPSDSWHERFFFSKPRILINLLL LEGAVIVYQLYSLMSSEKWHOTISLALILFSNYYAFFKLLDRIL LUKHSKAVYKANGHYNVALPSDSWHERFFFFSKPRILINLLL LUGKAYSYSASPQROLDHFS 412 SSETEMBEKEILRRQURLLQGLLDDYKTLHGNAPAPGTPAASG WOPPTYHGGAFSARAYDESRRGVSSHGPSRWKYSLWNDPP PSDPPADHAVRPLHGARGGQPPVPQHVLERQVQLSQGONVVIK VKPPSKGSASASAGAGRSSLEFFEDTPMSDGRFREGGEPPRGO LOPSRPTRANGTGSVSEDPLLVCQKEPGKRWKYSLWNDPP PSDPPADHAVRPLHGARGGQPPVPQHVLERQVQLSQGONVVIK VKPPSKGSASASAGARSSLEFFEDTPMSDGRFREGGEPPRGO LOPSRPTRANGTGSVSEDPLLVCQKEPGKRWKYSUSVGSDFR PRRTVSSSVIAVKASFPSSALPPRTUVALGRKLGSHLVASCAPQ LLGDRRVDASHTOGPUSSVGGFARASENVYTCR TKKFKKNYKWVAASSKSPVARRALSPRVARENCKASAGHAN KVENGULLADPEPPKRFRATSSKGGARGASLEKFUKASAGAPAS SSHWASHANASSKSPVARRALSPRVARENCKASAGHAN KVENGULLADPEPPKRFRATSSKGGARGASELEKFUKTCRLPPSRAHLPTKRA SSLHAVRTAFTSKVIKTRYRIVKKTRALSPLSAPFPLSLPSHPTKRA RLSLSKSLIANARVYGANGGGRAPPLEKVKASSPSSASSS SPRWGSBAGSKDHARGTSSLEGGGRAPGCSCRFCTYHTOPKV AVCTEPVGGTCKKTTGTCPPSHHVSKKKMPVCSYFLKGGULY KVSANKLSKTSGQPSDAGGRPLLKTGRLPPAGSCSSLLASRAVV CRISALTIRGAGGRREKKEKTGCTSPSHHVSKKKHLLCPPPSRRALBPTKRA SSLHAVRTAFTSKVIKTRYRIVKKKTRASPLSLSAPSHOPKFBAGGGRAPCHCGGSAPSSKCAS CPYSHVYVSKAEVCSDFLKKYCHYFTKRALTVRIVAKKHTLLCPPPBRG ACPRGAGCGULHRTOKRHSRRAATSPAGPSDATARSRVSASHG PKKPSASQ				
REYBEREPONSKLIKTSMLKRIGUTTRINLELAUSDCFMENVRS VEQQADSFKATRFINLETEWKINNY PLREIDENELFEKAKRIELD EVISLSQVTPKHWEBILQOSLWERVSTHVIENIYLPAAQTMINSG TENTIVDIKLKWITKGLPHKAVEVAWETLQBEFSRFMTEPKSK BEIDDIFPKLKEVAVKBSSIKSHKWINDFSLRVIQBEFSRFMTEPKSK KRITCBGCQUNINTKNELEKMIKKINEBLSLRVIQBHALBERSI SDKQWDAAIYFMERALQARLKOTENAIENIVAGPD)WKKRRLVW KRITCBGCQUVINTKNELEKMIKKINEBLAKJASDEITTVIRNLE SRGVEVDPSLIKOTHHQVYRRHFLKTALIMENLCRRGFYYYQRH FVUSSELEKONDVVLFWRIQRMLAITANTLRQOLTWITEVRILE SRGVEVDPSLIKOTHHQVYRRHFLKTALIMENLCRRGFYYYQRH KEVLEDPABBGBKKIKLITGKRVQLABDLKKVRRIQBEKDAFIE ALHQEK PVFVPAPCAVLEQAS/ASPPLATOTVVVPLÖHCKIPELFVQASIL FELQLFFCGLIALFVHYINIYKTVWWYPPSRPPSHTSLINFHLID PHLIMVTIVLORRFIGSIVKEASQRSUFFRSILLFITFTV LTATGWSLCRSLIHLFRTYSFINLL/FPLLSVMDVHSVPAABER P\RKTSLFNHMASMGPRBAVSGLAKRDYLLTIR,RRGSTODS CMARTPCF/PHACCLSPSLIRSEVEFLMDFINNRMKEVLVSSML SAYYVAPVPWFVKNTHYYDKRRSCELFLLVSISTSVILMHHLI PASYCDLHKRAAHLGGAGVPPALCSVLQHDWTSECMPQGV LVKHSKNVYKAVGHYNVAIPSDUSHFRFHFFFSKURTINILLL LEGAVIVYQLYSIMSSEKWHOTISLALLIFSNYYAPFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSTREMEBEREILRQURLUQGLDDYKTLHGNAPAFGPAASG WOPPTYHGGAFSARYPPSRRGYSSHHGPSWKKXSLVNRPPG PSDPPADHAVRPLHGARGGQPVPQQHVLERQVGLSQGGNVVIK VXPSKSSGASASGAGNSLEFETDFDORFREGEGEPPRG LOPSRPTRAGGTCSVEDDFLLVCQKEPGKPRWKXSGVVGDSPRE PRRTVSSSSAJSAGNGSSLEFETDFDDRFREGEEPPRG LOPSRPTRAGGTCSVEDDFLLVCQKEPGKPRWKXSGVVGDSPRE PRRTVSSSVIJAVKASPSSALPRTVALGRKLGSHSVASCADQ LLGDRRVDAGHTDQPVPSGSVGGPAPASGPRARASLVVTCR TMKFRKINNYKWAASSKSPRVARRALSPRVAABENVCKASAGMAN KVEKQULADPEEVRRAFASSLAPPRTONALGRKLGSHSVASCADQ LLGDRRVDAGHTDQPVPSGSVGGPAPAKKMASSPASSSS SFRWGSEAGSKDHASQLSPVLSRSPSGD\RPRAVCKASAGMAN KVEKQULADPEEVRRAFASSLAPRTONALGRKLGSHSVASCADQ LLGDRRVDAGHTDQPVPSGSVGGPAPAKSKVKASSDASSS SFRWGSEAGSKOHASQLSPVLSRSPSSPNKKMASSPSASSSS SFRWGSEAGSKOHASQLSPVLSRSPSGPNRRKKGSCSKLADRAVQ RELSIALIKGRRAFATSPTKOSGGSKADGSPSVKKKASSPSASSSS SFRWGSEAGSKOHASQLSPVLSRSPSGPNRRKKGSTCIGGVLY KVSANKLSKTSGOPBDAGSRPLLKTGRLDPARGSCRSTLADRAVQ RELSIALIKGRRAFATSPRAGGPSPWRRKSKYCIGGNLY KVSANKLSKTSGOPBDAGSRPLLKTGRLDPARGGRCSPTLEDPKW AVCTFPURGTCKKTDGTCPSHHVSRKMPPCPGGSASPSSKAS SSSSSSSSSSSPASLUBERSUQARALAAACSN]	
USQQADS FRATERNLETEMINNY PELRELDENELFEKARNE ILD EVISLOVPKHWEEILQQSLWERVSTHVIENTYLPAAQTWINSG TENTIVDIKLKOWTDKOLENKAVEVAMETIQEEFSRPHTE KSK BEIDDIFPKKLERAVKESSIK SHRKWINFARDSLRVJQHNALEDRSI SDKQQMODAN IYEMEELAQALKUTERAN EEMVOJQHNALEDRSI SDKQQMODAN IYEMEELAQALKUTERAN EEMVOJQHNALEDRSI SOKUPUS DELIKDITHQOVIRHELIKAN EEMVALKONEEHPAYLASDEITTVEKINLE SOKUPUS DELIKDITHQOVIRHELIKAN ELIKAN HORIOLORGETYTVORI FVDSELECNDVVLFWRIQRMLAITANTLRQQLTITTEVRINLE SOKUPUS LIKDITHQOVIRHELIKAN KRYLLABDLKKVERIQEKLOAFIE ALHQEK ALHQEK FVDSELECNDVVLFWRIQRMLAITANTLRQQLTITTEVRINLE SOKUPUS LIKDITHAN TINTUK TINTUK VERVELOEKLOAFIE ALHQEK PROFOSAL HELDON TINTUK TINTUK VERVELOEKLOAFIE FLOLFFOOLIALPYHVINIY XIVUW YPPSH PSHTSLNFHLID FRILMVTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTFTYV LITATUS LOKASLIHLFRTYSFINLL/FPLISVOHUNSVPAABLE PRETSSLFINMASMOPRAVSGLAKSROYLLTUR (ROSSTODS CMARTPCCP/FHACCLSPSLIRSEVSFLKMDDINMKEVLVSSML SAYVAVPVPWFVKNITYTYNKRYNGELFILLVSISTSVILMHLL PRAYCDLLHKRAAHLGOWG VOPALCSWULQHDWTEECHWDOGV LVKHSKNIVYKAVGHYNVAIPSDVSHFRPFPFFSKPLRILILLL EGAVIVYQLYSIMSSEKWIQTISLALLIFSNIVYAPFKLIRDRL VLGKAYSYSASPQRDLEHRS SSFTEMEBEKEILRRGINLLQGLIDDYKTLHGNAPAPGTPAASG WOPPTYHSIGRAFSARYPRPSRRGYSSHIGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGARGGQPPVPQQHULERCOVLOSGONVVIK VLPPSKSGSASASGAGRGSLEEFEITJEWSDQRPREGEGEPPRQ LOPSRPTTARGTCSVEDDLLVCQKEEGKPRWKVSVOSVODSPRR PRRTVSESVIJAVKASPESSALPPRRTUSLEGVOLLOGGONVVIK VLPPSKSGSASASGAGRGSLEEFEITJEWSDQRPREGEGEPPRQ LLGDERVDAGHTOPVPSGSVGGPARPASGFQARRASLIVVTCR TIKERKONYKWAVAASSKSPAVARRILVASVOSVODSPRR PRRTVSESVIJAVKASPESSALPPRRTUSKOSVODSPRR SPRRTVSESVIJAVKASPESSALPPRRTUSKOSVODSPRR PRRTVSESVIJAVKASPESSALPPRRTUSKOSVODSPRR SPRRTVSESVIJAVKASPESSALPPRRTUSKOSVODSPRR SPRRTVSESVIJAVKASPESSALPPRRTUSKOSVODSPRR PRRTVSESVIJAVKASPESSALPPRRTUSKOSVODSPRR SPRRTVSESVIJAVKASPESSALPPRRTUSKOSVODSPRR SPRRTVSESVIJAVKASPESSALPPRRTUSKOSVODSPRR PRRTVSESVIJAVKASPESSALPPRRTUSKOSVODSPRR SPRRTVSESVIJAVKASPESSALPPRRTUSKOSVODSPRR SPRRTVSESVIJAVKASPESSALPPRRTUSKOSVODSPRR SPRRTVSESVIJAVKASPESSALPPRRTUSKOSVODSPRR PRRTVSESVIJAVKASPESSALPRRTUSKOSVODSPRR SPRRTVSESVIJAVKASPESSALPPRRTUSKOSVO				_ ·
BUTISLSGYPT KHWERILQGSLWERVSTHVIENTYLPARQTMNSG TPHTTYDIKLKQWTDKQLPNKAVEVAWETLQEFSERPHTEPKGK BHDDIFPKKKEAVKEBSI KRHKWNDFAEDSLRVIGENSLEDSIS SDKQMDARIYMERALQARLKOTENAI ENWUGDOD WKKRNLWW KRRTQEGCUNIETKNBELKMLKCNEBHEPAYLADDITTYRKNLE SRGVEVDESLIKDTHQVYRRHFLKTALMHCHLGREGFYTYGRIE SRGVEVDESLIKDTHQVYRRHFLKTALMHCHLGREGFYTYGRIE SRGVEVDESLIKDTHQVYRRHFLKTALMHCHLGREGFYTYGRIE FUNDSLEENDVLJERIGGRALATTALTRQQLTRTEVRRIEBN KEVLEDPABDGEKKIKLLTGKRVQLAEDLKKVREIQEKLDAFIE ALHQEK PVFYBARGAVLEQAS/ASPPLATQTVVPLQHCKIPELFVQASIL FELGLFFCGLIALFYHYINIYKTVWWYDPSHPSHTSLNFHLID FELGLFFCGLIALFYHYINIYKTVWWYDPSHPSHTSLNFHLID FELGLFFCGLIALFYHYINIYKTVWWYDPSHPSHTSLNFHLID FELGLFFCGLIALFYHYINIYKTVWWYDPSHPSHTSLNFHLID FELGLFFCGLIALFYHYINIYKTVWWYDPSHPSHTSLNFHLID FALGAUFTULUGREGSLIKBEVEFLKMDFNWRMKEVLVSSML SAYYVAFVPWWFVKNTHYYNKWSCELFILLVSITSTVIIMGHLID PASYCDLHKRAAHLGGCOKVDPALCSVLQHDWTBECWMPQGV LUKHSKNYKAVGHYNNAIPSDVSHFRHFPFSKRUPIINILLL LEGAVIYVGLYSIMSSEKWHQTTISLALLLFSNYYAFFKLLEDRI VLGKAYSYSASPQRDLDHRFS SFRTEMBEEKEILRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WOPPTYHIGGAFSARYPRPSRRGYSSHHGPSWRKXYSLVNRPPG PBDPPADHAVRPLHGARGGOPPVPQGHVLERQVGLSQGGNVVIK VKPPSKSGSASASGAGGRSLEFFETDTFMSDGRFREGEGEPRGG LOPSRPTRAGGTCSVEDPLLVCQKEPGRPRWKKYGGVUDSPGR PRRTYSESSVLAVKAFPSSALPPRTVALGKKLGSHSVAGCAPQ LLGDRRVDAHTHQPVPSGSVGCPARPASGCAPATAKSHGLK KVEKQLIADPEBVRRKPATSSKPGAPSKYKKKASSPSASSS SFRWGSEAGSKDHAGQLSFVLSKSPBGD\RRACKYGSVCDSPRR PRRTYSESVLAVKASPFSALPRTVANSGCRAPATKKKASSPSASSS SFRWGSEAGSKDHAGQLSFVLSKSPBGD\RRACKYGRCGGVLY KVSANKLSKTSGQPSDAGSRPLLKTGRLDPAGSCRSILLDFWRA RELSLSRSLVLINILRPVASGGKAQPGSPWWRKGYCCIGGVLY KVSANKLSKTSGQPSDLKSCYCTLARGCRESCPTLHDPEKV AVCTRPVGGTCKKTDGTCPFSHTVSRCKKHTLLCCPPFARG ACPRGAQCOLLHRTOKRRISRAATSPAPGPSDAARSKYGAGE CYPSHVYYSKRAFCKSTCYCTYNTRFGRCNGGECCPTHDPEKV AVCTRPVGGTCKKTDGTCPFSHTVSRCKKHTLLCCPPFARG ACPRGAQCOLLHRTOKRRISRAATSPAPGPSDAARSKYGSAGS SSSSSSSSPASLIDHEARSLQEAALDAACSNRLCKLPSFISLGS SSSSSSSSPASLIDHEARSLQEAALDAACSNRLCKLPSFISLGS SSSSSSSSSSSSSPASLIDHEARSLQEAALDAACSNRLCKLPSFISLGS SSSSSSSSSPASLIDHERSGCACPHIKPRL AXAPPTEGESSEPEAKLYHTKELKRAVRADENDLLLLCKLPSFISLGS SSSSSSSSSSSSSSSCASGARRARALT	1			1 · · · · · · · · · · · · · · · · · · ·
TENTIVOIKLKONTUKOLPUKAUVEVAAMETLOEBESRIMTEPKEK EHDDIFKKLKEAVKEBSIKRHKMOPPABEDSLRVIOHNALEDRSI SDKQQMDAAIYFMERALQARLKOTENAIENMYGP) WKKRNLW KNRTCGCCVINETKNELEKMIKKCHERHPAYLASDEITTVEKNILE SGRUEVOPDSIIKDTNEVYRHEHKITALHICHLCERGFYYYORK FVDSSLECNDVULFNEVORMLAITANTLRQOLTNTEVERLEKNV KEVLEDFABDGEKKIKLLTGKRVQLAEDLKKVERIGEKTOV KEVLEDFABDGEKKIKLLTGKRVQLAEDLKKVERIGEKLDAFIE ALHQEK 6090 194 1560 PVFVPAPGAVLEQAS/ASPPLATQTVVPPLQTKIPELPVQASIL FELQIFCOLIALFVHYINIYKTVMWYPPSHPPSTTSINPHLID FPLLMVTTIVLGREFIGSIVKEASQRGKVSLFRSILLFLTFTV LTATTOMSLCRSILHEFTYSFILMIPFLSUSVANDHVSPAABLEK ANYAVAYPVHVFKVNTHYDKRRSCHLLVSISTSVILMGHLI PASYCDLLHKRAAHLGCWGVDPALCSNULQHBWTEECMBPGGV LVHSKKNYKAVGHVNATPSDKNSCHLLVSISTSVILMGHLI PASYCDLLHKRAAHLGCWGVDPALCSNULQHBWTEECMBPGGV LVHSKKNYKAVGHVNATPSDKNSCHLLVSISTSVILMGHLI LEGAVIVYOLYSIMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDRRFS 6091 3279 412 SSRTEMBEKE ILERGIRLIQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWKKYSLVNRPPG PSDPPADHAVPPLIGARGGQPVPGVLERGVOLSOGGNVIIK VKPPSKSGSASASQARGSLEEFEDTDWSDORPREGGEPPRGQ LOPSRPTRARGTCSVEDPLLVCQKEPGVPLERGVOLSOGGNVIIK VKPPSKSGSASASGARGSLEEFEDTDWSDORPREGGEPPRGQ LOPSRPTRARGTCSVEDPLLVCQKEPGVPREARSLSVUTCR TKKFRKNYKWADASKSBPVARRALSPRVABRSLVCKASAGMAN KVEKPQLLADPERPRKPATSSKPGSARPARGABSLVVTCR TKKFKNYKWADASKSBPVARRALSPRVABRSLKVLKSSGRSSSSSSSSSSSSSSSSSSPVARRALSPRVABRSLKKPLGGEVLY KVEKNQLKADPERPRKPATSSLPGDKKSGTSPAATAKSHLSL RRQALRGKSSPVLKKTPNKGLVQVTTRRLCRLPPSRAHLPRKBA SSILMAVRAPSPSSULVTRYRIVKTRAPLSKPSLPDPARSLARGRUNL RRQALRGKSSPVLKKTPNKGLVQVTTRRLCRLPPSRAHLPRKBA SSLHAWRTAPTSSVLTKTRYRIVKTAPSLSPLSPPPLSLEPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWSKSGYRCLGGVLY KVSANKLSKTSQQPSDAGSRPLLRTGRLPPSRAHLSPRKBA RRJSLSRSLVLNRLRPVASGGGKAQPGSPWWSKSGYRCLGGVLY KVSANKLSKTSQQPSDAGSRPLLRTGRLPPSRAHLSPRKBA RRJSLSRSLVLNRLRRPVASGGGKAQPGSPWRSKGTGCGSVLY KVSANKLSKTSQQPSDAGSRPLLRTGRLPPSRAHLSRNSASHG PRKPSASQRPTRGTPSSAALTAAAVAAAPPHCPGGSASPSSKAS SSSSSSSPPASLDHEARRAATSPAPGGSBATARSRVSASHG PRKPSASQRPTRGGESEPSSAALTAAAVAAAPPHCPGGSASPSSKSS SSSSSSSSPPASLDHEARRAATSPAPGGSBATARSRVSASHG PRKPGBSSEPERKVUMTKRILVVEAVHRIDDILLCNKTAYQ SSP			1	1
### ### ##############################	1			1
SDKQQWIDAJTYFMERALQARLKOTENAIENMUGPD\MKKRRLYW KNRTQGQCVINETKNELEKMLKCNEEHPAYLASDEITTVRKNILE SRGWEVDPSLIKIDTMIQVYRRHFLKTALAHCRICERGFYTYQRH FYDSELECNDVUFWRIQRMLAITANTLRQQLTNTEWRRLEKW KEVLEDFAEDGEKKIKLITGKRVQLAEDLKKVREIQEKLDAFIE ALHQEK 6090 194 1560 PYFYPPAGAVLEQAS/ASPPLATQTVVPLQHCKIPELPVQASIL FELQUFFCQLIALFVHYINIYKTVWWYPPSHPPSHTSLNFHLID FHILMVTTIVUGREFIGSIVKEASQRGKVSLFRSILLFLTFTV LTATGWSLCRSLIHLFRTYSFINLL/FPLSLWDVHSVPAABLR P\RKTSLENNHAASMGPRRAVSGLAKSRDVLLTLR\RRGSSTQDS CWARTPCP/FHACCLSPSLIRSEWEFLKMDFFWRMKKEVLVSSML SAYYVAFVPWFWKVNHYYDKWRSUFLLWSISTSVILMGHLI PASYCDLLHKAAAHLGCWQKVDPALCSNVLQHPWTEECMMPQGV LVKHSKNYYKAVCHYNVAI PSDVSHFRHFFFSKPLRILNILLL LEGAUVYQUYSINSEEKHQTISLLJESNYYLFFKLIRDRI VUGKKAYSYSASPQRDLDHRFS 3279 412 SSRTREMEEKSILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WOPPTYHSGRAFSARYRPSRRGYSSHHGFSWRKKYSLVNRPP PSDPPADHAVRPLHGARGGQPPVQQWLLERGVQUSSQGONVVIK VKPSKSGSASASGARGSLEEFEDTFWSDORPRREGGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWVKSVGSVODSPR PRRTYSSSVIAVKASFPSSALPPRTGVALGRKGSHSVASCAPQ LLGDRRVDAGHTDQPVPGGSVGGPARPASGPRQAREASLVVTCR TMKFRKNNYKNVAASKSPRVARRALSPRVAARNUCKASAGMAN KVEKPQLIADPPRPRKPATSSKPGSPASKYKWKASSPSSASSS SFRWGSEAGSBCHASGLSFVLSRSPSGD\RPAVGISGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSIR RRQALGKSSPVLKKTPNGLVUYTRICKLCHPSRAHLPTKEA SLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPPPLSLPSWRA RRISLSRSLVINRILRFVASGGGKAQGGSWRKSKGYRCIGGVLY KVSANKLKSTTSQGPSDAGSRPLLATGLCLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSPASSFSKASRAV RSLAIIRQARQRRSKRKEXCMYYNRFGRCNGGRCPYHDPEKV AVCTRFVRGTCKKTDGTCPSHVYKKERMPVCSYPLKGICSNSN CYYSHYYNSKAEVCSDFLKGYCPLGAKCKKHTILLCDPPARRG ACPRGGQCQLLHRTGRRRAATSPAPGRSDATARSRVSSHG PRKPSSGORPTGTGPSSAALTAAAVAAPPHCPGGSSRSPSSKAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSSSSSSSSPPASLDHEAPSLQEAALAAACSNR			1.	
KNRTOEQCUMETINBLEKMLKCNEEHPAYLASDEITTVEKNLE SRGVEVDPSLIKDTWHQVYRRHJEKALNHCNLCRGFYYYQRH FVDSSLECNDVVLFWRIQRMLAITANTLRQQLTNTEVRRIERNV KEVLEDFABDGEKKIKLLTGKRVQLAEDLKKVRBIQEKLDAFIE ALHQEK 6090 194 1560 PVFVPAPGAVLEQAS/ASPPLATQTVVPLQHCKIPELPVQASIL FELQLFFCQLIALFVHY NII YRTVWWYPSHPPSHTSINHLID FPLLWYTTIVLGRFIGISIVKEASQRGKVSLFRSILLFLTRFTV LTATUMSLCRSLIHLFRTYSFLNLL/FPLLSWNDVHSVPAAELR P\RKTSLFNHAASMSPREAWSGRASPDVLLTR IR RGSSTDOL GMARTPCP/PHACCLSPSLIRSEVEFLKMDFNWRMKEVLVSSML SAYYVAFVPWFVKNTHYYDKWSCELFLLVSISTSVILMQHLL PASYCDLHKRAANHLGGWGRDALCSUNLQHPWTEXCMMPQC LVKHSKNVYKAVGHYNVAIPSDVSHFRFHFFPSKPLRILNILLL LEGAVIVYQLYSLMSSEKWHQTISLAILFSNYYAFFKLLADL LLEGAVIVYQLYSLMSSEKWHQTISLAILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDHRFS 6091 3279 412 SSRTREMEEKSILRRQIRLGGLIDDYKTLHGNAPAPAPGTPAASG WQPPTYHSGRAFSARYFRSFRSYSSHHGPSWRKKYSLVNNPPG PSDPPADHAVRPLHGARGGQPPVPQQHULERQVQLSQCGNVVIK VKPPSKSGSASASGAGRGLEEFEITPWSDQRFREGGEPPRG LOPSKPTTARATCSVEDPLLVCQKEPGKPRWKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALVPRTSVALGRKLGSHSVASCAPQ LLIGDRRVDAGHTDQPVPSGSVAPAPASGFRQAREASLVVTCR TNKFRKNNYKWAASSKSPVARRALSPRVAAENVCKASAGMAN KVEKQLLIADPEPKPRKPATSSKPGSAFSKYKWKASSPSASSS SFRWGSEAGSKNHASQLSPVLISRSPSGD\RPAVCHSGLKULSGE TPLSAYKWKSRKILTRRRGSTSLPGDKKSGTSPAATAKSHLSLR RQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPFPDSLESWRA RRISLSRSLVLNRRLPVASGGGKAPGPSSWMSKGYRCIGGVLY KVSAKKLSKTSGOPSDAGSRPLLRTGRLPPSRAHLPTKER SSLHAVRTAPTSKVIKTRYRIVKKYPASPLSAPFPDSLESWRA RRISLSRSLVLNRRLPVASGGGKAPGPSSWMSKGYRCIGGVLY KVSAKKLSKTSGOPSDAGSRPLLRTGRLPPSRAHLPTKER ACPRGAQCQLHHRTQKRHSRRAATSPRAPGSBATARSRVSASHG PRKPPSASGPTRGTCSPSHAVSKKKPPVCSYFLKGICSNSH ACPRGAQCQLHHRTQKRHSRRAATSPAPGPSBATARSRVSASHG PRKPSASGPTRGTCSPSSALALTAAAVAAPPHCPGGSASFSSSKSH PRKPSASGPTRGTCSPSSALALTAAAVAAPPHCPGGSASFSSSKSH SPSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPPASLDHEAPSLQEAALAAACSNRL	1			
SRGVEVDSLIKTOTWHQVYRRIELKTALMHCNLCRRGFYYYQRH FVDSELECNDVVLFWRIQRMLAITANTLRQQLTMTEVRRLEKNV KEVLEDFABDEEKKIKLLTGKRVQLAEDLKKVRBIQSKLDAFTE ALHQEK 6090 194 1560 PVFVPAPGAVLEQAS/ASPPLATQTVVPLQHCKIPELPVQASIL FELQLFFCQLIALPVHYINIYKTVWWYPPSHPPSHTSLNPHLID FNLLMVTTIVUGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTY LTATAWSLCRSILHLERTYSFINLL/FPLSSWUDWISVPAABLR P\RKTSLFNHMASMGPREAVSGLAKSRDYLLTLR\RRGSSTQDS CMARTPCF/PHACCLSPSLIRSEVEFLKUPSHWINKYSVLVSSML SAYYVAFVPWFVNNTHYYDKRKSCELFLLVSISTSVILMGHLL PASYCDLHKAAAHLGKWGKVDPALCSNVLOHPWTESCMMPQGY LVKHSKNVYKAVGHYNVAIPSDVSHFFPFFSKPLRILNILLL LEGAVIVYQLVSLMSSEKMHQTISLALTLFSNYAFFKLERDRL VLGKAYSYSASPQRDLDHRFS 6091 3279 412 SSRTREMEEKSILBRQIRLLOGGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGRAGGGPPVPQCHVTURRVOLOGQGNVVIK VKPSKGSGASAGAGGSLEFEDTPWSDCRPREGEGEPPRG LOPSRPTRARGTCSVEDPLLVCQKEPGKPRWKSVGSVGSPRR PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGRQAREASLVVTCR TMKFRKNNYKWAASSKSPRVARRALSFRVAAENVCKASAGMAN KVEKPQLIADPEPPRFRAFTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGRPAREASLVVTCR TMKFRKNNYKWVAASSKSPRVARRALSFRVAAENVCKASAGMAN KVEKPQLIADPEPPRFRAFTSVAFFNCKASAGMAN KVEKPQLIADPEPPRFRAFTSVAFFNCKASAGMAN KVEKPQLIADPEPPRFRAFTSVAFFNCKASAGMAN KVEKPQLIADPEPPRRFATSKAFGSSPAAFAKSHSLIK RRQALRGKSSPVLKTFNKGLUQVTTHRLCRLIPPGRAHLPTKBA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPPDLSPWRA RRLSLGRSLVLNRIRPVASGGKAQGSPWWRSKGYRCIGGVLY KVSAMKLSKTSGGPSDAGSRPLLRTGRLIPPGASCGRSLASRAVQ RSLAITGAARQRREKREYCMYYNRRGRNGREGREPYHDPEKV AVCTFFVRGTCKTDGTCPFSHLVSKEKMPVCSYFLKGICSNSN CPYSHVYNSKAEVSGFTLAGACKKKHTLLCPDFRRG ACPGRAQCQLHRTQKRASRAATSPRAPGSBATARSRVSASHG PRKPSASGRPTRGTPSSAALTAAAVAAPPHCPGGSGSFSSKAS SSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSSPASLDHEAPSLQEAALA	-			
FVDSELECNDVVLPWRIQRMLAITANTLRQQLTNTEVRRIERWV KEVLEDFABDGEKKIKLITGKRVQLAEDLKKVBELOEKLDAFIE ALHQEK 6090 194 1560 PVFVPAPGRAVLEQAS/ASPPLATQTVVPLQHCKT PELPVQASTL FELQLIFCQLIALFVHYINIYKTVWWYPPSHPPSHTSLNPHLID FELLWTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTV LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSWWDVHSVPABELR P\RKTSLFNHMASMGPREAVGGLAKSRDYLLTLR\RRGSSTQDS CMARTPCP/PHACCLSPSLIRSEVEFLKMDPRWRMKZVLVSSML SAYYVAFVPWFVNNTHYYDKRRSCELFLUSISTSVILMGHLL PASYCDLHKRAAHLGGWGXVDPALCSNVLGHPWFECMMPGL LVKHSKNVYKAVGHYNVAIPSDVSHFRPHFPFSKPLRILNILLL LEGAVIVVQLYSLMSSEKHQTISLALLLFSNYVAFFKLLRDRL VLSKAYSYASSPQRDLHHRFS 6091 3279 412 SRFTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTTHSGRAFSARYPRSRRGYSSHHEGSWRKKYSLVNRPPG PSDPPADHANYPLHGARGGGPPVPQQHVLERQVQLSQGONVVIK VKPPSKSGSASASGAQRGSLEFFEDTPWSDQRPRSGGSEPPRGQ LQPSRFTRARGTCSVEDPLLVCQKEPGKPRWVKSVGSVGDSPRE PRRTVSESVIANKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPAPPASGPRQAREASLVVTCR TNKFRKNNYKNVAASSKSPVARRALSPRVAAENVCKASAGMAN KVEKRQLLADEPRPRRPATSSKPGSAPSKYKWKASSPSASSS SFRWGSEAGSKDHASQLSPVLSRSPSGON PRAVENSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTNNKGLVQVTTHRLCRLPPSRAHLSTKR RRLSLSLVLNRLRPMASGGGAQPGSPWMSKSGYRCIGGVLY KVSANKLSKTSQQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSIALIIRQARQRREKREYCMYYNNRGRORRGRECRPYTHDPEKY AVCTRRVBTGYKKTTDGFORSHVSKEMPVCSYPLKGICGNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDPARRG ACPRGAQCQLLHRTQKRHSRRAATSPRAPGSBATARSRVSASHG PRKPSASGRPTRGTTSAAVAAPPHCPGGSASSSSKAS SSSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSPGAQPRVRAPRAPALTKRSKYRAVVEAVHRIDDLICKNTAYQ	1			1
KEVLEDFAEDGEKKIKLTGKRVQLAEDLKKVRBIQEKLDAFIE ALHQEK 6090 194 1560 PVPVPAPGAVLEQAS/ASPPLATQTVVPLQHCKIPELPVQASIL FELQLFFCQLIALFVHYINIYKTVWWYPPSHPSHTSLNFHLID FNLIMVTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTFTV LTATGWSLCRSLIHLFRTYSFLALL/FPLLSVMDVHSVPAAELR P\RKTSLFNHMASMGPRAVGLAKSROYLLTUR\RRGSSTQDS CMARTPCP/PHACCLSPSLISEVEFLKMDFNMEMKSVLVSML SAYYVAFVPWFVKNTHYYDKRWSCELFLLVSISTSVILMQHLL PASYCDLHKAAAHLGCQKVDPALCSNVLQHBWTEECWMPQGV LVKHSKNYVKAVGHYNVAI PSDVSHFRFHFPFSFDFLSILNILL LEGAVLVYQLYSLMSSEKWHOTISLALILFSNYYAFFKLLRDRL VUGKAYSYASPQRDLDHRFS 6091 3279 412 SSRTEMBEKEILRRQIRLLGGLTDDYKTLHGNAPAPGTFAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVI IK VKPSKSGSASASGAGRGSLEFFEDTBWSDQRFRBGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGKKIGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TMKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLLADPEPRFRKPATSKPGSAPSKYKWKASSPSSSSS SFRWQSEAGSKDHASQLSPVLSRSPSGQ\RPAVCHASGLKBLSG TPLSAYKVSRTKIIRRRGSTSLFGGAPSKYKWKASSPSSSSSSSFRWQSEAGSHVKKTAKSLSLLER RRQALRGKSSPVLKETPMKGLVQVTTHRLCRLPPSRAHLEFKEA SSLHAWRTAPTSKVLKTPKRLVQVTTHRLCRLPPSRAHLEFKEA SSLHAWRTAPTSKVLKTPKRLVQVQTTHRLCRLPPSRAHLEFKEA SSLHAWRTAPTSKVLKTPKGLVQVTTHRLCRLPPSRAHLEFKEA SSLHAWRTAPTSKVLKTPKGLVQVTTHRLCRLPPSRAHLEFKEA SSLHAWRTAPTSKVLKTPKGLVQVTTHRLCRLPPSRAHLEFKEA CPYSHVYVSRKAECVGSPBAGSRPLLKTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRSYCMYYMFGRGNGBECPYIHDPEKV AVCTRPVRGTCKKTDGTCPSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKKTYGKELPAGGECRSVIHDPERK AVCTRPVRGTCKKTDGTCPSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKKTYGKERAPATSPAGSBATARSRVSASHG PRKPSASQRPTKRRSPACTSPAGGRACKKKKHTLLCPDFARG ACPRGQCQLLHRTQKRRRRARTSPAGSBATARSRVSASHG PRKPSASQRPTKRRSPAGCHARGRCPYIHDPERK ACPRGAQCQLLHRTQKRRRRRARTSPAGSBASHG PRKPSASGRPTKRSPAGGRAALTAAAVAAPPHCGGSASPSSKAS SSSSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAGPRVRAPARAPLTKOSGKPLHKFRL 6092 143 3190 KKRPPTGESSERPEAKVLHTKRIVFRLVERVVERVÜRLDLILCNKTAVQ	}			1
ALHQEK PVFVPAPAVALGAS/ASPPLATQTVVPLQHCKIPELPVQASIL PVFVPAPAVALGAS/ASPPLATQTVVPLQHCKIPELPVQASIL PVFVPAPAVALGAS/ASPPLATQTVVPLQHCKIPELPVQASIL FELQLFFCQLIALFVHYINIYKTVMWYPPSHPPSHTSLNPHLID FNLLMVTTIVLGRRPIGSIVKEASQRGKVSLFRSILLFLTRTFVV LITATGWSLCRSLIHLFRTYSFLNLL/FPLLSVMDVHSVPAABLR P\RKTSLFNHMASMGPRBAVSGLAKSRDYLLTLR\RRGSSTQDS CMARTPCP/PHACCLSPSLIRSEVEFLKMDFNNRMKSVLVSSML SAYYVAFVVWFVKNTHYYDKRWSCELFLLVSISTSVILMQHLL PASYCDLHKAAAHLGCUGKVDPALCSNVLQHBWTEECMWPQGV LVKHSKNYVKAYGHYNVAIPSDUSHFRPHFPFSKPLRIINILLI LEGAVIVVQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASFQRDLDHRFS SSRTREMEBKEILRRQIRLLGGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWKKYSLVNRPPG PSDPPADHAVRPLHGARGGQPPVPQGHVLERQVQLSQGGNVVIK VKPSKSGSASASGAQRGSLEFFBITWSDORPREGEGEPPRGQ LQPSRTRARGTCSVEDPLLVCQKEPGKPRWKSVGSVGGRAVIK VKPPSKSGSASASGAQRGSLEFFBITWSDORPREGEGEPPRGQ LQPSRTRARGTCSVEDPLLVCQKEPGKPRWKSVGSVGGRAVSIK VKRPGRTGSVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARAASPCKARASMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWGSEAGSKDHASQLSPVLSRSPSCD\RPAVCHSGLKPLSGE TPLSAYKVKSRYKITRRGSTSLPGDKKSGTSPAATAKSHLSIK RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAWRTAPTSKVIKTRYRIVKTPSPLSAPFPLSLPSWRA RRLSLSRSLVLNRLEPVASGGGKAQPGSPWRSKGYRCIGGVLY KVSANKLSKTSQQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAITQARQRREKRKSYCMYNRFFGRGNRGERCPYTHDPEKV AVCTRPVRGTCKKTDGTCPSFHHVSKEKMPVCSYFLKGICSNEN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTOKRRBARRAATSPAGSRGG ACPRGAQCQLLHRTOKRRBARRAATSRAGSRASGSSSSAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SSPSGAGPRVRAPARAPITKSOKPHHKIYRKVVEXVVERVURLDLLLCKKTAYQ	1		•	=
194 1560 PVFVPAPGAVLEQAS/ASPPLATQTVVPLQHCKIPELPVQASIL FELQLIFCQLIALFYHYINIYKTVWYPPSHPSHTSLMPHLID FRILMYTTIVLGREFIGSIVKEASQRGKVSLPRSILLFTRFTVV LTATGWSLCRSLIHLFRTYTYVLTVGREFIGSIVKEASQRGKVSLPRSILLFTRFTVV LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSVWDVHSVPAAELR P\RKTSLFHHMASMGPRRAVSGLAKSGRVLLITIR\RKGSSTQDS CMARTPCP\PHACCLSPSJLRSSVBFLKMDFNRMKWSVLVSSML SAYYVAFVPVWFVKNTHYYDKRWSCELFILLVSISTSVILMQHLL PASYCDLLHKAAAHLGCWQKVPPALGSNVLQHBYTEECMWPQGV LVKHSKNVYKAVQHYNVATASDSVSHPFFHFFPSKPLRINILLL LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VU.GKAYSYSASPQRDLDHHFS 6091 3279 412 SSRTRPMEEREILRRGGUPDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGARGGQPPVQQHVLBCQVQLSQGGNVVIK VKXPSKSGSASASGAQRGSLEFFEDTPWSDQRPRGEGBPPRGO LQPSRTFRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALSPRTQVALGSKLGSHSVASCAPQ LLGDRRVDAGHTOQPVPSSCAPPRTQVALGSKLGSHSVASCAPQ LLGDRRVDAGHTOQPVPSSCAPPADAGGRQAPSVKKASSPSASSSS SFRWQSEAGSKDHASQLSPVLRSPSGAPQARRASLWVTCR TKKFRKNNYKWAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEFKPRKPATSSKPGSAPSKYKKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVI KTRRGSTSLPGBKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVI KTRYRJVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSWWRSKGYRCIGGVIY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPSGSSRSLASRAVQ RSLAIIRQARQRREKRKEYVMYNNFGRCNRGERCPY HDDPEKV AVCTRPVRGTCKKTDDTCFFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKABVCSDFLKKYCPLGAKCKKHTLLCPDPARRG ACPRGAQCQLLHRTQKHRRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRGTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSSSPASLDHEAPSPLCHAAAAACSNRLCKLPSFISLQS SPSPGAQRQRVRAPRAADAAAAACSNRLCKLPSFISLQS SPSPGAQRQRVAPAPADLTKOKKPHRLDLLLCNKTAVQ	-			
FELQLFFCQLIALFVHYINIYTVWWYPPSHPPSHTSLNFHLID FNLLMVTTIVLGRRFIGSIVKEASGRKVSLFRSILLFITFTV LTATGWSLCFSILHFRTYSFLNLL/FPLLSWDVHSVPAABLR P\RKTSLFNHMASMGPRBAVSGLAKSRDYLLTLR\RRGSSTODS CMARTPCP/FHACCLSPSLIRSEVFLKMDFRWRKEVLVSSML SAYYVAFVPWFVKNTHYYDKRWSCELFLLVSISTSVILMQHLL PASYCDLLHKAAAHLGCWQKVDPALGSNULQHBWTEECMMPQGV LVKHSKNVYKAVGHYNVAIPSDVSHFRFHFFFSKPLRILNILL LEGAVIVYQLYSIMSSEKHQTISLALILFSNYYAFFKLLRDRL VLGKAXSYSASPQRDLDHRFS 6091 3279 412 SSRTREMEBKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTHSGRAFSARYPRSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGARGGQPPVPQQHVLERQVOLSQGGNVVIK VKPPSKSGSASASGAQRSSLEEFEDTPWSDQRPREGGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTOVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGPARPASGPRQAREASLVVTCR TMKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKKASSPSASSSS SFRWGSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RQALRGKSSPULKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVKTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRISLSRSLVLNRLRPVASGGGRAQPGSPWWRSKGTRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAITRQARQRREKRKEYGWNFRFGRCNRGERCPY HDDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKABVCSDFLKGYCPLGAKCKKKHTLLCPDPARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRGTPSSAALITAAAVAAPPHCPGGSASPSSSKAS SSSSSSSSPASLLDHEAPGLGCAALAAACSNRLCKLPSFISLQS SPSPGAQRVRAPRAPLTKDSKCPHIKPRL				~
FRILMYTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFIRTTV LTATGWSLCRSLHLFRTYSFLNLL/FPLLSVMDVHSVPAAELR P\RKTSLFNHMASMGPRBAVSGLAKSRDYLLTIR\RGRSTODS CMARTPCP/PHACCLSPSLIRSEVBFLKMDFNWRMKEVLVSSML SAYYVAFVPWFVKNTHYYDKRMSCEFFLLWSISTSVILMQHLL PASYCDLLHKAAAHLGWQKVDPALCSNVLOHPWTECCMPQGLV LVKHSKNVYKAVGHYNVAIPSDVSHFRFHFPFSKPLRILNILLL LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLHRFS 6091 3279 412 SSRTREMEEKEILRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGARGQPPVPQHVLERQVQLSQGNVVIK VKPPSKSGSASAGAQRGSLEEFEDTPWSDQRPRRGEGEPPRGQ LQPSRPTRAGGTCSVEDPLLVCQKEPGKPRWKSVGSVGDSPRE PRRTVSESVIAVKASFPSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTTQPVPSGSVGGPARPASGPRQAEASLVVTCR TNKFRKNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKKKASSPSASSS SFFMQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSIR RRQALRGKSSPVLKKTNNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVKTAPTSKVI KTRYRIVKTYPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLKTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKREYCMYYNKFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGACQLLHRTQKRTRSRRAATSPAPGGSASPSSKAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPAGQPRVRAPRAPLTKDSKPLHIKFRLY	6090	194	1560	
LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSVWDVHSVPAAELR P\RKTSLFNHMASMGPREAVSGLAKSRDYLTLTR\RRGSSTODS CMARTPCP/PHACCLSPSLTRSEVEFLKWDFNMRKEVLVSSML SAYYVAFVEVWFYKNTHYYDKRWSCELFLLVSISTSVILMQHLL PASYCDLHKAAAHLGGWQXVDPALCSNVLOHPWTEECMWPQGV LVKHSKNVYKAVGHYNVAIPSDVSHFRFHFPFSKPLRILNILLL LEGAVIVYQLYSLMSSEKWHGTISLALLLFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDHRFS 6091 3279 412 SSRTREMEEKEILRRQTRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWKKYSLWNRPPG PSDPPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQQNVVIK VKPPSKSGSASAGAQRGSLEEFEDTTWSDGRPRRGEGEPPRQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMKSVGSVGSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPQAREASLVVTCR TMKFRKNNYKWVAASSKSPVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPFRRPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLFGDKKSGTSPAATAKSHLSIR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVKTAFTSKVIKTRYRIVKKTPASPLSAPPFDLSLPSWRA RRLSLSRSLVLINRLRPVASGGGKAQPGSPWWRSKGYRCTGGVLY KVSANKLSKTSQGPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKKREYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRPVRGTCKKTDGTCPFSHVVSKEKMPVCSYFLKGICSNSN CPYSHYVYSRKAEVCSDFLKGYCPLGARCKKHTLLCPDPARRG ACPRGAQCQLLHRTQKRHSRRAATSPAGPGPSDATARSRVASHG PRKPSASQRPTRGTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPAGQPRVRAPRAPLTKDSKPLHIKFRLY	ı			
P\RKTSLFNHMASMGPREAVSGLAKSRDYLLTLR\RRGSSTQDS CMARTPCP/FHACCLSPSLIRSEVEFLKMDFNMRMKEVLVSSML SAYYVAPVPWFWYNTHYYDKRWSCELFLLWSISTSVTLMOHLL PASYCDLLHKAAAHLGCWQKVDPALCSNVLQHPWTEECMWPQGV LVMSKNVYKAVGHYNVAIPSDVSHFRFHFFFSKPLRTLNILLL LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDHRFS 6091 3279 412 SSRTREMEEKBILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGGNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPRBGEGEPPRGQ LQPSRFTRARGTCSVEDPLLVCQKEPGKPRWVKSVGSVGDSPR PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TMKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWGEEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGKKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTYRIVKKTPASPLSAPPPPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGTCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARGREKKSYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRRAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSWASHG PRKPSASGRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSSPPASLDHEAPSLGEAALAAACSNRLCKLPSFISLQS SPPGAQPRVRAPRAPLITKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEARVLHTKRLYVRAVVEAVIREDLILCNKTAYQ	1		1	··· · · · ·
CMARTPCP/PHACCLSPSLIRSEVEFLKMDFNWRMKEVLVSSML SAYYVAFVPWWFVRNTHYYDRWSCZLFLLVSISTSVILMQHLL PASYCDLHKAAAHLGCWQKVDPALCSNVLQHPWTEECMWPQGV LVKHSKNVYKAVGHYNVAIPSDVSHFRFHFFFFSKPLRILNILLL LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDHRFS 6091 3279 412 SSRTREMEEKSILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGARGGQPVPQQHVLERQVQLSQGONVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPRBGEGEPPRGQ LQPSRFTRARGTCSVEDPLLVCQKEPGKPRWVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLGGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLISKTSGQPSDAGSRPLLRTGRLDPAGSCGRSLASRAVQ RSLAIIRQARQRREKRSYCMYYNRFGRCNRGERCPYHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHYVYSTCKKTGGTCPFSHVSKEKMPVCSYFLKGICSNSN CPYSHYVYSTKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPPGAQQPRVRAPRAPLTKDSGKPLHIKPRL	1		1.	
SAYYVAFVPWFVKNTHYYDKRWSCELFLLVSISTSVILMQHLL PASYCDLLHKAAAHLGCWQKVDPALCSNVLQHBWTEECMWPQGV LVKHSKNVYKAVGHYNVAI PSDVSHFRFHFFFSKPLRILNILLL LEGAVIVYQLVSLMSSEKHHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDHRFS 6091 3279 412 SSRTREMEEKEILRRQIRLIQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRYYSSHHGPSWRKKYLVNRPPG PSDPPADHAVRPLHGARGGQP PVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLFGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLV KVSANKLSKTSGQPSDAGSRPLLKTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKKEYCMYYNRFGRCNRGERCPYHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAFGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDGKPLHIKPRL SPSPGAQPRVRAPRAPLITKDSKPLHIKFRLF	1		'	' · · · · · · · · · · · · · · · · · ·
PASYCDLIHKAAAHLGCWQKVDPALCSNVLQHPWTEECMWPQGV LUKHSKNVYKAVGHYNVALPSDVSHFRFHFFFSKPLRILNILLL LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLERDRL VLGKAYSYSASPQRDLDHRFS 6091 3279 412 SSRTREMEEKEILRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRFSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGARGQQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRQQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWKKSVGSVGSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPPAPASGPQAREASLVVTCR TIKKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKRKPATSSKPGSAPSKYKKKASSPSASSS SFRWGSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKYEGS TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR RQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTYRIVKKTPASPLSAPFPFLSLPSWRA RRLSLSSRLVLNRLRPVASGGKAQPGSPWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLKTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVVYSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTOKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSSPPASLDEBAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRIDDLILCNKTAYQ		· ·		
LVKHSKNVYKAVGHYNVAIPSDVSHFRFHFFFSKPLRILNILLL LEGAVIVYQLYSIMSSEKWHQTISLALILFSNYYAFFKLIRDRL VLGKAYSYSAS PQRDLDHRFS 6091 3279 412 SSRTREMEEKE ILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGARGQPPVPQOHVLERQVQLSGGONVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TMKFFKRNYKWVAASSKSPRVARRALSPRVAABENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSQQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKREYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKHTLLCPDFARRG ACPRGAQCQLLHRTQKHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS				
LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSAS PQRDLDHFS 6091 3279 412 SSRTREMEEKEILRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPHGARGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWKKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TMKFRKNNYKWVAASSKSFRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATKASHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPFPPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLKTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKREYCMYYNRFGRCNRGERCPY HDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKRPL 6092 143 3190 AKAPPTGESSEPERKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ		·	ì	-
VLGKAYSYSAS PQRDLDHRFS 6091 3279 412 SSRTREMEEKEI LRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVI K VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPRGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLFGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAI IRQARQRREKKEYCMYYNRFGRCNRGERCPY IHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSAHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSSSPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPS PGAQPRVRAPRAPLTKDSGKPLHIKRPL 6092 143 3190 AKAPPTGESSEPERKVLHTKRLYRAVEAVHRLDLILCNKTAYQ			,	
G091 3279 412 SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWKKSYGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGBAPSKYKWKASSPSASSSS SFRWGSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTBSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSKKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRELYRAVVERVHRLDLILCNKTAYQ				
WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGONVJK VKPPSKGSASASAGRGSLEEFEDTPWSDQRPRGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRRPATSSKPGSAPSKYKAKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKREYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVGGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSSPSPALDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKFRL				
PSDPPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPFPPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPPRAPLTKDSGKPLHIKPRL	6091	3279	412	
VRPPSKSGSASAGQRGS LEEFEDTPWSDQRPRBGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TMKFRKMNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLLADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLHRTGKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPITKDSGKPLHIKPRL			1	-
LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRRTSSKPGSAPSKYKKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHYVYSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL		1		
PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTTYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWRKSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL	1			
LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTTYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKREYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ	1			
TNKFRKNNYKWAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTTYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKREYCMYYNRFGRONRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ				
KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKREYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ				
SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQREKKREYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ				
TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKREYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ		İ		
RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKREYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ	1			
SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKREYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS SSSSSSSPPASLDHEAPSLQEAALAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ			İ	
RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSPPASLDHEAPSLQEAALAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ				
KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ	1			
RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ				
AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ				
CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ	1			
ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ	1		1	
PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ		1		
SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ	-		1	ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG
SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL 6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ	1		1	
6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ				
6092 143 3190 AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ EVFKPENISLRNKLRELCVKLMFLHPVDYGRKAEELLWRKVYYE				
EVFKPENISLRNKLRELCVKLMFLHPVDYGRKAEELLWRKVYYE	6092	143	3190	AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ
	j	1	ł	EVEKPENISLRNKLRELCVKLMFLHPVDYGRKAEEDLWRKVYYE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	bequence	\=possible nucleotide insertion)
ļ	sequence		VIQLIKTNKKHIHSRSTLECAYRTHLVAGIGFYQHLLLYIQSHY
}			QLELQCCIDWTHVTDPLIGCKKPVSASGKEMDWAQMACHRCLVY
j	1	ļ	LGDLSRYQNELAGVDTELLAERFYYQALSVAPQIGMPFNQLGTL
	1	Ì	AGSKYYNVEAMYCYLRCIQSEVSFEGAYGNLKRLYDKAAKMYHQ
1			LKKCETRKLSPGKKRCKDIKRLLVNFMYLQSLLQPKSSSVDSEL
j		ļ	TSLCOSVLEDFNLCLFYLPSSPNLSLASEDEEEYESGYAFLPDL
ł		}	
}	}		LIFOMVIICLMCVHSLERAGSKQYSAAIAFTLALFSHLVNHVNI
1	1	(RIQAELEEGENPVPAFQSDGTDEPESKEPVEKEEEPDPEPPPVT
ļ		}	PQVGEGRKSRKFSRLSCLRRRRHPPKVGDDSDLSEGFESDSSHD
}		{	SARASEGSDSGSDKSLEGGGTAFDAETDSEMNSQESRSDLEDME
}			EEEGTRSPTLEPPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQ
}	į.		MFQTKRCFRLAPTFSNLLLQPTTNPHTSASHRPCVNGDVDKPSE
1			PASEEGSESEGSESSGRSCRNERSIQEKLQVLMAEGLLPAVKVF
1			LDWLRTNPDLIIVCAQSSQSLWNRLSVLLNLLPAAGELQESGLA
ł		1	LCPEVQDLLEGCELPDLPSSLLLPEDMALRNLPPLRAAHRRFNF
1		1	DTDRPLLSTLEESVVRICCIRSFGHFIARLQGSILQFNPEVGIF
1	į.		VSIAQSEQESLLQQAQAQFRMAQEEARRNRLMRDMAQLRLQLEV
ļ	1	1	SQLEGSLQQPKAQSAMSPYLVPDTQALCHHLPVIRQLATSGRFI
ł	}	{	VIIPRTVIDGLDLLKKEHPGARDGIRYLEAEFKKGNRYIRCQKE
j		l .	VGKSFERHKLKRQDADAWTLYKILDSCKQLT\LAQGAGEEDPSG
į ·			MVTIITGLPLDNPSLLSGPMQAALQAAAHASVDIKNVLDFYKQW
Ì		{ .	KEIG
6093	76	1002	ACGRRAMLALRVART/SRWGAL\RGAVWAPGTRPSKRRACWALL
ţ		†	PPVPCCLGCLAERWRLRPAALGLRLPGIGQRNHCSGAGKAAPR\
]			PAAGAGAAAEAPGGQWGPASTPSLYENPWTIPNMLSMTRIGLAP
		1.	VLGYLIIEEDFNIALGVFALAGLTDLLDGFIARNWANQRSALGS
J		1	ALDPLADKILISILYVSLTYADLIPVPLTYMIISRDVMLIAAVF
1		∤.	YVRYRTLPTPRTLAKYFNPCYATARLKPTFISKVNTAVQLILVA
{		[ASLAAPVFNYADSIYLQILWCFTAFTTAASAYSYYHYGRKTVQV
			IKD
6094	23	1010	PFLRCLRGDQKAKMSERKVLNKYYPPDFDPSKIPKLKLPKDRQY
			VVRLMAPFNMRCKTCGEYIYKGKKFNARKETVQNEVYLGLPIFR
[FYIKCTRCLAEITFKTDPENTDYTMEHGATRNFQAEKLLEEEEK
	:	1	RVQKEREDEELNNPMKVLENRTKDSKLEMEVLENLQELKDLNQR
			QAHVDFEAMLROHRLSEEERRRQQQEEDEQETAALLEEARKRRL
}			LEDSDSEDEAAPSPLQPALRPNPTAILDEAPKPKRKVEVWEQSV
		ļ	GSLGSRPPLSRLVVVKKAKADPDCSNGQPQA/APHPRSPAEQEG
}	}	}	GQPYTPDAWRVLPEPTGCIPGQ
6095	1	1599	TRGRAAERSRGRGHGFLGGGFA\SVVDYFPSEDFYRCGYCKNES
0095		1333	GSRSNGMWAHSMTVQDYQDLIDRGWRRSGKYVYKPVMNQTCCPQ
1		}	YTIRCRPLQFQPSKSHKKVLKKMLKFLAKGEVPKGSCE\DEPMD
}		}	STMDDAVAGDFALINKLDIQCDLKTLSDDIKESLESEGKNSKKE
1		1	
	L	<u> </u>	EPQELLQSQDFVGEKLGSGEPSHS

TRADOCS:1416257.1(%CSH011.DOC)

			lades and second containing gignal montide
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Giutamic Acid, Fernenylatanine, Gedrycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			VKVHTVPKPGKGADLSKPPCRKAKEIRKERKRLKLMQQNPAGEL
	1		EGFQAQGHPPSLFPPKAKSNQPKSLEDLIFESLPENASHKLEVR
1			VVRSSPPSSQFKATLLESYQVYKRYQMVIHKNPPDTPTESQFTR
			FLCSSPLEAETPPNGPDCGYGSFHQQYWLDGKIIAVGVIDILPN
Į.			CVSSVYLYYDPDYSFLSLGVYSALREIAFTRQLHEKTSQLSYYY
			MGFYIHSCPKMKYKGQYRPSDLLCPETYVWVPIEQCLPSLENSK
		•	YCRFNQDPEAVDEDRSTEPDRLQVFHKRAIMPYGVYKKQQKDPS
1			EEAAVLQYASLVGQKCSERMLLFRN
6096	2277	575	ORVRAALLSSAMEDSEALGFEHMGLDPRLLQAVTDLGWSRPTLI
. 0030	22//	2/3	QEKAIPLALEGKDLLARARTGSGKTAAYAIPMLQLLLHRKATGP
1		i	VVEQAVRGLVLVPTKELARQAQSMIQQLATYCARDVRVANVSAA
			EDSVSQRAVLMEKPDVVVGTPSRILSHLQQDSLKLRDSLELLVV
1		1	DEADLLFSFGFEEELKSLLCHLPRIYQAFLMSATFNEDVQALKE
			LILHNPVTLKLQESQLPGPDQLQQFQVVCETEEDKFLLLYALLK
1.		ľ	
1			LSLIRGKSLLFVNTLERSYRLRLFLEQFSIPTCVLNGELPLRSR
	· ·		CHIISQFNQGFYDCVIATDAEVLGAPVKGKRRGRGPKGDKASDP
i			EAGVARGIDFHHVSAVLNFDLPPTPEAYIHRAGRTARANNPGIV
1			LTFVLPTEQFHLGKIEBLLSGENRGPILLPYQFRMEEIEGFRYR
1			CRDAMRSVTKQAIREARLKEIKEBLLHSEKLKTYFEDNPR\DLQ
i			LLRHDLPLHPAVVKPHLGHVPDYLVPPALRGLVRPHKK\GRSCL
1			PLVGRPREQSPRTHCAASSTKERNSDPQPSPPEVVGPLWS
6097	1673	192	APGTMSGGKKKSSFQITSVTTDYEGPGSPGASDPPTPQPPTGPP
			PRLPNGEPSPDPGGKGTPRNGSPPPGAPSSRFRVVKLPHGLGEP
			YRRGRWTCVDVYERDLEPHSFGGLLEGIRGASGGAGGRSLDSRL
	i :		ELASLGLGAPTPPSGLSQGPTSWLRPPPTSPGPQARSFTGGLGQ
ļ	· ·		LVVPSKAKAEKPPLSASSPQQRPPEPETGESAGTSRAATPLPSL
			RVEAEAGGSGARTPPLSRRKAVDMRLRMELGAPEEMGQVPPLDS
1			RPSSPALYFTHDASLVHKSPDPFGAVAAQKFSLAHSMLAISGHL
1.	[DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQI
1			RELAERNAALEQENGLLRALA\SPEQLGSAGPPRGVPR\LGPPA
			PNGPFVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVFPGVG
1		į	VOALSNGPWSPGPLPHLLIIPSLDGGGEGFRTGRQQGAPFGEET
j		ļ	OPPPSLPGTPQQ
6098	168	1074	NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD
			EGKIPKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK
			RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE
			NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL
	}		\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR
			TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D
	1	}	ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD
6000	120	1074	NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKELD
6099	168	1074	EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK
			RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE
1			
1			NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL
1			\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR
1	1		TAWEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D
<u></u>		<u> </u>	ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD
6100	2	713	FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL
			QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF
1			RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM
		1	VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN
1			VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP
1	1	1	SASQRNSRDIGSNSGCC
6101	1	1399	FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR
		1	GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAQIAEDKPY
1		1	AELWMGTHPRGDAKILDNRISQKTLSQWIAENQDSLGSKVKDTF
L		- L	

	I Dec 31 about	1 m 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
ID NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
140:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	1	S=Serine, T=Threonine, V=Valine,
}	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			NGNLPFLFKVLSVETPLSIQAHPNKELAEKLHLQAPQHYPDANH
			KPEMAIALTPFQGLCGFRPVEEIVTFLKKVPEFQFLIGDEAATH
1			LKQTMSHDSQAVASSLQSCFSHLMKSEKKVVVEQLNLLVKRISQ
1			QAAAGNNMEDIFGELLLQLHQQYPGDIGCFAIYFLNLLTLKPGE
			AMFLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTLCE
1			MLSYTPSSSKDRLFLPTRSQEDPYLSIYDPPVPDFTIMKA\EVP
J .			G\SVTEYKDLALDSASILLMVQGTVIASTPTTQTPIPLQRGGVL
			FIGANESVSLKLTEPKDLLIFRACCLL
6102	70	2415	QTPQATLAANGAEDSRGGEMLPAGEIGASPAAPCCSESGDERKN
			LEEKSDINVTVLIGSKQVSEGTDNGDLPSYVSAFIEKEVGNDLK
			SLKKLDKLIEQRTVSKMQLEEQVLTISSEIPKRIRSALKNABES
			KQFLNQFLEQETHLFSAINSHLLTAQPWMDDLGTMISQIEEIER
			HLAYLKWISQIEELSDNIQQYLMTNNVPEAASTLVSMAELDIKL
	,		QESSCTHLLGFMRATVKFWHKILKDKLTSDFEEILAQLHWPFIA
			PPQSQTVGLSRPASAPEIYSYLETLFCQLLKLQTSHELLTEPK\
]			HSQKNTLFLPPLLSS/WPIQVMLTPLQKRFRYHFRGNRQTNVLS
•			KPEWYLAQVLMWIGNHTEFLDEKIQPILDKVGSLVNARLEFSRG
			LMMLVLEKLATDIPCLLYDDNLFCHLVDEVLLFERELHSVHGYP
			GTFASCMHILSEETCFQRWLTVERKFALQKMDSMLSSEAAWVSQ
,			YKDITDVDEMKVPDCAETFMTLLLVITDRYKNLPTASRKLQFLE
1 1			LQKDLVDDFRIRLTQVMKEETRASLGFRYCAILNAVNYISTVLA
1			DWADNVFFLQLQQAALEVFAENNTLSKLQLGQLASMESSVFDDM
			INLLERLKHDMLTRQVDHVFREVKDAAKLYKKERWLSLPSQSEQ
]			AVMSLSSSACPLLITLRDHLLQLEQQLCFSLFKIFWQMLVEKLD
	•	-	VYIYQEIILANHFNEGGAAQLQFDMTRNLFPLFSHYCKRPENYF
			KHIKEACIVLNLNVGSALTAGKDVLPVQLQGSFPAT
6103	207	2523	ESNSTMTTYLEFIQQNEERDGVRFSWNVWPSSRLEATRMVVPVA
			ALFTPLKERPDLPPIQYEPVLCSRTTCRAVLNPLCQVDYRAKLW
	:		ACNFCYQRNQFPPSYAGISELNQPAELLPQFSSIEYVVLRGPQM
1 1			PLIFLYVVDTCMEDEDLQALKESMQMSLSLLPPTALVGLITFGR
	,		MVQVHELGCEGISKSYVFRGTKDLSAKQLQEMLGLSKVPVTQAT
1			RGPQVQQPPPSNRFLQPVQKIDMNLTDLLGELQRDPWPVPQGKR
			PLRSSGVALSIAVGLLECTFPNTGARIMMFIGGPATQGPGMVVG
1 1	j		DELKTPIRSWHDIDKDNAKYVKKGTKHFEALANRAATTGHVIDI
·			YACALDQTGLLEMKCCPNLTGGYMVMGDSFNTSLFKQTFQRVFT
			KDMHGQFKMGFGGTLEIKTPR\EIKISGAIGPCVSLNSKGPCVS
	<u>:</u>		ENEIGIGGTCQWK1CGLSPTTTLAIYFEVVNQHNAPIPQGG\RG
			A\IQFVTQY\QHSSGQRRIRVTTIARN\WADAQTQIQNIAASFD
1 1			QEAAAILMARLAIYRAETEEGPDVLRWLDRQLIRLCQKFGEYHK
			DDPSSFRFSETFSLYPQFMFHLRRSSFLQVFNNSPDESSYYRHH
 			FMRQDLTQSLIMIQPILYAYSFSGPPEPVLLDSSSILADRILLM
			DTFFQILIYHGETIAQWRKSGYQDMPEYENFRHLLQAPVDDAQE
]			ILHSRFPMPRYIDTEHGGSQARFLLSKVNPSQTHNNMYAWGQES
6104	3.24	722	GAPILTDDVSLQVFMDHLKKLAVSSAA
0104	124	732	KVSEYIILSKDKILFHALAMLVLVVSPWSAARGVLRNYWERLLR
			KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL
			LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH
1	1		LKQKHVLCAYCYEKVCKETAEIRRQIGKQEGGPFKAPTIETVVL
6105			YTGETPSEQDQGKRIIERDRKRPSWFTQN
6105	3	989	PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAVPLLLLCF
]	1		GSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHF
]			CGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAM
[YARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPD
, .		. i	PSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDT\PR
] [l		
			CNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSAGPLV CLVGQSWLQAGVISWGEGCARONRPGVYIRVTAHHNWIHRIIPK

050	Dec 31 and 3	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted		(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			LQVQPSEVGRPEVTPPGPGAP
6106	3	1302	GRPPTAPHTGRPPTANRGDPRLDLKRGCARLLTSIESRGRPAAS
0100	ļ		AGLERDRCALERWPLERAPLARATERRAGSPERCAPEPRACPOG
		·	WSRARHOPGGLCLLLLLLCOFMEDRSAQAGNCWLRQAKNGRCQV
	ļ		LYKTELSKBECCSTGRLSTSWTEEDVNDNTLFKWMIFNGGAPNC
]		IPCKETCENVDCGPGKKCRMNKKNKPRCVCAPDCSNITWKGPVC
			GLDGKTYRNECALLKARCKEQPELEVQYQGRCKKTCRDVFCPGS
	,		STCV\VDQTNNAYCVTCNRICPEPASSEQYLCGNDGVTYS\SAC
]			1 ' "
			HLRKATCLLGRSIGLAYEGKCIKAKSCEDIQCTGGKKCLWDFKV
1		-	GRGRCSLCDELCPDSKSDEPVCASDNATYASECAMKEAACSSGV
			LLEVKHSGSCNSISEDTEEEEEDEDQDYSFPISSILEW
6107	623	168	SRCSSPRPEPGRGRGK/LSPSEHRKWVEVFKACDEDHKGYLSRE
[DFKTAVVMLFGYKPSKIEVDSVMSSINPNTSGILLEGFLNIVRK
1			KKEAQRYRNEVRHIFTAFDTYYRGFLTLEDFKKAFRQVAPKLPE
			RTVLEVFREV\DRDS\DGHVSF
6108	3	1348	GGSLRFSPPRVPSCSRVFCPVPPGGCGLPSPMSASRPQSPTTPW
İ	!		CLPRRYMKHKRDDGPEKQEDEAVDVTPVMTCVFVVMCCSMLVLL
			YYFYDLLVYVVIGIFCLASATGLYSCLAPCVRRLP\SASAGESA
			LLAPTIPHNSLPYFHKRPQARMLLLALFCVAVSVVWGVFRNEDQ
l	ľ	1	WAWVLQDALGIAFCLYMLKTIRLPTFKACTLLLLVLFLYDIFFV
-			FITPFLTKSGSSIMVEVATGPSDSATREKLPMVLKVPRLNSSPL
1	ì		ALCDRPFSLLGFGDILVPGLLVAYCHRFDIQVQSSRVYFVACTI
i .			AYGVGLLVTFVALALMQRGQPALLYLVPCTLVTSCAVALWRREL
1			GVFWTGSGFAKVLPPSPWAPAPADGPQPPKDSATPLSPQPPSEE
1		1	PATSPWPAEQSPKSRTSEEMGAGAPMREPGSPAESEGRDQAQPS
	·		PVTOPGASA
		1201	CRSRAGAASGAILEGTKLRRQRVDTNKPLDPLVPSALRAAMLY
6109	1	1381	LEDYLEMIEQLPMDLRDRFTEMREMDLQVQNAMDQLEQRVSEFF
1			
į ·		•	MNAKKNKPEWREEQMASIKKDYYKALEDADEKVQLANQIYDLVD
1			RHLRKLDQELAKFKMELEADNAGITEILERRSLELDTPSQPVNN
1	Į.		HHAHSHTPVEKRKYNPTSHHTTTDHIPEKKFKSEALLSTLTSDA
1			SKENTLGCRNNNSTASSNNAYNVNSSQPLGSYNIGSLSSGTGAG
		,	GI\TMAAAQAVQATAQMKEGRRTSSLKASYEAFKNNDFQLGKEF
			SMARETVGYSSSSALMTTLTQNASSSAADSRSGRKSKNNNKSSS
ľ		1	QQSSSSSSSSSSSSSSSSSSTVVQEISQQTTVVPESDSNSQVDWT
			YDPNEPRYCICNQVSYGEMVGCDTQDCPIEWFHYGCVGLTEAPK
	1	:	GKWYCPQCT\AAMKRRGSRHK
6110	77	2464	ACPSAATMSDQDHSMDEMTAVVKIEKGVGGNNGGNGNGGGAFSQ
]		ARSSSTGSSSSTGGGGQESQPSPLALLAATCSRIESPNENSNNS
			QGPSQSGGTGELDLTATQLSQGANGWQIISSSSGATPTSKEQSG
			SSTNGSNGSESSKNRTVSGGQYVVAAAPNLQNQQVLTGLPGVMP
			NIQYQVIPQFQTVDGQQLQFAATGAQVQQDGSGQIQIIPGANQQ
1			IITNRGSGGNIIAAMPNLLQQAVPLQGLANNVLSGQTQYVTNVP
			VALNGNITLLPVNSVSAATLTPSSQAVTISSSGSQESGSQPVTS
			GTTISSASLVSSQASSSFFTNANSYSTTTTTSNMGIMNFTTSG
1			SSGTNSQGQTPQRVSGLQGSDALNIQQNQTSGGSLQAGQQKEGE
		1	Q\NQQTQAAPKSLSRPQLVQGG\QALQ\AFQAAPLSGQTFTTQA
	1		ISOETLONLOLOAVPNSGPIIIRTPTVGPNGQVSWQTLQLQNLQ
			VQNPQAQTITLAPMQGVSLGQTSSSNTTLTPIASAASIPAGTVT
			VONPOAQIITTLAPMOGVSLGQTSSSNIILITPIASAASIPAGIVI
		1	VNAAQLSSMPGLQTINLSALGTSGIQVHPIQGLPLAIANAPGDH
1			GAQLGLHGAGGDGIHDDTAGGEEGENSPDAQPQAGRRTRREACT
			CPYCKDSEGRGSGDPGKKKQHICHIQGCGKVYGKTSHLRAHLRW
1	}		HTGERPFMCTWSYCGKRFTRSDELQRHKRTHTGEKKFACPECPK
			RFMRSDHLSKHIKTHQNKKGGPGVALSVGTLPLDSGAGSEGSGT
			ATPSALITTNMVAMEAICPEGIARLANSGINVKEGGQFCSPINT
			SANGF
·		<u> </u>	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
6111	1637	797	RVDPRVRGAMAPWGKRLAGVRGVLLDISGVLYDSGAGGGTAIAG
ł		İ	SVEAVARLKRSRLKVRFCTNESQKSRAELVGQLQRLGFDISEQE
1	}		VTAPAPAACQILKERGLRPYLLIHDGV\ASEFDQIDTS/STPNC
			VVIADAGESFSYQNMNNAFQVLMELEKPVLISLGKGRYYKETSG
1			LMLDVGPYMKALEYACGIKAEVGGKPSPEFFKSALQAIGVEAHO
		İ	AVMIGDDIVGDVGGAQRCGMRALQVRTGKFRPSDEHHPEVKADG
L	1		YVDNLAEAVDLLLQHADK
6112	77	196	MSSHKSFKSKRFLAKKQKPNRPILQWIWLKTGNKIRHNWK
6113	1779	567	WEGRSWAACGVNLQGAWGERSGVRASEAESPGKRADVSWWSRQL
			ETMVDHLANTEINSQRIAAVESCFGASGQPLALPGRVLLGEGVL
			TKECRKKAKPRIFFLFNDILVYGSIVLNKRKYRSQHIIPLEEVT
			LELLPETLQAKNRWMIKTAKKSFVVSAASATERQEWISHIEECV
] .			RRQLRATGRPA\STEHAAPWIPDKATDICMRCTQTRFSALTRRH
1			HCRKCRVVVCAECSRQRFLLPRLSPKPVRVCSLCYRELAAQQRK
		•	EEAEEQGAGVPRAASHLARPICGRPVEMTMTPTRTRRAAGTATG
1			PAAWSSTPRGWPGLPSTADPRPAEHLSPSQLHCPGPQEGSSRSC
			PGLRDPIPWWQVQRWGVALSGLPVPFCWTLCPYGFTAGNAFPFR
6114	010	546	KPQNTHRSW
0114	818	246	PTSRPRPSPGSPAMSWSACVSAAPSSSWPASSSWPCGPRRCCTR
			RRRCSPRCGLAAGSMCSCSPSWRCTPVPACWPSPPP\PAEQVQC
			GHLPPHADRRALRLPVAAPARGPGPGHPAGPAGPRPARTPPASP HGPGRPTVPAPPCPLLAATEPTPSRPHQRWTREDRMLGRGSQVT
1			GRPOWFLRGLVLFSL
6115	324	71	DVCGRVCAHPHLYTHIHMHICAHAC\IHTHAQLC/ITASHALAH
			SHLYTCMVMLTASHTPSHTHPHTAVHKEHRADVLRGTLTPLR
6116	595	1430	TGVMPPGRWHAA/ISSSGPVFEGARA\LQTVKKEEEDESYTPVQ
			AARPQTLNRPGQELFRQLFRQLRYHESSGPLETLSRLRELCRWW
			LRPDVLSKAQILELLVLEQFLSILPGELRVWVQLHNPESGEE\L
			WPCWRSCRGTLMGHPGGTRALP\EPRCALDGYRS\LRSAQIWSL
			ASPLRSSSALGDHLEPPYEIEARDFLAGQSDTPAAQMPALFPRE
		•	GCPGDQVTPTRSLTAQLQETMTFKDVEVTFSQDEWGWLDSAQRN
			LYRDVMLENYRNMASLGK
6117	1433	. 222	VGVPSPAPPCSWEVGPGGGWTPGILKEGQGGRRTPLLLLATRTR
			GLLSLFPPAAMHPAAFPLPVVVAAVLWGAAPTRGLIRATSDHNA
[]			SMDFADLPALFGATLSQEGLQGFLVEAHPDNACSPIAPPPPAPV
	•	•	NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVHNVNSNELLNM
		*	VWNSEBIQQQIWIPSVFIGERSSEYLRALFVYEKGARVLLVPDN
			TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHRKRLQRNRLTK
			\EQLKQI\PTHDYQKGDQYDVCAICLDBYEDGDKLRVLPCAHAY
			HSRCVDPWLTQTRKTCPICKQPVHRGPGDEDQEEETQGQEEGDB
			GEPRDHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL
6118	1044	247	SPPSSPVILV
	1022	44/	STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK
}	1		KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQEKQERRKGK
	ł		EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE
	İ		DSQMEFLEIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP
			ITWKAKKYLHQLIAANPVLPLVVFANKODLEAAYHITDIHEALA
	ļ		II
6119	1217	462	DPRFVTENTTKAPAORRTTOPRSSREGTLRSTMEYLSALNPSDL
		102	LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR
	•	Î	QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM
	1	ĺ	VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKONPR
	Ì		DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ
	j		GLGHMLLGISSTLRHAVEGAEQWQQKGRLHSY
		1	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
•	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
J	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
•	sequence	Bedacuce	\=possible nucleotide insertion)
6120	785 '	179	LERAGGGGLSSRALVGSGACLSLVARANGKGLPRGRKEFVEAVR
6120	/63	1,3	VRYVAFRYRTPRAVCLRLWSCRREVIMSGRGKQGGKVRAKAKSR
			SSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAE
]			ILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQG
İ			G\VLPNIQAVLLPKKTESQKDEGANDP
6121	1612	107	FVRAOARGSROPVRRPLLGAGSRLRCRSCGRMEPLKVEKFATAN
6121	1612	107	RGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKE
ĺ	İ		KLMRCSOCRVAKYCSAKCOKKAWPDHKRECKCLKSCKPRYPPDS
ļ			
Ì	Ī		VRLLGRVVFKLMDGAPSESEKLYSFYDLESNINKLTEDKKEGLR
l			QLVMTFQHFMREEIQDASQLPPAFDLFEAFAKVICNSFTICNAE
			MQEVGVGLYPSISLLNHSCDPNCSIVFNGPHLLLRAVRDIEVGE
			ELTICYLDMLMTSEERRKQLRDQYCFECD\CFRCQTQDKDADML
i		!	TGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCQAIISSNSERL
			PDINIYQLKVLDCAMDACINLGLLEEALFYGTRTMEPYRIFFPG
			SHPVRGVQVMKVGKLQLHQGMFPQAMKNLRLAFDIMRVTHGREH
			SLIEDLILLLE/AMRRQHQSILRERSQREIRRVSLLNALLRSHT
			LCFVSCVNLSYWKFCSVFV
6122	2	2324	RFRKMADGGAASQDESSAAAAAAADSRMNNPSETSKPSMESGDG
			NTGTQTNGLDFQKQPVPVGGAISTAQAQAFLGHLHQVQLAGTSL
!	\		QAAAQSLNVQSKSNEESGDSQQPSQPSQQPSVQAAIPQTQLMLA
	•		GGQITGLTLTPAQQQLLLQQAQAQAQLLAAAVQQHSASQQHSAA
1			GATISASAATPMTQIPLSQPIQIAQDLQQLQQLQQQNLNLQQFV
1			LVHPTTNLQPA\QFIISQTPQGQQGLLQA\QNLLTQLPRQSQAN
l]	LLQSQPRI\TLTSQPATPTCTIAATPIQTLPQSQSTPKRIDTPS
	•		LEEP\SDLEELEQFAKTFKQRRIKLGFT\QGDAGLAMVKLYGND
· ·			FSPTTIFRFEALNLSFKNMCKLKPLLEKWLNDAENLSSDSSLSS
1			PSALNSPGIEGLSRRRKKRTSIEA\NIRVALEKSFLEN\QKPTS
[EEITMIADQLNMEKGVIRVWFCNRRQKEKRINPPSSGG\TSSSP
1			IKAIFPSPTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVTNLS
		ļ '	VTGTSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEA
1			SSASETSTTQTTSTPLSSPLGTSQVMVTASGLQTA/AQLLPFKG
			AAQLPANASLAAMAAAAGLNPSLMAPSQFAAGGALLSLNPGTLS
1			GALSPALMSNSTLATIQALASGGSLPITSLDATGNLVFANAGGA
			PNIVTAPLFLNPQNLSLLTSNPVSLVSAAAASAGNSAPVASLHA
			TSTSAESIQNSLFTVASASGAASTTTTASKAQ
6123	3	2944	HLLHRWFGTDMQMINFTTGEFQLTEACPYLGTHSEESRFGILHL
			HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG
]		,	ARELLKVGGRLPGAGGSLRFKVPESTLMDCRRQLKDSKQILSIT
			KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT
1			SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL
			PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM
			EFMKTRQRQNASSSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS
			DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK
1			HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI
			SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS
			MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL
			PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK
1			PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGNL
			QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS
	!		SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK
1			KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM
1			VDAOHFLPAGDSVSQNDFPSBAPISLNLSHNICNPMTGNSLPQY
			AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE
			NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLELNDYNAFP
			EENMNYANGFPCPADVQTDFIDHNSQSTWNTPP\NMPAS\WGNA
			QFPSSSRPYLKSTPKACLPMSGLFGPI\WAP\QSDVYENCCPIN
L		<u> </u>	1-1

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	i -	\=possible nucleotide insertion)
			PTTEHSD/THMENQA\VVCKEYYPGF\NPFRAYMNLDIWTTT\A
			NRNANFPLSRDSSYCGNV
6124	1573	236	SDEALRLAGERGMGRVQLFEISLSHGRVVYSPGEPLAGTVRVRL
			GAPLPFRAIRVTCIGSCGVSNKANDTAWVVEEGYFNSSLSLADK
			GSLPAGEHSFPFQFLLPATAPTSFEGPFGKIVHQVRAAIHTPRF
1			SKDHKCSLVFYILSPLNLNSIPDIEQPNVASATKKFSYKLVKTG
i			SVVLTASTDLRGYVVGQALQLHADVENQSGKDTSPVVASLLOKV
1			SYKAKRWIHDVRTIAEVEGAGVKAWRRAQWHEQILVPALPOSAL
1			PGCSLIHIDYYLQVSLKAPEATVTLPVFIGNIAV/NPCPSEPPA
			RPGAASWGPTPGG\PSAPPQEEAEARAAAGGPHFLDPVFLSTKS
ļ			HSQRQPLLATLSSVPGAPEPCPQDGSPASHPLHPPLCISTGATV
			PYFAEGSGGPVPTTSTLILPPEYSSWGYPYEAPPSYEQSCGGVE
6125			PSLTPES
0125	1	904	KTCPKLTCAFTVSVPDSCCRVCRGDGELSWEHSDGDIFRQPANR
	ļ		EARHSYHRSHYDPPPSRQAGGLSRFPGARSHRGALMDSQQASGT
			IVQIVINNKHKHGQVCVSNGKTYSHGESWHPNLRAFGIVECVLC
			TCNVTKQECKKIHCPNRYPCKYPQKIDGKCCKVCPG/KKAKEBL
1			PGQSFDNKGYFCGEETMPVYESVFMEDGETTRKIALETERPPQV
1			EVHVWTIRKGILQHFHIEKISKRMFEELPHFKLVTRTTLSQWKI
6126	1224	389	FTEGEAQISQMCSSRVCRTELEDLVKVLYLERSEKGHC RLLSEAFCPRSRRRFQMNPEWGQAFVHVAVAGGLCAVAVFTGIF
		307	DSVSVQVGYEHYAEAPVAGLPAFLAMPFNSLVNMAYTLLGLSWL
			HRGGAMGLGPRYLKDVFAAMALLYGPVQWLRLWTQWRRAAVLDQ
			WLTLPIFAWPVAWCLYLDRGWRP\WLFLSLECVSLASYGLALLH
	,		PQGFEVALGAHVVPAVGQALRT\HRHYG/SATPSATYLALGVLS
•			CLGFVVLKLCDHQLARWRLFQCLTGHFWSKVCDVLQFHFAFLFL
			THENTHPREHPSGGKTR
6127	1335	463	VLPRRCLVFVVNTMDSSREPTLGRLDAAGFWQVWQRFDADEKGY
			IEEKELDAFFLHMLMKLGTDDTVMKANLHKVKQQFMTTQDASKD
			GRIRMKELAGMFLSEDENFLLLFRRENPLDSSVEFMQIWRKYDA
1 1	.		DSSGFISAAELRNFLRDLFLHHKKAISEAKLEEYTGTMMKIFDR
			NKDGRLDLNDLARILALQENFLLQFKMDACSTEKRKGDFEKIFA
			YYDVSKTGALEGP\EVDGFVKDMMELVOPSISGVDLDKFREILL
			RHCDVNKDGKIQKSELALCLGLKINP
6128	2511	843	TCRMSRRQLERWVWSSQQVQARGRNVRAPRLGKIAMGLEMSSKD
:		•	SPGSLDGRAWEDAQKPQSAWCGGRKTRVYATSSRRAPPSEGTRR ·
1 . 1	1		GGAARPEKTABEGPPAAPGSLRHSGPLGPHACPTALPEPQVTSA
			MSSQVVGIEPLYIKAEPASPDSPKGSSETETEPPVALAPG\PAP
			TRCLPGHKEEEDGEGAGPGEQGGGKLVLSSLPKRLCLVCGDVAS
į į			GYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITKRRRKAC
1			QACRFTKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDPLPFPGP
1			FPAGPLAVAGGPRKTAAPVNALVSHLLVVEPEKLYAMPDPAGPD
			GHLPAVATLCDLFDREIVVTISWAKSIPGFSSLSLSDQMSVLQS
1	ſ	ı	VWMEVLVLGVAQRSLTLQDELAFAEYLVLDEEGARPAGLGELG\ AALLQLVRRLQALRLEREEYVLLKALALANSDSVHIEDEPRLWS
			SCEKLLHEALLEYEAGRAGPGGGAERRRAGRLLLTLPLLRQTAG
			KVLAHFYGVKLEGKVPMHKLFLEMLEAMMD
6129	1764	771	ARFARSAHEGKMPKKKTGARKKAENRREREKQLRASRSTIDLAK
		· · -	HPCNASMECDKCQRRQKNRAFCYFCNSVQKLPICAQCGKTKCMM
ļ	1		KSSDCVIKHAGVYSTGLAMVGAICDFCEAWVCHGRKCLSTHACA
			CPLTDAEC\VECERGVWDHGGRIFSCSFCHNFLCEDDQFEHQAS
			CQVLEAETFKCVSCNRLGQHSCLRCKACFCDDHTRSKVFKQEKG
[[KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEEGDGASGYDA
[YWKNLSSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS
			DLFTNLNLGRTYASGYAHYEEQEN
6130	3	577	GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCTFIEKYDPTIE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DFYRKEIEV\DSSPSVAGISWTQQGTEQF\ASMRDLYIKKGQGC
İ			ILVYSLVNQQSFQ\DIKPMRDQIIRVKVSEKVPVI\LVGN\SVD
1.			LESEREVSSSEGRALAEEWGCPFMETSAKSKTMVDELFAEIVRQ
			MNYAAQPDKDDPCCSACNIQ
6131	3	1811	SSPREKTSDSSHRPSRHGFLFLRLVGLSPFSYLCVPPSRPVPGS
1			PRSLSAMRLLPLAPGRLRRGSPRHLPSCSPALLLLVLGGCLGVF
}			GVAAGTRRPNVVLLLTDDQDEVLGGMTPLKKTKALIGEMGMTFS
1			SAYVPSALCCPSRASILTGKYPHNHHVVNNTLEGNCSSKSWQKI
1			QEPNTFPAILRSMCGYQTFF\AGKYLNEYGAPDAGGLEHVPLGW
1			SYWYALEKNSKYYNYTLSINGKARKHGENYSVDYLTDVLANVSL
			DFLDYKSNFEPFFMMTATP\APHSPWTAAPQYQKAFQNVFAPRN
1			KNFNIHGTNKHWLIRQAKTPMTNSSIQFLDNAFRKRWQTLLSVD
1			DLVEKLVKRLEFTGELNNTYIFYTSDNGYHTGQFSLPIDKRQLY
			EFDIKVPLLVRGPGIKPNQTSKMLVANIDLGPTILDIAGYDLNK
			TQMDGMSLLPILRGASNLTWRSDVLVEYQGEGRNVTDPTCPSLS
1			PGVSQCFPDCVCEDAYNNTYACVRTMSALWNLQYCEFDDQEVFV
1		}	EVYNLTADPDQITNIAKTIDPBLLGKMNYRLMMLQSCSGPTCRT
1 _			PGVFDPGYRFDPRLMFSNRGSVRTRRFSKHLL
6132	96	1241	AAGLLPPGLVPEDPRRTRNLLPFGIQGPPFALSRPLFSCVESGW
l			AWEAMEPEFLYDLLQLPKGVEPPAEEELSKGGKKKYLPPTSRKD
			PKFEELQKPA\VLMEWINATLLPEHIVVRSLEEDMFDGLILHHL
			FQRLAALKLEAEDIALTATSQKHKLTVVLEAVNRS\CSWRSGRP
			SGA/WESIFNKDLLSTLHLLVALAKRFQPDLSLPTNVQVEVITI
			ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVFDELFKLAPEKVNA
İ			VKEAIVNFVNQKLDRLGLSVQNLDTQFADGVILLLLIGQLEGFF
1			LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAQLPC/LALK/
			TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN
6133	2	4256	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
Ī			TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
			KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
İ			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
			STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
			TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
			VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
			GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
1			RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
			/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
1	,	1	GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1			LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
			KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
1			VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
			CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
			SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
1			IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
			CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
			SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
			NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTPLAPALPSPA
			STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
			LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
			RRIRRWLRRFOASQGENLEGKYLSFEAEEKLAEWVLTOREOOLP
			VNEETLFOKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
			VAHTLPKDVAENAGLFIDFVORQIHNODLPLSMIVAIDEISLFL
			DTEVLSSDDRKENALOTVGTGBPWCDVVLAILADGTVLPTLVFY
			RGOMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
1			RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIOPL
			I WOWGEIT ALIDCUK IUDONE ATMINOMOGITELWA ALUGCOOVIOLD

650	T page of the state of		
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ı	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
ı	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
f	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
-	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	sequence	sequence	Codon, /=possible nucleotide deletion,
 	sequence		\=possible nucleotide insertion)
-	•		DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
1.			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
			LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES FYGFERADLDLMEI
6134	2	4256	
0,134	_	4256	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
1			TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
1			KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
1			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
{	1		IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
	1		STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
1			TATOPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
			VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
J	1		RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
1	! .		THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
†			GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1			LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
			KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
			VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
ĺ	Ĭ		CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
			SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
		:	IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
	·		CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
1		,	SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
			NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
			STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
1			LASGGGGSGCVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
1			RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQRBQQLP
1 :		÷ .	VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
			VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
		·	DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
			RGOMDOPANMPDSILLEAKESGYSDDEIMELWSTRVWOKHTACO
			RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
			DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
			LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
	·		FYGFEEADLDLMEI
6135	2	4256	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
			TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
			KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
1		.	STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
			TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
			VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
	1	Í	GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
		!	RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
) .			/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
			GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1		.	LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
			KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
			VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
			CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
	Ī		SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
]	1		IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
	[CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location		1
ļ		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGOTRDRVHDR
l			NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
}			STATPPPTPTHPOALALPPLATEGAECLNVDDODEGSPVTOEPE
	İ]	LASGGGGSGGVGKKEOLSVKKLRVVLFALCCNTEOAAEHFRNPO
ľ		ŀ	RRIRRWLRRFQASQGENLEGKYLSFEABEKLAEWVLTOREOOLP
ŀ]		
	1	ł	VNEBTLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
ļ			VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
}	}	1	DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
			RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
	1		RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
ļ.			DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
ļ			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
1			LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
İ		,	FYGFEEADLDLMEI
6136	1704	539	FGVRMALEGMSKRKRKRSVQEGENPDDGVRGSPPEDYRLGOVAS
]]]	SLFRGEHHSRGGTGRLASLFSSLEPQIQPVYVPVPK\ESALASA
1	<i>'</i>	Ĭ	DLEEEIHQKQGQKRKNSQPGVKVADRKILDDTEDTVVSQRKKIQ
1 .		i e	INQEEERLKNERTVFVGNLPVTCNKKKLKSFFKEYGOIESVRFR
			-
-			SLIPAEGTLSKKLAAIKRKIHPDQKNINAYVVFKEESAATQALK
1			RNGAQIADGFRIRVDLASETSSRDKRSVFVGNLPYKVEESAIEK
			HFLDCGSIMAVRIVRDKMTGIGKGFGYVLFENTDSVHLALKLNN
			SELMGRKLRVMRSVNKEKFKQQNSNPRLKNVSKPKQGLNFTSKT
L			AEGHPKSLFIGEKAVLLKTKKKGQKKSGRPKKQRKQK
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG
			MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK
ļ	i	,	1 .
1	1	}	YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES
i			YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDABGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLFRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLFRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLITLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLPGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY
6138	4587	974	LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG
6138	4587	934	LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLGHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL
6138	4587	934	LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL
6138	4587	934	LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLOHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ
6138	4587	934	LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDABGRTSFYBEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGBKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK
6138	4587	934	LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLOHVRIPYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE
6138	4587	934	LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLHELKNKETHFQRRRTTCAL TLEAGBKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM
6138	4587	934	LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLOHVRIPYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE
6138	4587	934	LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLHELKNKETHFQRRRTTCAL TLEAGBKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM
6138	4587	934	LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLITLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL
6138	4587	934	LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFFFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFFFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRTTCAL TLEAGBKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD
6138	4587	934	LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLHELKNKEHPQRRRTTCAL TLEAGBKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFREKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS
6138	4587	934	LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLHELKNKEHPQRRRTTCAL TLEAGBKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAE
6138	4587	934	LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLHELKNKEHPQRRRTTCAL TLEAGBKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFREKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS

WO 01/53312

SEQ	Predicted	Predicted end	Amino acid segment containing
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ĺ			NQREBFEGTRESILVWLTBMDLQLTNVEHFSESDADDKMRQLNG
			FQQEITLNTNKIDQLIVFGEQLIQKSEP\LDAVLIEDELEBLHR
			YCQEVFGRVSRFHRRLTSCTPGLEDEKEASENETDMEDPREIQT
1			DSWRKRGESEEPSSPQSLCHLVAPGHERSGCETPVSVDS\IPLE
			WDHTGRRGGPSSSH\EEDEEAQYY\SALSGKSISDGHSWHVPDS PSCPEHHYKQMEGDRNVPPVPPASSTPYKPPYGKLLLPPGTDGG
Ì			KEGPRVLNGNPQQEDGGLAGITEQQSGAFDRWEMIQAQEL\HNK
			LKIKQNLQQLNSDISAITTWLKKTEABLEMLKMAKPPSDIQEIE
	ĺ		LRVKRLQEILKAFDTYKALVVSVNVSSKEFLQTESPESTELQSR
			LRQLSLLWEAAQGAVDSWRGGLRQSLMQCQDFHQLSQNLLLWLA
]		SAKNRRQKAHVTDPKADPRALLECRRELMQLEKELVERQPQVDM
			LQEISNSLLIKGHGEDCIEAEEKVHVI\EKKLKQLREQVSQDLM
1 .		•	ALQGTQNPASPLPSFDEVDSGDQPPATSVPAPRAKQFRAVRTTE
			GEEETESRVPGSTRPQRSFLSRVVRAALPLQLLLLLLLLLLACLL
			PSSEEDYSCTQANNF\ARSFYPMLRYTNGPPPT
6139	52	1131	LGDWVWSRTCGVLETPTSVLRRARARGPCPTDSKWALPRLREGE
}			TERRPWEASSWKTL/LAGWIGGAASVIVGHPLDTVKTRLQAGVG
1			YGNTLSCIRVVYRRESMFGFFKGMSFPLASIAVYNSVVFGVFSN
1			TORFLSQHRCGEPRASPPRTLSDLLLASMVAGVVSVGLGGPVDL
			IKIRLQMQTPPVSGRQPRFEVQGSGSCG\EPAYQGPVHCITTIV
			RNEGLAGLYRGASAMLLRDVPGYCLYFIPYVFLSEWITPEACTG PSPCAVWLAGGMAGAISWGTATPMDVVKSRLQADGVYLNKYKGV
			LDCISQSYQKEGLKVFFRGITVNAVRGFPMSAAMFLGYELSLQA
1			IRGDHAVTSP
6140	694	136	RPELELWRLRSRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP
			RCQRP/QPPAPEPSSPNAAVPEAIPTPRAAASAALELPLGPAPV
			SVAPQAEAEARSTPGPAGSRLGPETFRQRFRQFRYQDAAGPREA
	_		FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR
6141			ARRIRRTDVRITG
9141	2	984	AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS
			ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS
	İ		PSEILYCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI
	•		NGENIVGWRHYDVAKKLKELKKEBLFTMKLIEPKKAFEIELRSK
	• }		AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD
1 1			VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP
			DEFVFDVWGVIGDAKRRGL
6142	116	602	EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN
	ł		LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR
	ļ		FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL
			REKQLSHSLRAVSTDPPHHDHHDEFC\LMP
6143	2802	270	FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q
			\QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED
]	ļ		LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN
	ĺ		SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM
			FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE
			KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK
			YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI
1		•	FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF
		j	TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS
			QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD
] [YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN
			AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF
			GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL
L			TIYNAYLGWKKARQEGGYRSEITYCRRNFLNRTSLLTLEDVKQE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	,		
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
Į.	sequence		\=possible nucleotide insertion)
			LIKLVKAAGFSSSTTSTSWEGNRASQTLSFQEIALLKAVLVAGL
ł	Į.		YDNVGKIIYTKSVDVTEKLACIVETAQGKAQVHPSSVNRDLQTH
			GWLLYQEKIRYARVYLRETTLITPFPVLLFGGDIEVOHRERLLS
1			IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENDKI
	1		LQIITBLIKTENN
6144	1289	568	SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPYQN
			VSASGGARHGGRGSGGPVICTYGPDLFPLVA\TIGAAFVAKVMS
	[VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSS
	1		FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFHDV
ļ	3		QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVMTE
	1		, · · · · · · · · · · · · · · · · · · ·
C7.45	1100	100	DKGVDLGQKPNPYFYSCCHH
6145	1109	196	GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGPVL
]			GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMEDT
1			DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYALD
			QGVNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALYPV
			\VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDPQD
			/TKAWLKEHVEPVF\GFP\QFVRF\SWRTAQTI\LEKEAEDVIR
1	İ		EDSASENQEGLRKITSYFLNEGSQARPRSSHRYFLERGLESTTS
ļ	ŀ		L
6146	428	781	LKKKGKEKAEAQQVEALPGPSLDQWHRSAGEEEDGPVLTDEQKS
			R/YPGHEAHDQGG\WDARQSIIRKVVDPETGRTRLIKGDGEVLE
	İ	1	BIVTKERHREINKOATRGDCLAFOMRAGLLP
6147	i	2304	GTRQLPPPSPGSGPGDSPEGPEGEAPERRKAHGMLKLYYGLSE
			GEAAGRPAGPDPLDPTDLNGAHFDPEVYLDKLRRECPLAQLMDS
			ETDMVRQIRALDSDMQTLVYENYNKFISATDTIRKMKNDFRKME
į.			DEMDRLATNMAVITDFSARISATLODRHERITKLAGVHALLRKL
İ			QFLFELPSRLTKCVELGAYGQAVRYQGRAQAVLQQYQHLPSFRA
ł			IODDCOVITARLAOOLRORFREGGSGAPEOAECVELLLALGEPA
	ļ		EELCEEFLAHARGRLEKELRNLEABLGPSPPAPDVLEFTDHG\S
1			•
Į		,	SGFVGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGSRYFALV
1			ERRLAQEQGGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT
Ì			EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP
[GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF
1			CSQGVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLLS
			RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA
	1		RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV
		1.	VEDTTAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG
1	1	1	GGDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS
			CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS
	<u> </u>		CILPLPHSTGSINSDHVPTK
6148	3056	353	VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ
		-	KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT
			SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV
	1		PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT
}	1	1	SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES
			VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE
	1		LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ
	Į.	1	LKNIVSYPPSKPPTYEEODLVWEFRYYLTNODKALTKILTSVIW
		}	DLPOGAKOALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR
		†	LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS
		1	ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG
			ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK
			THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM
		1	KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK
			IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLRQD
			QLILQIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSV

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
"""	location	corresponding	Glutamic Acid, F-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, K-Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	B-Broline, M-Methionine, N-Asparagine,
İ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
ı			PVAEVLDTEGSIQNFFRKYAPSENGPNGISAEVMDTYVKSCAGY
ļ			CVITYILGVGDRHLDNLLLTKTGKLFHIDFGYILGRDPKPLPPP
j ,			MKLNKEMVEGMGGTQSEQYQEFRKQCYTAFLHLRRYSNLILNLF
			SLMVDANIPDIALEPDKTVKKVQDKFRLDLSDEEAVHYMQSLID
			ESVHALFAAVVEQIHKFAQYWRK
6149	1	1413	RVDPRVRENGTANPIKNGKTSPASKDQRTGKKTSVQGQVQKGND
			ESESDFESDPPSPKSSEEEEQDDEEVLQGEQGDFNDDDTEPENL
1	·		GHRPLLMDSEDEEEEEKHSSDSDYEQAKAKYSDMSSVYRDRSGS
1 1			GPTQDLNTILLTSAQLSSDVAVETPKQEFDVFGAVPFFAVRAQQ
1			PQQEKNEKNLPQHRFPAAGLEQEEFDVFTKAPFSKKVNVQECHA
			VGPEAHTIPGYPKSVDVFGSTPFQPFLTSTSKSESNEDLFGLVP
			FDEITGSQQQKVKQRSLQKLSSRQRRTKQDMSKSNGKRHHGTPT
			STKKTLKPTYRTPERARRHKKVGRRDSQSSNEFLTISDSKENIS
1 1		•	VALTDGKDRGNVLQPEESLLDPFGAKPFHSPD\LSWHPP\HQGL
1			S\DIRADHNT\VLPGR\PRQNSLHGSFHSADVLKMDDFGAVP/F
L			LTELVVQSITPHQSQQSQPV\BLDPFGAAPFPSKO
6150	372	37	MSNIKKYIIDYDWKASIEIEIDHDVMTEEKLHQINNFWSDSEYR
1 1			LNKHGSVLNAVLIMLAQHALLIAISSDLNAYGVVCEFDWNDGNG
1			QEGWPPMDGSEGIRITDIDTSGIF
6151	1555	521	DSNQQSVSGTAASTLLHSFKATIYYQGTGHVQQFYGVTSPYSQT
		-	TPPIVQSYAQPSLQYIQGQQIFTAHPQGVVVQPAAAVTTIVAPG
1 1			QPQPLQPSEMVVTNNLLDLPPPSPPKPKTIVLPPNWKTARDPEG
1 1			KIYYYHVITRQTQWDPPTWESPGDDASLEHEAEMDLGTPTYDEN
1 1			PMK\ASKKPKTAEADTSSELAKKSKEVFRKEMSQFIVQCLNPYR
1 1	•		KPDCKVG\RITTEDFKHLARKLTHGVMNKELKYCKNPE\DLEC
			APDICAGE ATTTTED FRIDARY THE WINNER RECEIVED THE CONTROL OF THE CO
1 1			NENVKHKTKEYIKKYMQKFGAVYKPKEDTEFRVTVGPGWEDGWS
6152	1366		GKTDSRERKSCGPFCSTPVSTVLLMIHHPGEFNPADVN
6132	1366	648	NRTWSTPSTWMGVALPPLCSTGPWPVTRQITARTTCGAVPAKCP
1 . [,		PWC/DVHEPRCQPPDCHGHGTCVDGHCQCTGHFWRGPGCDELDC
] . [GPSNCSQHGLCTETGCRCDAGWTGSNCSEECPLGWHGPGCQRPC
		•	KCEHHCPCDPKTGNCSVSRVKQCLQPPEATLRAGELSFFTRTAW
1 1			LALTLALAFLLLISTAANLSLLLSRAERNRRLHGDYAYHPLQEM
-			NGEPLAAEKEQPGGAHNPFKD
6153	2	3368	GRVGARSPGRAYALLLLICFNVGSGLHLQVLSTRNENKLLPKH
1 1			PHLVRQKRAWITAPVALLEGEDLSKKNPIAKIHSDLAEERGLKI
1		•	TYKYTGKGITEPPFGIFVFNKDTGELNVTSILDREETPFFLLTG
] : [YALDARGNNVEKPLELRIKVLDINDNEPVFTQDVFVGSVEELSA
] 1	ſ		AHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDT
1	ľ		GEIYTTSVTLDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIR
1	ļ		ILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVFDADEIGSDN
	1		WLANFTFASGNEGGYFHIETDAQTNEGIVTLIKEVDYEEMKNLD
1	1	ł	FSVIVANKAAFHKSIRSKYKPTPIPIKVKVKNVKEGIHFKSSVI
1	ļ		SIYVSESMDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNW
		ļ	ISVDSVTSEIKLAKLPDFESRYVQNGTYTVKIVAISEDYPRKTI
		ļ	TGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPN
j 1	}	}	SGPFSFSVIDKPPGMAEKWKIARQESTSVLLQQSEKKLGRSEIQ
	İ		FLISDNQGFSCPBKQVLTLTVCEVLHGS\GCREAQHDSYVGLGP
1	İ		AAIALMILAFLLLLLVPLLLLMCHCGKGAKGFTPIPGTIEMLHP
1]		
] [ļ		WNNEGAPPEDKVVPSFLPVDQGGSLVGRNGVGGMAKEATMKGSS
į l			SASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAI\MTTE
; l]		TTITARATGASRDVAGAQAAAVALNEEFLKNYFTDKAASYTEED
			ENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFLDDLGL
			KFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTM
	1		VNSENTYSSGSSFPVPKSLQEANAEKVTQEIVTERSVSSRQAQK
	1	J	
		ł	VATPLPDPMASRNVIATETSYVTGSTMPPTTVILGPSQPQSLIV TERVYAPASTLVDQPYANEGTVVVTERVIQPHGGGSNPLEGTQH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
į	sequence	-	\=possible nucleotide insertion)
			LQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
Ì			APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGH
			SNSTITTSSTRVTKHSTVQHSYS
6154	3660	2146	KKKTKMKNTLQKTVNFGAWPKPTISDKSHLLQMVSKLDLTDAKN
			SDTAHIKSIEITSILNGLQASESSAEDSEQEDERGAQDMDNNGK
			EESKIDHLTNNRNDLISKEEQNSSSLLEENKVHADLVISKPVSK
]	SPERLRKDIEVLSEDTDYEEDEVTKKRKDVKKDTTDKSSKPQIK
	}	ļ	RGKRRYCNTEECLKTGSPGKKEEKAKNKESLCMENSSNSSSDED
ſ			EEETKAKMTPTKKYNGLEEKRKSLRTTGFYSGFSEVAEKRIKLL
		1	NNSDERLQNSRAKDRKDVWSSIQGQWPKKTLKELFSDSDTEAAA
			SPPHPAPEEGVAEESLQTVAEEESCSPSVELEKPPPVNVDSKPI
			EEKTVEVNDRKAEFPSSGSNFSA*IPLPYLHLNRLHQSL*QKGS
		1	RQQSSVTVSEPLAPNQEEVRSIKSETDSTIEVDSVAGELQDLQS
1			ERE*LASRF*CQCELEQ**SARTRTS*KSLYRSEKSERCSGRRK
			FIKKAEKKP*SNSGKQQKEGK
6155	869	121	HLLPELRGKSWITMKYVFYLGVLAGTFFFADSSVQKEDPAPYLV
			YLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDG
i			TEOTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQALN
i			P\PTTNVRPGTVCLLSGLDWSQENSGRHPDLRQNLEAPVMSDRE
			COKTEOGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKLQGIE
1			VGHFMGGDVGIYTNVYKYVSWIENTAKDK
6156	5725	3984	GTSTVTMATKKHFSIILNLLGMLLKKDNODTRKLLMTWALEVAV
			VMKKSETYAPLFCLPSFHKFCKGLLADTLVEDVNICLQACSSLH
1			ALSSSLPDDLLQRCVDVCRVQLVHRGTCIRQAFGKLLKSIPLGV
			FLSNNNHTEIOEISLALRSHMSKAPSNTFHPQDFSD/VISFILY
			GNSHRTGKDNWLERLFYSCQRLDKRDQSTIPRNLLKTDAVLWQW
İ			AIWEAAOFTVLSKLRTPLGRAQDTFQTIEGIIRSLAGHTLNPDQ
		Ì	DVSOWTTADNDEGHGNNOLRLVLLLQYLENLEKLMYNAYEGCAN
1	•		ALTSPPKVIRTFLYTNROTCODWLTRIRLSIMRVGLLAGOPAVT
1			VRHGFDLLTEMKTTSLSQGNELEVSIMMVVEALCELHCPEAIQG
1		}	IAVWSSSIVGKHLLWINSVAQQAEGRFEKASVEYQEHLCAMTGV
			DCCISSFDKSVLTLASAGCKSASLKHCLNGESRKSVLSKPTDSS
1			PEVINYLGNKACECYISTADWAAVQEWQNAIHDLKKSTSSTSLN
			LKADFNYIKSLSSFESGKFVECTEQLELLPGENINLLAGGSKEK
			IDMKKLLRNM
6157	946	329	MANRGPSYGLSREVQEKIEQKYDADLENKLVDWIILQCAEDIEH
	1		PPPGRAHFQKWLMDGTVLCKLINSLYPPGQEPIPKISESKMAFK
1			QMEQISQFLKAAETYGVRTTDIFQTVDLWEGKDMAAVQRTLMAL
			GSVAVTKDDGCYRGEPSWFHRKAQQNRRGFSEEQLRQGQNVIGL
			QMGSNKGASQAGMTGYGMPRQIM*DAASCP
6158	441	1482	LGSLIVLSLHCKVIFSSQSLERAMKEKAVDLVPILAQNPGLAQN
			PILEGKDHNONTGVDPIIDHVQDRKTD/SRSKSPHKKRSKSRER
			RKSRSRSHSRDKRKDTREKIKEKERVKEKDREKEREREKEREKE
			KERGKNKDRDKEREKDREKDKEKDREREREKEHEKDRDKEKEKE
1	1	-	QDKEKEREKDRSKEIDEKRKKDKKSRTPPRSYNASRRSRSSSRE
			RRRRSRSSSRSPRTSKTIKRKSSRSPSPRSRNKKDKKREKERD
			HISERRERESTSMRKSSNDRDGKEKLEKNSTSLKEKEHNKEPD
			SSVSKEVDDKDAPRTEENKIQHNGNCQLNEENLSTKTEAV
6159	53	84	AVIAPLHISLGDRARPYLKNTEKSSTTCSRRRNQSFPPVMSLTH
0133	33 .	""	RLHLCKYWGCAVSNVCRFWEGRPLPLMIVVPYTLPVSLPVGSCV
	1		IITGTPILTFVKDPQLEVNFYTGMDEDSDIAFQFRLHFGHPAIM
			NSCVFGIWRYEEKCYYLPFEDGKPFELCIYVRHKEYKVMVNGQR
	1		IYNFAHRFPPASVKMLQVFRDISLTRVLISD*GRCVRITAVQEF
			DVSVSCDCTTAYOPG
6160	1626	1790	AGAKPFP*F*KVADAQPTESEKEIYNQVNVVLKDAEGILEDLQS
3100	1020	1,30	YRGAGHEIREAIQHPADEKLQEKAWGAVVPLVGKLKKFYEFSQR
		<u> </u>	THORISTIAL AND THE PROPERTY OF THE PARTY THE P

r	75 31		
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			LEAALRGLLGALTSTPYSPTQHLEREQALAKQFAEILHFTLRFD
]			ELKMTNPAIQNDFSYYRRTLSRMRINNVPAEGENEVNNELANRM
1			SLFYAEATPMLKTLSDATTKFVSENKNLPIENTTDCLSTMASVC
		ļ	RVMLETPEYRSRFTNEETVSFCLRVMVGVIILYDHVHPVGAFAK
1			TSKIDMKGCIKVLKDQPPNSVEGLLNALRYTTKHLNDETTSKQI
			KSMLQ*QLLTLVNKG
6161	455	1569	PVSGSESSLRRAWASILRLMLGPRVAVSILCEDGISH*LLEKH*
J			KSHVLEPLSSLALEEQCLALSLDWSTGKTGRAGDQPLKIISSDS
ì			TGQLHLLMVNETRPRLQKVASWQAHQFEAWIAAFNYWHPEIVYS
1			GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIQSSPHREHILAT
			GSYDEHILLWDTRNMKQPLADTPVQGGVWRIKWHPFHHHLLLAA
			CMHSGFKILNCQKAMEERQEATVLTSHTLPDSLVYGADWSWLLF RSLQRAPSWSFPSNLGTKTADLKGASELPTPCHECREDNDGEGH
			ARPQSGMKPLTEGMRKNGTWLQATAATTRDCGVNPEEADSAFSL
1			LATCSFYDHALHLWEWEGN
6162	1	586	RTIHATGRAGASPMHRLIVWRLAEANKQHVRCQKCLEFGHWTYE
			CTGKRKYLHRPSRTABLKKALKEKENRLLLQQSIGETNVERKAK
			KKRSKSVTSSSSSSSSSSSSSSSSSSESEETSTSSSSEDSDTDESS
1	ļ		SSSSSASSTTSSSSSDSDSDSSSSSKQ*HQHR*QL*R*TTKEE
L			EKEIELLHSYWTDGLKTLM
6163	1081	785	RIRSTTEGCAVRLHPTQNTGKARIMILLSVSLGRHWAFTYKFFL
			TPVVFVFFFFFFHRKE*VMQKNPMKSREDEWMEKLNNLHVQRAD
1			MNRLIMNYLVTEGFKEAAEKFRMESGIEPSVDLETLDERIKIRE
1			MILKGQIQEAIALINSLHPELLDTNRYLYFHLQQQHLIBLIRQR
1 .			ETEAALEFAQTQLAEQGEESRECLTEMERTLALLAFDSPEESPF
			GDLLHTMQRQKVWSEVNQAVLDYENRESTPKLAKLLKLLLWAQN
6164	90	406	ELDQKKVKYPKMTDLSKGVIEEPK
0104	, ,	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
	,		VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
			NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
:]			WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
			YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
! !	•		GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
! !			RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
			LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
] . [KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE
'	.]		PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
	1		ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
1 1		i	HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
			PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
	İ		EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
	l		VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT
		1	SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
	ŀ	ļ	GGERFG WWVFSSGTMLSRQLPGYPQEYQRN
6165	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
			SCISRTAPRILCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
			VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
	1		NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
	ļ		WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
			YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
			GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
j			RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHR
	Ì		LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
			KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE

	,		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į į	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
			PNEEOSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
1			ALKROYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
1			HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
1			PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEONEASKTNGLGAA
			EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
1			VOAKLGALELNORDAAAETELRVHPPCORHCPEPPSAPEENKAT
			SKAPOGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
1		1	HFPOMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
1	1	l .	GGERFG
63.66		1206	HKLWRTVAMAGAEWKSLEECLEKHLPLPDLQEVKRVLYGKELRK
6166	2	1206	LDLPREAFEAASREDFBLQGYAFBAAEEQLRRPRIVHVGLVQNR
i			IPLPANAPVAEOVSALHRRIKAIVEVAAMCGVNIICFQEAWTMP
			FAFCTREKLPWTEFAESAEDGPTTRFCQKLAKNHDMVVVSPILE
			RDSEHGDVLWNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYYM
		1	EGNLGHPVFQTQFGRIAVNICYGRHHPLNWLMYSINGAEIIFNP
ļ		j	SATIGALSESLWPIEARNAAIANHCFTCAINRVGTEHFPNEFTS
ļ			GDGKKAHQDFGYFYGSSYVAAPDSSRTPGLSRSRDGLLVAKLDL
}			NLCQQVNDVWNFKMTGRYEMYARELAEAVKSNYSPTIVKE*PAS
			VPALG
6167	1220	1844	YGIVTGPSLCAGDKQPKKQEKNPVLVSPEFVDEALCACEEYLSN
İ			LAHMDIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQ
			VQRCEDILQQLQAVVPQIDMEGDRNIWIVKPGAKSRGRGIMCMD
1	j		HLEEMLKLVNGNPVVMKDGKWVVQKYIERPLLIFGTKFDLRQWF
į.			LVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDK*APLYLTPEGWS
į			LFLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDMEG
	1		DRNIWIVKPGAKSRGRGIMCMDHLBEMLKLVNGNPVVMKDGKWV
			VQKYIERPLLIFGTKFDLRQWFLVTDWNPLTVWFYRDSYIRFST
			QPFSLKNLDK
6168	84	1392	VWPVPSVSAMPPKKQAQAGGSKKAEQKKKEKIIEDKTFGLKNKK
			GAKQQKFIKAVTHQVKFGQQNPRQVAQSEAEKKLKKDDKKKELQ
ł			ELNELFKPVVAAQKISKGADPKSVVCAFFKQGQCTKGDKCKFSH
			DLTLERKCEKRSVYIDARDEELEKDTMDNWDEKKLEEVVNKKHG
			EAEKKKPKTQIVCKHFLEAIENNKYGWFWVCPGGGDICMYRHAL
			PPGFVLKKKKKKKKEDEISL*DLIERERSALGPNVTKITLESF
			LAWKKRKRQEKIDKLEQDMERRKADFKAGKALVISGREVFBFRP
			ELVNDDDEEADDTRYTQGTGGDEVDDSVSVNDIDLSLYIPRDVD
j			ETGITVASLERFSTYTSDKDENKLSEASGGRAENGERSDLEEDN
			EREGTENGAIDAVPVDENLFTGEDLDELEEELNTLDLEE
6169	112	662	APAAAMAERPEDLNLPNAVITRIIKEALPDGVNISKEARSAISR
			AASVFVLYATSCANNFAMKGKRKTLNASDVLSAMEEMEFQRFVT
			PLKEALEAYRREQKGKKEASEQKKKDKDKKTDSEEQDKSRDEDN
			DEDEERLEEEEQNEEEEVDN*KGRETVAPWKVPLEMRRATCFCE
1			AFPCWAE
6170	62	667	STKVMLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIA
	1		AKTAQPHPKLLGTIYTAABEIEAVGGKALPCIVDVRDEQQISAA
1	1		VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG
1			TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW*VV
			G*GDGLCLICFELNLCMSDVITICT
6171	382	941	HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST
1 01/1	1		MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRRHAN
1	1		SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD
1			RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT
1			NATLRYTKSK
6172	651	54	GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR
07/2	621	3-4	SAOERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV
1			TSHVDDEYRWAGVEDPKVMITTSRDPSSRLKMFAKELKLVFPGA
í		1	TOTAL DESIGNATION OF THE PROPERTY OF THE PROPE

SEQ	Predicted	Predicted end	l amino and d
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	*		QRMNRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLIVSHLP
1	İ	1	FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV
			SDILRYLFPVPKDDSHRVITFANQDDYISFRHHVYKKTDHRNVE
	}		LTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYTNTARKRVF
}			LSTE*AAPRPLGQLL
6173	3	288	SVDHREVQVLSQSMPLTPHQAVLRGERPYMCVECGKCFGRSSHL
l		,	LQHQRIHTGEKPYVCSVCGKAFSQSSVLSKHRTIHTGEKPYECN
i		İ	ECGKAFRVSSDLAQHHKIHTGEKPHECLECRKAFTQLSHLIQHQ
			RIHTGERPYVCPLCGKAFNHSTVLRSHQRVHTGEKPHRCNECGK
			TFSVKRTLLQHQRIHTGEKPYTCSECGKAFSDRSVLIQHHNVHT
			GEKPYECSECGKTFSHRSTLMNHERIHTEEKPYACYECGKAFVQ
1			HSHLIQHQKVHRKL*PTCVLSVGSALAGVPTSFSISVSTLERSP
			MCAVYVGRPSARAQSLVNTGQFTQVRSPMSVMSVEKPLE
6174	1060	959	PRPPGKRWMVAGLGNPGLPGTRHSVGMAVLGQLARRLGVAESWT
			RDRHCAADLALAPLGDAQLVLLRPRRLMNANGRSVARAAELFGL
			TAEEVYLVHDELDKPLGRLALKLGGSARGHNGVRSCISCLNSNA
1	1		MPRLRVGIGRPAHPEAVQAHVLGCFSPAEQELLPLLLDRATDLI
			LDHIRERSQGPSLGP*H*WFSKKA
6175	2204	334	RYFRADPRSRSGQPRAEGLGAFAEGPLRAMAAPVKGNRKQSTEG
1			DALDPPASPKPAGKQNGIQNPISLEDSPEAGGEREEEQEREEEQ
1			AFLVSLYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYE
			LVTGRRLWKNVYNELGGSPGSTSGATCTRRHY*RLVLPYVRHLK
1		1	GEDDKPLPTSKPRKQYKMAKENRGDDGATERPKKAKEERRMDQM
			MPGKTKADAADPAPLPSQEPPRNSTEQQGLASGSSVSFVGASGC
			PEAYKRLLSSFYCKGTHGIMSPLAKKKLLAQVSKVEALQCQEEG
1]		CRHGAEPQASPAVHLPESPQSPKGLTENSRHRLTPQEGLQAPGG
1		,	SLREEAQAGPCPAAPIFKGCFYTHPTEVLKPVSQHPRDFFSRLK
]		DGVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGSRKGILYP
			KPKACWVSPMAKVPAESPTLPPTFPSSPGLGSKRSLEEEGAAHS
1 .			GKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLLGPALGPVPPEA
			YRGTMLHCPLNFTGTPGPLKGQAALPFSPLVIPAFPAHFLATAG
			PSPMAAGLMHFPPTSFDSALRHRLCPASSAWHAPPVTTYAAPHF
6176	1040	402	FHLNTKL
31/6	1040	402	PLSALRAMAEVHVIGQIIGASGFSESSLFCKWGIHTGAAWKLLS
			GVREGQTQVDTPQIGDMAYWSHPIDLHFATKGLQGWPRLHFQVW SQDSFGRCQLAGYGFCHVPSSPGTHQLACPTWRPLGSWREQLAR
			SQUSFGREQLAGIGFCHVPSSPGTHQLACPTWRPLGSWREQLAR AFVGGGPQLLHGDTIYSGADRYRLHTAAGGTVHLEIGLLLRNFD
			RYGVEC*GTLPPTSPPSTPRTPSDGGGWHSGOEHRL
6177	1400	992	VPIESLVGKVHNFPLIAFYCCEKGKRQPHKSLHDRCFGEALDPN
		عرر	CSHCYLDQIKRSDFLGFSGYSPHFVAISTNSEHKMQPSSMQQAL
			PSQ*PYWTDPRPALVPCCSHRPDVHRSRPGPGLPGTSGCSDRPP
			VCPI
6178	1027	254	STQRGGIKGVARAASLVGRRRAGTGMALLLCLVCLTAALAHGCL
			HCHSNFSKKFSFYRHHVNFKSWWVGDIPVSGALLTDWSDDTMKE
	ļ		LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELR
]	ĺ		NIFREQVHLIQNAIIESRIDCQHRCGIFQYETISCNNCTDSHVA
			CFGYNCESSAQWKSAVQGLLNYINNWHKQDTSMRPRSSAFSWPG
			THRAAPAFLVLPALRCLEPPHLANLSLEDAA*CLKQH
6179	806	276	RGETREMAGNLLSGAGRRLWDWVPLACRSFSLGVPRLIGIRLTL
		-· •	PPPKVVDRWNEKRAMFGVYDNIGILGNFEKHPKELIRGPIWLRG
	1		WKGNELQRCIRKRKMVGSRMFADDLHNLNKRIRYLYKHFNRHGK
			FR*KRKLRTSEKAHLSPWRRETVLFPVRKRLCIFSVIKWGFFGI
6180	156	1833	DHHILKAASTTHVCARGNIFAIPNTRCLEC*ATATPSSLECON*
			SHLSLCPLPATTSGLTPNSMIPEKERQNIAERLLRVMCADLGAL
			SVVSGKEFLKLAQTLVDSGARYGAFSVTEILGNFNTLALKHLPR
i			MYNQVKVKVTCALGSNACLGIGVTCHSQSVGPDSCYILTAYQAE

Deginning nuclectide location cortesponding to first anino acid anino	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No. nuclectide corresponding to first amino acid residue of santo acid residue of amino acid sequence h=histidine, I=lscleucine, N=Apparagine, n=histidine, I=lscleucine, N=Apparagine, n=histidine, I=lscleucine, N=Apparagine, n=histidine, I=lscleucine, N=Apparagine, n=histidine, I=lscleucine, N=Apparagine, n=histidine, I=lscleucine, N=Apparagine, n=histidine, I=lscleucine, N=Apparagine, n=histidine, I=lscleucine, N=Apparagine, n=histidine, I=lscleucine, N=Apparagine, n=histidine, I=lscleucine, N=Apparagine, n=histidine, I=lscleucine, N=Apparagine, n=histidine, I=lscleucine, N=Apparagine, n=histidine, I=lscleucine, N=Apparagine, n=histidine, I=lscleucine,				
Location Corresponding Lofirst amino acid amino acid residue of amino acid residue of amino acid amino acid sequence Septence Location Lo				
to first anino acid residue of residue of anino acid residue of anino acid sequence S=Serine, T=Threenine, V=Vallne, anino acid sequence S=Serine, T=Threenine, V=Vallne, anino acid sequence S=Serine, T=Threenine, V=Vallne, S=Serine, T=Threenine, V=Vallne, W=Tryptophan, Y=Typtophan, Y=Typtophan, Y=Unknown, *stop Codon, /=possible nucleotide deletion, _possible nucleotide insertion) ONNIKSYVLOVKGADIRDSGDLYHHWVGNVLSBYDWSERTRYYY TDCRWSTASPSKAMCHACSACALNSVGSUSKERTLORGANSHE VIELINVCEDLAGSTGLAKEFTOSLEETSPPCOKNSVTDSLLLV HERYSGLCEYSTASKAMCHACSACALNSVGSUSKERTLORGANSHE VIELINVCEDLAGSTGLAKEFTOSLEETSPPCOKNSVTDSLLLV HERYSGLCEYSTASKAMCHACSACALNSVGSUSKERTLORGANSHE LSNESQDTLQLVLFTVVNLERLENLANLANLTDYKQAYIE LSNESQDTLQLVLFTVVNLERLENLANLANLTDYKQAYIE LSNESQDTLQLVLFTVVNLERLENLANLANLTDYKQAYIE LSNESQDTLQLVLFTVVNLERLENLANLANLANLTDYKQAYIE LSNESQDTLQLVLFTVVNLERLENLANLANLANLTDYLCOST SELLHITVOISISHPENSGREYSTRUSPLGISTYPOKET KESMAREADPEPAAKKPRSAAVENPAAQEDDRIGKREVTDYDLOS VSLLELHITVOISISHPENSGREYSTRUSPLGISTYPTUKE YTLIQFCGHSWHFTRNTTVFFFSSGESMMUTFYAAGLANLKGSCVNCOST VSLLELHITVOISISHPENSGREYSTLEPILGISTYPTUKE YTLIQFCGHSWHFTYNSHLYSGRSULTSTLLEPILGISTYPTUKE YTLIQFCGHSWHFTYNSHLYSGRSULTSTLLEPILGISTYPTUKE YTLIQFCGHSWHFTYNSHLYSGRSULTSTLLEPILGISTYPTUKE YTLIQFCGHSWHFTYNSHLYSGRSULTSTLLEPILGISTYPTUKE YTLIQFCGHSWHFTYNSHLYSGRSULTSTLLEPILGISTYPTUKE YTLIGFCGHSWHFTYNSHLYSGRSULTSTLLEPILGISTYPTUKE YTLIGFCGHSWHFTYNSHLYSGRSULTSTLLEPILGISTYPTUKE YTLIGFCGHSWHFTYNSHLYSGRSULTSTLLEPILGISTYPTUKE YTLIGFCGHSWHFTYNSHLYTTSLLEBMAANYFPUC VKNYPSERIATOKALSYLGECLDHWFTSLGFTHLSALHKIGGHFMEFF VKNYFSERIATOKALSYLGECLDHWFTSLGFTHLSALHKIGGHFMEFF VKNYFSERIATOKALSYLGECLDHWFTSLGFTHLSALHKIGGHFMEFF VKNYFSERIATOKALSYLGECLDHWFTSLGFTHLSALHKIGGHFMEFF VKNYFSERIATOKALSYLGECCHSMCCVACXGRC CAARASISTISSTEGAMTINFSLITMVTFFLGRSSPTLIKTSCRCHTI STOT 6183 1118 452 HERBITTERFORMANNANTATYCLLESSENGRACASCOSCOSSSCOSCOSS COCOSSSCOCHOCOSSGRGGCOSCOSSSCOSCOSSSCOSCOSS COCOSSSCOCHOCOSSGRGGCOSCOSSSCOSCOSSSCOSCOSS COCOSSSCOCHOCOSSGRGGCOSCOSSSCOSCOSSSCOSCOSS COCOSSSCOCHOCOSSGRGGCOSCOSSSCOSCOSSSCOSCOSS COCOSSSCOCHOCOSCO	NO.			
to first amino acid residue of amino acid residue of amino acid amino acid sequence S=Serine, T=Threonine, V=Valine, amino acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Valine, acid sequence S=Serine, T=Threonine, V=Dronic Serine, T=Serine, acid sequence S=Serine, T=Threonine, V=Dronic Serine, T=Serine sequence S=Serine, T=Threonine, V=Dronic Serine, T=Serine sequence sequence sequence S=Serine, T=Threonine, V=Dronic Serine, T=Serine sequence sequenc			•	• •
amino acid residue of amino acid sequence whytophan, Y-Tyroshen, Y-Waline, and acid sequence whytophan, Y-Tyroshen, Y-Wanknown, *-Stop Codon, /-possible nucleotide deletion, Y-possible nucleotide deletion, Y-possible nucleotide deletion, Y-possible nucleotide deletion, Y-possible nucleotide deletion, Y-possible nucleotide deletion, Y-possible nucleotide insertion on the sequence of the sequence	1			
residue of amino acid sequence (Codon, /=possible nucleotide deletion) (Codon, /=possible nucleotide deletion) (Codon, /=possible nucleotide deletion) (Codon, /=possible nucleotide deletion) (Codon, /=possible nucleotide deletion) (Codon, /=possible nucleotide insertion) (Codon, /=possible nucleotide insertion) (Codon, /=possible nucleotide insertion) (Codon, /=possible nucleotide insertion) (Codon, /=possible nucleotide insertion) (Codon, /=possible nucleotide insertion) (Codon, /=possible nucleotide insertion) (Codon, /=possible nucleotide insertion) (Codon, /=possible nucleotide insertion) (Codon, /=possible nucleotide insertion) (Codon, /=possible nucleotide) (Codon, /=			••••	
amino acid sequence				, , , , , , , , , , , , , , , , , , , ,
A-possible mucleotide insertion	1			
GNNILKSYL/GAVKGADIRDSGDLYHHWONILSEFYNSEITPTYY TDCRYSTASTSKARCHICGSCALGANSVOGSUSKAPCARSHE VIELINVCEDLAGSTGLAKETPGSLEFTSPPCNNSVTDSLLIL HERYPG)(TESYSAKKMILGSURALITIPVKQAVIE LSNESQPTIQL/ULPTYVPLEKLFTAKANDAGTVGKLCHLFLEAL KENFSKYHPAIKKANTLIDPQCALKFULSIKALILAVPAVGALISEV KESSABEADEEPAAKKROAAVENPAQEDDRLGKNEVYDYLOE ELSNESQPTIQL/ULPTYVPLEKLFTAKANDAGTVGKLCHLFLEAL KESSABEADEEPAAKKROAAVENPAQEDDRLGKNEVYDYLOE KESSABEADEEPAAKKROAAVENPAQEDDRLGKNEVYDYLOE ELSNESQPTIQL/ULPTYVPLEAGERKEWRERWEPAGEDDRLGKNEVYDYLOE KESSABEADEEPAAKKROAAVENPAQEDDRLGKNEVYDYLOE KESSABEADEEPAAKKROAAVENPAQEDDRLGKNEVYDYLOE KESSABEADEEPAAKKROAAVENPAQEDDRLGKNEVYDYLOE KESSABEADEEPAAKKROAAVENPAQEDDRLGKNEVYDYLOE KESSABEADEEPAAKKROAAVENPAQEDDRLGKNEVYDYLOE KESSABEADEEPAAKKROAAVENPAQEDDRLGKNEVYDYLOE KESSABEADEEPAAKKROAAVENPAQEDRLGKNEVYDYLOE KESSABEADEEPAAKKROAAVENPAGAETTISTAKUR SIGNILA YTHILISPYLLEGERKEWRERWERPAGEADLAURGYKNENALFIS YTHILISPYLLEGERKEWRERWERPAGEADLAURGYKNENALFIS YTHOLICILLAKEROJTEERYKLEKLIGSTLEILKEWSTAKATURSCOTT KULLINICAS KENTAL STATE KULLINICAS K			sequence	
TDCRVSTSAPSKAGMCLRCSACALMSVYGSVLSKRTLQASMUL VIELUMVCENLAGSTGLARFTSPPOMSVTOSLLLV HERVEDICEFYSRAKKMILGSIMKHLISHLANLTDVKQAVIE LSNESSPPIGLULTPVYRUKEKLPTAKNDAGTVERKHLIPVERAVIE LSNESSPPIGLULTPVYRUKEKLPTAKNDAGTVERKHLIPVERAVIE KESMAERADFERAKKMERJARDLAGFYPPYQHEEIIGKVCELINEV KESMAERADFERAKKMERJAVERPPAQEBDERGKMENYTDTLAG FLORTPDLFQVUKSCVTQHITTLAKLARFULLAPVAGASSGCVN MCGQALLIKRRELSSPEDMKLMFIKASMUL 6181 169 1032 TRTLISPVLLEGFERKFWRRERPBEPJALPAMLQPFYRKMAYLFI YTLIQFCOHSWIFTIMTVEPSFRKDSWNDTFYAIGLVRRLOG VSLLELHITVGISSPRLUMPFIADFANLQPFYRKMAYLFI YTLIQFCOHSWIFTIMTVEPSFRKDSWNDTFYAIGLVRRLOG VSLLELHITVGISSPRLUMPFISSPRKJERSSHUTTYSGEVOS KYVVCULPVWNLLDMYRTYSMLSVGISSPAULWESGTLMB IYPLCVLAERAFATYSSLFYSERRDILGFFIKKKMM*STAPGCDTR KDRIMTGCSK*NTOSLIVVERFUY VLAMLEIGHTYTYSELIVSERRDILGFFIKKKMM*STAPGCDTR KDRIMTGCSK*NTOSLIVVERFUY VLAMLEIGHTYTSELIVSERRDILGFFIKKKMM*STAPGCDTR KDRIMTGCSK*NTOSLIVVERFUY VROPSSSWITTGKLISVLGSCLUBFFICOVOVKILIARCPIAVR FSHQASGPCCLITTNRIALTSSELLYTYGALDSRVRALVEV PSHQASGPCCLITTNRIALTSSELLYTYGALDSRVRALVEV CWARAHSITSSI FRGMITMSESHTITYSTKETTELLIKERFFIF YFGMFAFRIKSI TRINGGRGRUMPLDETRINGSHVATHENSKUT CWARAHSITSSI FRGMITMSESHTINGVFTFTSIKKETI KTLADAEBKCVIEGHNCTEVRDLSFIKRSCONTSTLELLIKERFFIF YFGMFAFRIKSI TRINGGRGRUMFESHITYTGSFFTISHISKRN SQSOLQKFVDLARESAMILQEDTDRPSISSRFFMGLVSLLIUM KTLADAEBKCVIEGHNCTEVRDLSFIKRSCONTSTLELLIKERFE YFGMFAFRIKSI TRINGGRGRUMFTSISHITYTSISKRTI STOT 6183 1118 452 HLDBYIKSPGSSSTPAPPSHLLLYLLHPQSTRTMGCCGSRGG GGGGGSGGGGGGGGGGGGGGGGGGGGGGGGG		sequence		
VIELINVCEDLAGSTGLAKETIGSLESTSPPCMNSTTDSLILV HERYEDICETYSPAKMILISHAANILITSVKOAVIE LSNESOPILOLVLPTYVRLEKLPTAKANDAGTVGKICHIFLEAL KENFSKYHPAIKKAMILIOPOOKIRSKLISHAANILITSVKOAVIE LSNESOPILOLVLPTYVRLEKLPTAKANDAGTVGKICHIFLEAL KENFKYHPAIKKAMILIOPOOKIRSVPTYGHESI OKA KESHABEADFEPAAKKRGAAVENPAGEBODRIGKINSVTOYLOE PLOATPDLEOVING CYTCHTELIKLAFILLAVPAVGARSGOVING MCOALLIKRRELSPEDMIKLAFILLAVPAVGARSGOVING MCOALLIKRRELSPEDMIKLAFILLAVPAVGARSGOVING VOLLELHITVOIGSNIHLIPFIQLTERIILIFVVITSGESOV KTYVCVLPVFWINLIBMYRTTSPHSKOSMOTPTYAIGLOVRICOS VSLLELHITVOIGSNIHLIPFIQLTERIILIFVVITSGESOV KTYVCVLPVFWALDHOWTTSTSMENVOISTSPHOURSCTLAMS TYPLCULLEAFFATYOSLPYFSKOSTOTSTRUPPOLSITPFYVLK YLMMEIGMTYTTSHINSERRBIGIFFIKKRYLTGSLIEDMAAVFPDCI VRPGSSVNTFGKLOCLDMFIDLDETRILSAHKISGNIFMEN FIRMASSPTKKREPOLTEENFKKRYLTGSLIEDMAAVFPDCI VRPGSSVNTFGKLOCLDMFIDLDETRILSAHKISGNIFMEN FSKQASGFOCDLITTINIKIATSSELITITYGALDSRVRALVFSVR CMARARISITSTEROPTCENFYKKRYLTGSLIEDMAAVFPDCI VRPGSSVNTFGKLOCLDMFIDLDETRILSAHKISGNIFMEN FSKQASGFOCDLITTINIKIATISSELITITYGALDSRVRALVFSVR CMARARISITSTEROPTCHORTUNGUPECKORSPHILOPSELITISSEN VRSGALGKRVDLARSEANILOGEPTORPETSSHPPUGLISLILDS APRIKSFTKKKSNKPALETVONLLESLKGNRTETELLILKETSVR SQSQLOKRVDLARSEANILOGEPTORPETSSHPPUGLISLILDS APRIKSFTKKKSNKPALETVONLLESLKGNRTENFTKTSGKRT STOT HLDRYYKGPGSGSTPAPPHILLYLLHEQSTRUPGCGGCSSGC GGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			· · · · · · · · · · · · · · · · · · ·
HERYEGICEFYSRAKKWILIOSIANHILISILAAILTPUKOAVIE LSNESOPTIQUUPTYVUELKIPTAKANDAGUKCHIPTEAL KEPISKVIPAHKVANILIDEQOKURPYVPEYDEEIIGKVCELINEV KESHAEEADFEPAAKKPRAAVEPPAQEEIIGKVCELINEV KESHAEEADFEPAAKKPRAAVEPPAQEEDIGKVCELINEV KESHAEEADFEPAAKKPRAAVEPPAQEEDIGKVCELINEV KESHAEEADFEPAAKKPRAAVEPPAQEEDIGKVCELINEV KESHAEEADFEPAAKKPRAAVEPPAQEEDIGKVCELINEV KESHAEEADFEPAAKKPRAAVEPPAQEEDIGKVCELINEV KESHAEEADFEPAAKKPRAAVENPAAQEDRILGKNEVYDYLOE PLOQATPDLOPGYNSCUTIGKTIKLAKLAFILLAVPAVGARSGCVV MCCOALLIKRRILISEDHMKUMFIKASMILITVUTTSGEEVQE VYILIOECHSMITTMITVEFFSGEMOMUTPYAIGLWARLOS VSLLELLHIVYGE SENHLENFIQUTERI ILIVVITSGEEVQE KYVVCULVPWINLIMWYYYSMISVIGISYAVITMISTISMI ITYLCULEAPAT YOSILVYERSFGYTSKIKLYDISTYTIKMI ITYLCULEAPAT YOSILVYERSFGYTSKIKLYDISTYTIMI ITYLCULEAPAT YOSILVYERSFGYTSKIKLYDISTYTIMI ITYLCULEAPAT YOSILVYERSFGYTSKIKLYDISTISTYTYIKX YLMMLEIGNYFTYSHINSERDILGIDHPTIKASYLTGISTAMAYPPOI VRYPEGSINTORGILOEDHOPLDETRINIAHIISONDIAMPPOI VRYPEGSINTORGILOEDHOPLDDETRINIAHIISONDIAMPPOI VRYPEGSINTORGILOEDHOPLDDETRINIAHIISONDIAMPPOI VRYPEGSINTORGILOEDHOPLDDETRINIAHIISONDIAMPPOI VRYPEGSINTORGILOEDHOPLDDETRINIAHIISONDIAMPPOI VRYPEGSINTORGILOEDHOPLDDETRINIAHIISONDIAMPPOI VRYPEGSINTORGILOEDHOPLDDETRINIAHIISONDIAMPPOI VRYPEGSINTORGILOEDHOPLDDETRINIAHIISONDIAMPPOI VRYPEGSINTORGILOEDHOPLDDETRINIAHIISONDIAMPILOPPOI VRYPEGSINTORGILOEDHOPLDDETRINIAHIISONDIAMPILOPPOI VRYPEGSINTORGILOEDHOPLDDETRINIAHIISONDIAMPILOPPOI VRYPEGSINTORGILOEDHOPLDDETRINIAHIISONDIAMPILOPPOI VRYNEGRIADHOUTARESELIANGUNGANIANIA VRYSHAAPANAULATURGICULDETRINIAHIISONDIAMPILOPPOI VRYPEGSINTORGINIAMPILOEDHOUTARAULATURGICULDETRINIAHIISONDIAMPILOPPOI VRYPUCCEKSKIKARATIATURGICCOCSCORGO GOOGGOGSGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			
LISNESOPTIOLULPTYVURLEKLPTAKANDATOSTICKICHIPEAL KENFRUHBAHKUMAILDOGORRPUPPYOREELIGKVCELINEV KESHAEEADFEPAKKPRSAAVENPAAQEDDRIGKNEVYDYLOE PLEVATTPOLTQYMS CUTCHITELAVLAFILLAVPAVGARSGCVN MCCQALLIKRRILSFEDMKLMFIKSMMI 6181 169 1032 TRTLISPVLLEGERKEPARRERWEGLALDAWLQPRYKRMAYLFI YYLIOECCHSHITIMMTVRFSERGDSMVDTPYAIGLVGRICOS VSLLELLHIYVGIESNHLLPRFLQUTERIILIFVUTSGEEVQE KYVVCULPVFMILLDWAYTYSHSUJGISTYMISGTLMM IYPLCVLAEAPATYQSLEYFESGTYSTKLPFDLSTYPFYUKX YLLMELHIYVGIESNHLLPRFLQUTERIILIFVUTSGEEVQE KYVVCULPVFMILLDWAYTYSHJSSTLAVBSTAFQCTOT KORLHIGOSK*NTGSILVEKPLVF 6182 1769 1224 AS*IDVQINTLLIKEPQTJEENDILGIPFIKKM*STAPQCTT KORLHIGOSK*NTGSILVEKPLVF VRAFGSSVNTPGKLGCDLDMFLDLDETRILSAHKISGNFLMEPQ VRAVPSBSIATQKILSFVLGSCLDHFGRGCVGVQKILNARCEJNR FSÜQASGPQCDLTINNRILLISSELLIYTGALEEMAAAVFPDCI VRAVPSBSIATQKILSFVLGSCLDHFGRGCVGVQKILNARCEJNR FSÜQASGPQCDLTINNRILLISSELLIYTGALEEMAAAVFPDCI VRAVPSBSIATQKILSFVLGSCLDHFGRGCVGVQKILNARCEJNR FSÜQASGPQCDLTINNRILLISSELLIYTGALELLKEFFFE YFORFAFDKNISINIRGGECNKPDSSPLYIQNPFETLELLLKEFFFE YFORFAFDKNISINIRGGECNKPDSSPLYIQNPFETLELLLKEFFFE YFORFAFDKNISINIRGGECNKPDSSPLYIQNPFETLELLKEFFFE YFORFAFDKNISINIRGGECNKPDSSPLYIQNPFETLELLKEFFFE YFORFAFDKNISINIRGGECNKPDSSPLYIQNPFETLELLKEFFFE YFORFAFDKNISINIRGGECNKPDSSPLYIQNPFETLELLKKEFFE YFORFAFDKNISINIRGGECNKPDSSPLYIQNPFETLELLKEFFF YFORFAFDKNISINIRGGECNKPDSSPLYIQNPFETLELLKEFFF ORDANGARGANGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1	1		
REMPEWHPAHKVAMILDPOGKLPUPPVQHEELIGKVCELINEV KESMAEEADFEPAAKKPRAAVSNPAAQBDRLGKVCYTOYLOG PLPQATPDLPQWSCVTQKHTKLAKLAFHLAVPAVQARSGCVN MCRQALLIKKRRLASFELAVPAVQARSGCVN MCRQALLIKKRRLASFELAVPAVQARSGCVN MCRQALLIKKRRLASFELAVAVQAVQAVGCV MCRQALLIKKRRLASFELAVAVQAVQAVGCV STATLSPVLLAGFERVEDAWARGCANAVQAVGCV STATLSPVLLAGFERVEDAWARGCANAVQAVGCV STATLSPVLLAGFERVEDAWARGCANAVATHINSTYSERVOG VSLIELLHIVQUE SENHLLPRIQUTERI ILIPVITSQEBVQB KYVVCVLFVFWNILDMVRYTYSMLSVIGISYAVITMISTYSENDE KYVVCVLFVFWNILDMVRYTYSMLSVIGISYAVITMISTYSENDE KYVVCVLFVFWNILDMVRYTYSMLSVIGISYAVITMISTYSENDE KYVVCVLFVFWNILDMVRYTYSMLSVIGISYAVITMISTYSENDE KYVVCVLFVFWNILDMVRYTYSMLSVIGISYAVITMISTYSENDE KYVVCVLFVFWNILDMVRYTYSMLSVIGISYAVITMISTYBPYUKX LAMMLFIGMYFTYSHLYSERGILGEIFPIKKKM*STAFQCDTR KORMYGCSK*NTGSLIVERSPTISTYSKLYPPYUKX LAMMLFIGMYFTYSHLYSERGILGEIFPIKKKM*STAFQCDTR KORMYGCSK*NTGSLIVERSPTISTISTYSKLYPPYUKX VKMYDSERLATQKLIVYGALDSRVALAYFDCT VRPFGSSVNTFGKLGCOLDMFEDLAKFSVILTYSALDSRVALAYFSVR CKARASISTISTS IPQANITNSTITMITTAMISTELSPELIKSPSV VKMYDSERLATQKLISVLASSELLITYGALDSRVALAYFSVR CKARASISTIST IPQANITNSTITMINTYFFICHSTALSISTIST KTLADABDKCVTGSNNTCTFURLISLIKSPFF YFGMFAFDKISSINTRQECGNORDSSPLIVAGFSPLITIDSI KTLADABDKCVTGSNNTCTFURLISLIKSPFF YFGMFAFDKISSINTRQECGNORDSSPLIVAGFSPLITIDSI KTLADABDKCVTGSNNTCTFURLISLIKSPFF YFGMFAFDKISSINTRQECGNORDSSPLIVAGFSPLITIDSI STQT ST				
RESHAREADFERAKKERSANYENPANGEDRILGKRIEVYDTUGE PEPGATPULPGYSCUTGKITIKALALFHILKALALFALIKALATATIKALATATIKALATATIKALATATIKALATATIKALATATIKALATATIKALATATIKALATATIKATATIKALATATIKATIK				LSNESQPTLQLVLPTYVRLEKLFTAKANDAGTVSKLCHLFLEAL
PLPGATPDLPGYMSCTTOKHTKLAKTAFHILAVAGARSGCVM MCSQALL IKRRILLSPEUNKUMFLKSMUN 6181 169 1032 TRTLLSPVLLPGPRWKPWRRRPWGPLALPAWLQFRYRKNAYLFI YTLLGPCGHSMIFTINHTVRFPSRYRDSWDDTFYAIGLUWRLCGS VSLLELLHIYGGESHHLPFINGLUERI ILLEVVLTSGEEVQB KYVVCVLFVFNNLLDWYRTTSMLSVIGISYAVLTMLSGTLWMP IYPLCVLLARPATYQSLSYHLFSENGTYSTKLFPDLSTYPFYVLKI YLMMLFIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR KDRIMICGS K*NTGSILWFFSFYGTYSTKLFPDLSTYPFYVLKI YLMMLFIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR KDRIMICGS K*NTGSILWFKIVFF KDRIMICGS K*NTGSILWFKIVFF KDRIMICGS K*NTGSILWFKIVFT KDRIMICGS K*NTGSILWFKIVFT KDRIMICGS K*NTGSILWFKIVFT KDRIMICGS K*NTGSILWFKIVFT KDRIMICGS K*NTGSILWFKIVFT KDRIMICGS K*NTGSILWFKIVFT KDRIMICGS K*NTGSILWFKIVFT KDRIMICGS K*NTGSILWFKIVFT KDRIMICGS K*NTGSILWFKIVFT KDRIMICGS K*NTGSILWFKIVFT KDRIMICGS K*NTGSILWFKIVFT KTADAEDKCVI BGNNCTFVRIJSR KFSGNTSTLELLKSFFF YFGNFAFDKNSINTRGGRSCKVEDSSCTVOVGKILNARCHIN FSKGASGFCCDINNCTFVRIJSR KFSGNTSTELLKSFFF YFGNFAFDKNSINTRGGRSCKVEDSSCTSSSCTSSCRGGCSSCGCSS COSAGGSGCGSSGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ł	ł		KENFKVHPAHKVAMILDPQQKLRPVPPYQHEEIIGKVCELINEV
MCEGALLIKRRELISEEMNIKLIMPLKSMIL TRYLLEPVILEPGERKKPMRERMEGELALPANLQESYRKNAYLFI TRYLLEPVILEPGERKKPMRERMEGELALPANLQESYRKNAYLFI TYTLOGOGISMIFINNTVEFFSGKDSWOTFTAIGLVMRLCQS VSLLELLHIYVGIESSHILLPRFLQLTERIIILFVITAGERVQE KYVVCVLPVFNILDMYRTYSHLYSGISTSAVLTHASGERVQE KYVVCVLPVFNILDMYRTYSHLYSGISTSAVLTHASGERVQE KYVVCVLPVFNILDMYRTYSHLYSGISTSAVLTHASGERVQE KYVVCVLPVFNILDMYRTYSHLYSGISTSAVLTHASGERVTLMW TYPLCVLARAFAIVQSLPYFSSFGTYSTKLFFDLSIYPYVLKI YLMMLPIGMYFTYSHLYSERRDIGIGFPIKKKKM*STAFQCDTR KDRLWIQCSK*NTDSILVEKFLVF KDRLWIQCSK*NTDSILVEKFLVF AS*IDVQLNTLLKEFQLTEEMTKLEVLTGLIEDMAAAYFDCI VRYPGSSVNTFGKLGCLDLMFLDLDETRILSAKKIGNFLMEFQ VRNYPSERIATQKILSVLGECLDBFGFGCVGVQKILNARCPLVM FSKQASGFCCDLTTNNRIALISSELLLYTGDSRVRALDSRVALVPSVX CWARAHSIJTSIPGAMITMFSLTMWIFFLQRRSPFILDFLDSI KTLADAEDKCVIGENONTFYNDLSRIKSGDSRVALDSRVALVPSVX CWARAHSIJTSIPGAMITMFSLTMWIFFLQRRSPFILDFLDSI KTLADAEDKCVIGENONTFYNDLSRIKSGNTSTELLLLKSFFF YFGNFAFDKNSINITGGRSQNKEDDSSPLVIONPFFIKTSGKTI STOT STOT STOT APPRIKASFTKKSNRFALFTVKNLLESLGKORTENFFKKTSGKTI STOT STOT STOT STOT APPRIKASFTKKSNRFALFTVKNLLESLGKORTENFFKKTSGKTI STOT STOT STOT APPRIKASFTKKSNRFALFTVKNLLESLGKORTENFFKKTSGKTI STOT STOT STOT APPRIKASFTKKSNRFALFTVKNLLESLGKORTENFFKKTSGKTI STOT STOT APPRIKASFTKKSNRFALFTVKNLLESLGKORTENFFKKTSGKTI STOT STOT APPRIKASFTKKSNRFALFTVKNLLESLGKORTENFFKKTSGKTI STOT STOT APPRIKASFTKKSNRFALFTVKNLLESLGKORTENFFKKTSGKTI STOT STOT APPRIKASFTKKSNRFALFTVKNLLESLGKORTENFTKTSGKTT STOT STOT STOT APPRIKASFTKKSNRFALFTVKNLLESLGKORTENFTKTSGKTT STOT STOT APPRIKASFTKKSNRFALFTVKNLLESGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			KESWAEEADFEPAAKKPRSAAVENPAAQEDDRLGKNEVYDYLQE
6181 169 1032 TRTLLSPVLLDGDRWRDMRRRPMBDLADPANLOPRYRNAVLF1 YYLDGVGUSNIFTHMTWY PERSYRDSWOFT ALIGLWRRLCOS VSLLELLHIYVGIESNHLLDRFLQLTERIIILFVVITSQEEVQE KYVVCVLFVFNNLLDWRXTYSMLSVGISYAVLTMLSQTUMP IYPLCVLLABAPATYQSLFYBSFGYTSYKLFFDLSIYFPYVLKI YLMMLPIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR KDRIMTQCS*NTOSILVERFIVF* KTRUMLYGS*NTOSILVERFIVF* 6182 1769 1224 AS*1DVQLMTLLKEFQLTEENTKLKYLTCSLIEDMAAAYFPDCI VRNPGSSVANTGKLLQCLDMFLDLDETRILSAHKISGMFLMEFQ VRNPGSSVANTGKLLQCDDMFLDLDETRILSAHKISGMFLMEFQ VRNPGSSVANTGKLLGVDMFLDLDETRILSAHKISGMFLMEFQ VRNPGSSRATATOKILSVLGECLDHFGPGCVGVQKILMAACPIVR FSHQASGFQCDLTTINRIALISSELLYTYQALDSRVALVFSVR CWARAHSLITSSIPGAMITHSSHTMVHTFLQRRSPFILDTLLKKFFF YFGNFAFDKNISINTRGGRSQNKDDSSPLYJQNSPFTLDSL KTLADAEDKCVIEGNKCTFVRDLSRIKFSGNFTERFKTSGKRTI STQT 6183 1118 452 HLDRYKKEPGSGSSTPAPSHLLLYLLHPQSTRTMGCCGCSRG GSGGGGGSCGGGGGGGGGGGGGGGGGGGGGG				PLFQATPDLFQYWSCVTQKHTKLAKLAFWLLAVPAVGARSGCVN
VYLLÖEGGISMITINMTVRFFSFGKDSMVPTYJAGLVMRLCOS VSLLELLHIYVGIBSNHLLPRPLQLTERI ILFWVITSGEVOB KYVVCVLFVFMNLLDMVRYTYSMLSVIGISYAVLTMLSQTLMNP IYPLCVLARAFATYQSLPYFESFGTYSTKLPFDLSTYPFVLKIK YLMMLFIGHYTYSHLSVERRILLGIFKKKMM*STAFQCDTR KDRLWTQCSK*NTGSILVERFIVF AS*IDVGUNTLLKERGDUTENTYKLKKKM*STAFQCDTR KDRLWTQCSK*NTGSILVERFIVF AS*IDVGUNTLLKERGDUTENTKLKKKM*STAFQCDTR KDRLWTQCSK*NTGSILVERFIVF AS*IDVGUNTLKERGDUTENTKLAFUTCSLIEDMAAAYFPDCI VRPPGSSVATFGKLGCDLDMPLDLDETRINLSAIKISGNFLMERG VKNVPSERIATQKILSVLGECLDHFDGCVVQKILNARCPIVR FSKQASGFQCDLTTNNRIALISSELLYIYGALDSRVRALIVFSVR CWARAISLITSSIPGAWITNFSITMWVIFFLQRSSPFILPTLDSL KTLADAEDKCVIEGNNCTFVRULSSIKGONTSTLELLKFFF YFGMFAFDKNSINTRQGRECNKPDSSPLY1QNFFTSILNISKNV SQSALKFVDLARESAWILQGEDTDFSISNNFWGLVSVRX SQSALKFVDLARESAWILQGEDTDFSISNNFWGLVSLLPS APNRKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI STQT 6183 1118 452 HLDRYYKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCCGCSRGC GSGGGGSGSGGGGSGGGGGSGGGGSSGGGGSSCGGCSSCGGCSS CGCSGSSGCGSSCCGSGCGGCSSCGGCSSCGGCSSCGGCGS GSGGGGSSGCGGGGGGGG		1		MCEQALLIKRRRLLSPEDMNKLMFLKSNML
USLLEILHTYGIBSNHLLPREJQLTERITITLEVUTTSQEEVOB KYVVCVLFVFNNLDMVRYTYSMLSVIGISYAVLTMLSQTLMMP 1YPLCVLARAFATYGSLPYFESFGTYSTKLPFDLSTYPPYUKI YLMMLPIGMYFTYSHLYSBERDILGIFFIKKKMSTAFQCDTR KDRIMATQCSK-MYTGSILDVERFLYFT KDRIMATQCSK-MYTGSILDVERFLYFT KDRIMATQCSK-MYTGSILDVERFLYFT KDRIMATQCSK-MYTGSILDVERFLYFT KDRIMATQCSK-MYTGSILDVERFLYFT KDRIMATQCSK-MYTGSILDVERFLYFT VRPPGSSVAPTFCKLQCLDMPDLDDEFTNLGARKIGGHFLMEPQ VRNVPSERIATQKILSVLGBCLDHFGPGCVGVQKILNARCPLVR PSHQASGFQCDLTTNNRIALITSSELLYTYGALDSKRALVFSVR CWARAHSIJSSIFGGMITHNSTLTMWYJTPFTLGRSPFILIPTLDSI KTLADAEDKCVIEGNNCTFVRDLSKIRSONTSTIEBLLIKEFFF YFGMFAFDRNSINIRGAGENRYDSSIVJOPPFTSIKISKNV SQSQLQKFVDLARESAWILQGDTDRPSISSNPWGLVSILLPS APRIKSFTKKKSNKRALETVKRLESLKGRRTENFTKTGSKRTI STQT 6183 1118 452 HLDRYTKSFGGSSTPAPPSHLLLYLLHPQSTTRTWGCGCSRG GSGGGSGSGGGGGGGGGGGGGGGGGGGGGGGG	6181	169	1032	TRTLLSPVLLPGPRWKPWRRRPMGPLALPAWLQPRYRKNAYLFI
KYVVCVLFVFWNLLDMWRTTYSMLSVIGISTALTMLSGYTLMING IYPLCVLAEAFAIYQSLPYFESFGTYSTKJPFLYLKI YLMMLPIGMYFTYSHLYSERRDILGIFFIKKKM-STAFQCDTR KDRLWIQCSK-NTGSILVEKFILVF AS-1DVQLWTLLKEFQUTEENTKLEVLTCSLIEDMAAAYPPDCI VRPPGSSVMTFGKLGCLDMPLDLDETKNLSAIKIJGNFLMEFQ VKNVPSERIATQKILSVLGECLDHFDGPGVCVQVQKILNARCPJVR FSÜQASGFQCDLTTNNRIALISSELLYIYQALDSRVRALVFSVR CWARAHSLTSSIPGAWITNFSLTMWVIFFLQRRSPFILPTLDSL KTLADABDKCVIEGNNCTFVFULSSR KONTETLELLIKFFFE YFGMFAPDKNSINTRQGEGNRFDSSPLYJQNFFTSLNISKNV SQSQLQKFVDLARESAWILQQEDTDRPSISSNRFWGLVSLLLPS APNRKSFTKKKSNKFAIETVRALLESLKGRRTENFTKTSGKRTI STQT 6183 1118 452 HLDRYIKSPGGSSTPAPPSHLLLYLLHPQSTRTWGCGGCSRG GSGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1	1	1	YYLIQFCGHSWIFTNMTVRFFSFGKDSMVDTFYAIGLVMRLCQS
KYVVCVLFVFWNLLDMWRTTYSMLSVIGISTALTMLSGYTLMING IYPLCVLAEAFAIYQSLPYFESFGTYSTKJPFLYLKI YLMMLPIGMYFTYSHLYSERRDILGIFFIKKKM-STAFQCDTR KDRLWIQCSK-NTGSILVEKFILVF AS-1DVQLWTLLKEFQUTEENTKLEVLTCSLIEDMAAAYPPDCI VRPPGSSVMTFGKLGCLDMPLDLDETKNLSAIKIJGNFLMEFQ VKNVPSERIATQKILSVLGECLDHFDGPGVCVQVQKILNARCPJVR FSÜQASGFQCDLTTNNRIALISSELLYIYQALDSRVRALVFSVR CWARAHSLTSSIPGAWITNFSLTMWVIFFLQRRSPFILPTLDSL KTLADABDKCVIEGNNCTFVFULSSR KONTETLELLIKFFFE YFGMFAPDKNSINTRQGEGNRFDSSPLYJQNFFTSLNISKNV SQSQLQKFVDLARESAWILQQEDTDRPSISSNRFWGLVSLLLPS APNRKSFTKKKSNKFAIETVRALLESLKGRRTENFTKTSGKRTI STQT 6183 1118 452 HLDRYIKSPGGSSTPAPPSHLLLYLLHPQSTRTWGCGGCSRG GSGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				VSLLELLHIYVGIBSNHLLPRFLQLTERIIILFVVITSQEEVQE
I TYPLCVLARAFATYQSLPYESFGTYSTKLPFDLSTYPPYJLKI YLMMLPIGMYTYSHLYSERROILLSFPIKKKMM*STAPCCDTR KORLMIQCSK*NTGSILVEKFLVF AS*IDVQINTLIKEFQLTEENTKLRYLTCSLIEDMAAAYFPDCI WPPGSSVNTFGKLGCLDMFUDLDETRILSAHKISGFLMEFQ VKNVPSSRIATGKILSULDMFUDLDETRILSAHKISGFLMEFQ VKNVPSSRIATGKILSULGECLDHFUDLDSTALKISGFLMEFQ VKNVPSSRIATGKILSULGECLDHFUDCHSLIKSFFLMEFQ VKNVPSSRIATGKILSULGECLDHFUDCHSCHAVGKILNARCPLVR FSHQASGPCQLTTINILALISSELLIYTGANDSRVRALVFSVR CWARAHSLTSSIPGAWITNFSLTMMVIFFLQRRSPPILPTLDSL KTLADAEDKCVIEGNNCTFVRDLSRIKPSONTETLELLLKSFFE YFGRFAFDINSININGGRENKPDSSTYJOPPFTSLINIS ISKV SQSGLKKFUDLARESAWILQGEDTDRPSISSNPPWGLVSLLLPS APNRKSFTKKKSNKPAIETVKNLLESLKGNRTENFTKTGSKRTI STQT 6183 1118 452 HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCCGSCRGC GSGGGGGGSGCGGCGSSGGGGGGGGGGGGG				
VLMMLPIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR KDRIMIQCSK*NTGSILVEKPIVF AS*IDYQLMTLLKERQLFENTKLRYLTCSLIEDMAAAYFPDCI VRPFGSSVMTFGKLGCDLDMFLDLDETRALSAKKISGNFLMERQ VKNYPSERIATOKILSVLGECLDBFGGGCGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1			l .
KDRLWIQCSK*NTGSILVERFIVF	1) -
AS * IDVQLMTLLKEFQLTEENTKLRYLTCSLIEDMARAYFPDCI VRPFGSSVNTFKKLGCLLDETRIKERYLMTENG VRAWPSERIATQKISVJEGELDHFGPGGCVGVQKILMARCPLWR FSHQASGFQCDLTTNNRIALITSSELLYIYGALDSRVRALWFSVR CMARAHSLTSSTFQAWINNSILMTFLQRESPTLPTLDSL KTLADAEDKCVIEGNNCTFVRDLSRIKPSQNTETLELLLKEFFE YFGMFAPDKNSINIRQREGNKFDSSPLYINGFFSTSLNTSKNV SQSQLQKFVDLARESAWILQGETDTDRPSTSSNFPMGLVSLLLPS APNRKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI STQV GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			
VRPPGSUNTFGKLGCDLMPFJDLDETRJLSHHKISGNFIMEPQ VKNVPSERIATQKILSVLGCCDHFGPGCVGVQKILNARCPLVR PSHQASGFQCDLTTNNRIALITSSELLYTYGALDSRVRALUFSVR CWARAHSLTSSIPGAMITMFSLTMMVIFFLQRSSPFLIPTLDSL KTLADAEDKCVIEGNNCTFVRDLSRIKPSQNTETLELLLKEFFE YFGMFAPDKNSINIRGGREQNKPDSSPLYIQNPFETSLNISKNV SQSQLQKFVDLARESAWILQGEDTRPSISNRFWGLVSLLLDS APNKKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI STQT 6183 1118 452 HLDRYTKSPGSSSTPAPPSHLLLYLLHPGSTRTMGCCGCSRGC GSGCGGCGSSCGGCGSSCGGGCGSCGGCSSCGGCGS RCYVPVCCCKPVCSWVPACSCTSCGSCGGSKGGGSCGGSCGGCS GSCGCSQSSCCKPCCCSSGCGSCGCGCSSCGGCGS RCYVPVCCCKPVCSWVPACSCTSCGSCGGSKGGGCSCGGSKGG GSCGCSQSSCCKPCCCSSGCCSSCCCPVC CQSSCCKPCCCSSNCCVPVCQCKI*GSGPPGFSGFSCLVXAFIM VP 6184 1 2191 TVTVREEDGAPAVAPPGVVVSRANKRSGAGFGGSGGGARGAEE EPPPPLQAVLVADSFDRFFFPISKDQPRVLLPLANVALIDYTLE FLITATGVQETFVPCCKKAAQIKEHLLKSKMCRPTSLMVVRIITS ELYRSLGDVLRPUDARALVRSFPLLVYGDVISNITITRALEFIRK LRRLL*KNVSVMTMIFKESSPSHPTRCHEDNVVAAVDSTTNRVL HPQXTGGLRRFAFPLSLFQGSSDGVVPVVDLDLCHISICSPQVA QLFTDNPDYGTRDDFVGGLIVMEEILGNQIHMHTTAKEYGARVS MLHMYSAVCADVIRRWVPLTPEAMFTDSTQSCTHSRHNIYRG PEVSLGGGSILEENVLLGGSTVIGSNCFTTNSV1GPGCHEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNTTLPEGSVISLHPPDAEEDDGBEFSDDGADQEK MCKMKGYNPABVAGAGKGTUKRAGMMEEEBELQONLWGLKI NMEESSESSESGSMDSBEPDSRGSSPQMDIKVFONEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVWQVLSHVVVLEPPLQQ MDSPLDSSRYCALLLPLIKAWSPVFNTIKRAAPHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRRNQOLQRFIOWLKBABEESDD GLRNQOLQRFIOWLKBABEESDD GFLGNVCNIPPSULLAEGNLIFLTGLSLILGLRKTFWFFFCR HKLKGTSFLLGSVVVLLERWIGHETTYGFFSIFKSFPPVAF GFLGNVCNIPPSGAMQTFTLTGUSSLILGERKTFWFFFCR HKKGTSFLLGSVVVVLLERWIGHETTYGFFSIFKSFPPVAF GFLGNVCNIPPSGAMQTTFTLTGUSSLLIGERKTFWFFFCR HKKGTSFLLGSVVVVLLERWIGHETTYGFFSIFKSFPPVAF GFLGNVCNIPPSGAMQTTFTLTGUSSLLIGERKTFWFFFCR HKKGTSFLLGSVVVVLLERWIGHETTYGFFSIFKSFPPVAF GFLGNVCNIPPSGAMQTTFTLTGUSSLLIGERTFRWFFTCR HKKGTSFLLGSGAMQTFRIGGGSTTLTGUGWTTTLTCTLSTLESLTGLFSKAPPVAF GFLGNVCNIPPSGAMQTTFTLTGUSSLNLDHWLKGAK REEWEPPPGSPALTHSPTTCTTLTTLTMEEK	6182	1769	1224	AS*IDYOLNTLLKEFOLTEENTKLRYLTCSLIEDMAAAYFPDCI
VKNYPSERIATQKILSVLGECLDHFGPGCVGVQKILNARCPLVN FSHQASGFQCDLTTNNRIAITSSELLYIYGALDSRVRALVFSVR CWARAHSLTSSI EGANITMFSILMVIFFLQALDSRVRALVFSVR KTLADAEDKCVI EGANICTFVRDLSRIKFSQNTETLELLKEFFE YFGNFAFDKNSINIRQGREQNRFDSSPLYIQNPFETSLNISKNV SQSQLQKFVDLARESAWILQGEDTDRPSISSNRPWGLVSLLLS APNRKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI STQT 6183 1118 452 HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTWGCGCSCRGC GSGGGGGGSGGGGGSGGGGGSGGGGGGGGGG				VRPFGSSVNTFGKLGCDLDMFLDLDETRNLSAHKISGNFLMEFO
FSHQASGFQCDLTTNNRIALISSELLYIYGALDSRVRALVFSVR CWARAHSLTSSIPGAWITNFSLTMWIJFTQRRSPFILPTLDSL KITLADAEDKCVIEGNNCTFVRDLSRIKPSGNTETLELLLKEFFE YFGMFAFDKNSINIRQGREGNKEDSSBLYIQNPFETSLNISKNV SQSQLQKFVDLARESAWILQQEDTDRPSISSNRPWGLVSLLLPS APNRKSFTKKKSNKFAIETVKNLLESLKGRRTENFFKTSGKRTI STQT 6183 1118 452 HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCGGCSRGC GSGGGCGGSSCGGGGGGGGGGGGGGGGGGG	1	l .	}	
CWARAHSLTSSIPGAWITMFSLTMWVIFFLQRRSPPILPTLDSL KTLADABDKCVIBGNNCTFVRDLSRIKFSGNTETLELLLKEFFE YFGHFAPTKNSINIRQGREGNKEDSSPLYIQNFFETSLNISKNV SQSQLQKFVDLARESAWILQCEDTDRPSISSNPWGLVSLLLPS APNRKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI STQT 6183 1118 452 HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCGCSGSG GSGGGGGSGGGGGGGGGGGGGGGGGGGGGG				
KTLADAEDKCVIBGNNCTFVRDLSRIKPSQNTETLELLLKEFFE YFGRFAPDKNSINIRGREQDNKEDSSELYIQNDFETSIANISKNV SQSQLQKFVDLARESANILQQEDTDRPSISSNRPWGLVSLLLPS APNRKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI STQT 6183 1118 452 HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCCGCSRGC GSGCGGGSGCGGGSGCGGCGSGCGGCGSCGGCGGCGGCGG				
YFGNFAPKNSINIRQGREQNKPDSSPLYIQNPFETSLNISKNV SQSQLQKFVDLARESAWILQGEDTDRPSISSRRPWGLVSLLLPS APPNKSFTKKKSNKFAIETVKNLLESLKGNRTENFFKTGSKRTI STQT HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCCGCSRGC GSGCGGGSSGCGGGCGSGGGGGGSSGGGGGSSGGGGGSSGGGGS RCYVPVCCCKPVCSWVPACSCTSCGSCGGKGGGGSCGGCGSKGGC GSGCSCSSCCKPCCCSSCCVSVCCQCKI*GSGPRPSGFSCLVKAFLM VP 6184 1 2191 IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGGSGGGAGAEE EPPPPLQAVLVADSPDRFFFISKDQPRVLLPLANVALIDYTLE FLYARGYQETFYFCCMKAAQIKEHLLKSKMCRPTSLNVVR.ITS ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR LRRIL*KNVSVMTMIFKESSPSHPTRCHEDNVVVADDSTTNRVL HPQKTQGLRRFAFPLSLFQGSSGGVEVRVDLLDCHISICSPQVA QLFTDNFDYQTRDFVDFVRLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWVYPLTPEAMFTDSTTQSCTHSRRNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIKQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDEFSDDSCADQEK DKVKMKGYNPASVGAAGKGYLMKAAGMNMEEEBELQQNLWGLKI NMEESESESEQSMDSEBPDSRGSSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYANNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVIMAFYQLEILAEETILSWFSQRDTTDKGQ QLRNQQLQRFIQWILKEAEEESSEDD 6185 791 44 PCTSCVLWATLHILPASTRKAPQAECGMISITEMQKIGVGITGFG IFFILEFTLLGTLLYFDSVLLAFGNLLFITGLSLIGLRKTFWFFFQR HKLKGTSFLLGGVIVTLLEWPLLGWFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSWV*KTEMSSLNLDHNLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQBAEMGTPRRLQGTSSWV*KTEMSSLNLDHNLKGAK	1	1		
SQSQLQKFVDLARESAWILQQEDTDRPSISSNRPWGLVSLLLPS APNRKSFTKKKSNKFAIBTVKNLLESLKGNRTENFTKTSGKRTI 5TQT 6183 1118 452 HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCGCSRGC GSGGCGGCGSGCGGCGSGGCGGCGGCGSGSCGGCGS RCYVPVCCCKPVCSWVPACSCTISCGSCGGGCGSGSKGGCGS GSCGCSQSSCCKPCCCSSGCGSGSGGCGSGCGSKGGCGSCGGSKGGCGSCGCSKGGCGSCGCSKGGCGSCCGSKGGCGSCCGSKGGCGSCGCSKGCGCSCCCPVCC CQSSCCKPCCCQSNCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM VP 6184 1 2191 TVTVREEDGAPAVAPFGVVVSRANKRSGAGPGGSGGGARGAEE EPPPPLQAVLVADSFDRRFFPISKDQPKVLLPLANVALDTYTLE FLYTATGVQETFVPCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS ELYRSLGDVLRDVDAKAALVRSDFLLVYGDVISNINITRALEEHR LRRKL*KNVSVMTMLFKESSPSHPTRCHEDNVVAVDSTTNRVL HFQKTQGLRFFAFPLSLFQGSSGVVEVRYDLLDCHISICSPQVA QLFTDNFPYQTRDDFVRGLLVAEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWVYPLTPEAMFTDSTTQSCTHSRINIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEFPGD NVVLDQTYLMQGVRVAAGAQIRQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDGGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI NMEESSESESCSMDSBEFDSRGGSPQMDDIKFVGNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHERALGISNAKVLMAFQUEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEAEEESSEDD GCRENGCGISSGAGGAGCGCGCSSCGCSCGCS GCGAEMGTPRRLAGGTSSWV*KTEMSSLNLDHNLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCGAEMGTPRRLAGGTSSWV*KTEMSSLNLDHNLKGAK		1		-
APNRKSFTKKKSNKFAIETVRNLLESLKGNRTENFTKTSGKRTI STQT 6183 1118 452 HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCCGCSRC GSGCGGCGSGCGGCGSCGGCGSCGCGCSCGCGCS RCYVPVCCCKPVCSWVPACSCTSCGCGSKGGCGSCGGSKGGC GSCGCSQSSCCKPCCCSSGCGSCCGSCCGSKGGC CQSSCCKPCCCSNCCVPVCCQCKI*GSGPRGSGCGGCSCGSKGGC CQSSCCKPCCCSNCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM VP 6184 1 2191 TVTUREEDGAPAVAPGVVVSRANKRSGAGPGSGGGGARGAE EPPPPLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE FLTATGVQETFVFCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS ELYRSIGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVAVDSTTNRVL HFQKTQGLRRFAFPLSLFQGSSDCVWRYDLLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVNEEILCMQIHMHVTAKEVGARVS NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLIGSGTVIGSNCFITNSVIDPGCHIEFOD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGFSDDGSADGEK DKVKMKGYNPASVGAAGKGTJWKAAGMMEEEBELQQNLWGLKI NMEEESESESEQSMDSEPDSRGGSPQMDDIKVFQNEVLGTLQR GKERNISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLKAMSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEET ILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKBABEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLLNVCNIPPIGALFRRLQGTSSMV*KTEWSSLNLDHNLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLITSNPQVDSR GCQEREMQTPRRLIGWGWYHTLTDYLWEEK	1			1
STQT	į	1	ĺ	
HLRRYIKSPGSGSTPAPPSHLLLYLHPQSTRTMGCCGCSRGC GSGCGCGSSCGGCGSGCGCGSGCGCGCGCGCGCGCGCGC	l	,		
GSGCGGCGSSCGGCGGGGGGGGGGGGGGGGGGGGGGGG	6183	1110	452	
RCYVPVCCKPVCSWVPACSCTSCGSCGGSKGGCGSCGGS GGCGGSCGCGSCCKPCCCQSSCCVPCCCCSSCCCPCCQSSCCVPCCCQSSCCVPCCCQSSCCVPCCCQSSCCVPCCCQSSCCCCCCCCCC	0100	1	. 232	
GSCGCSQSSCCKPCCCSSGCGSSCCQSSCCKPCCQSSCCVPVC CQSSCCKPCCCQSNCCVPVCCQCKI*GSGPPPSGFSCLVKAFLM VP 6184 1 2191 TUTVREEDGAPAVAPPGVVVSRANKRSGAGPGSGGGARGAEE EPPPPLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE FLTATGVQETFVFCCKKAAQIKEHLLKSKWCRPTSLNVVRIITS ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR LRRKL*KNVSWMTMIFKESSPSHPTRCHEDNVVVAVDSTTRRVL HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVNEE ILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEFGD NVVLDQTYLMQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKNKGYNPAEVGAAGKGYLWKAAGMNREEEBELQQNLWGLKI NMEEESESESEQSMDSEBPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEAEEESSEDD GLRKNQQLQRFIQWLKEAEEESSEDD HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTENSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEARMQTPRRLGWGWYHTITLYLWEEK	1			1
CQSSCCKPCCQSNCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM VP 6184 1 2191 TVTVREEDGAPAVAPPGVVVSRANKRSGAGPGGSGGGARGAEE EPPPPLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE FLTATGVQETFVFCCMKAAQIKEHLLKSKWCRPTSLNVVRIITS ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTIRVL HFQKTQGLRFFAFPLSLFQGSSGGVEVRYDLLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVMEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLMQGVRVAAGAQIHQSLLCDNASVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAFVGAAGKGYLWKAACMNMEEEELQQNLWGLKI NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLIKAWSPVFRNYIKRAADHLBALAAIED FFLEHEALGISMAKVLMAFYQLEILABETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEABEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWBDPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEABMQTPRRLGWGWYHTLTLYLWBEK				
VP	ł	<u> </u>		T: "
1 2191 IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGGSGGGARGAEE EPPPPLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE FLTATGYQETFVFCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL HFQKTGGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGSFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHBALGISMAKVLMAFYQLEILABETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEAEBESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEDPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWBEK				
EPPPPLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE FLTATGVQETFVFCCKKAQIKEHLLKSKWCRPTSLNVVRIITS ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEHRR LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL HFQKTQGLRRFAFFLSLFQGSSDGVEVRYDLLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWYPLTPEANFTDSTTQSCTHSRRNIYRG PEVSLCHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI NMEEESESESEQSMDSEBPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEABEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEARMQTPRRLGWGWYHTLTYLWEEK	6184	 	2191	
FLTATGVQETFVFCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR LRRKL*KNVSVMTMTFKESSPSHPTRCHEDNVVVAVDSTTNRVL HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPABVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGFLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEAEEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGGPSQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	0.204	1 . •	1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMMEEEBELQQNLWGLKI NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEAEEESSEDD 6185 791 44 PCTSCVLWATHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIGLRKTFWFFFQR HKLKGTSFLLGGVVIVVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWBEK	İ	1		
LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWYYPLTEEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPABVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEABEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEABMQTPRRLGWGWYHTLTLYLWEEK	1]	
HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWYYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMINEEEBELQQNLWGLKI NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEABEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFPSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWBEK				
QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI NMEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILABETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEABEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEABMQTPRRLGWGWYHTLTLYLWEEK	1			1 " "
NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI NMEESESESESQSMDSEBEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEABEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEABMQTPRRLGWGWYHTLTLYLWEEK	1		1	1
PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI NMEEESESESEQSMDSEBPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEABEESSEDG 1FFILFGTLLYFDSVLLAFGNLFLTGLSLIGLKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1			
NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEABEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1			
TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI NMEEESESESEQSMDSEBPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKANSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEABEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	į.			
DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI NMEEESESESEQSMDSEBPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEABEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1			
nmeeeseseseqsmdseepdsrgspqmddikvfqnevlgtlqr gkeeniscdnlvleinslkyaynislkevmqvlshvvlefplqq mdspldssrycalllpllkawspvfrnyikraadhlealaaied fflehealgismakvlmafyqleilaeetilswfsqrdttdkgq Qlrknqqlqrfiqwlkeabeessedd 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG iffilfgtllyfdsvllafgnllfltglsliglrktfwfffqr HKLKGTsfllggvvivllrwpllgmfletygffslfkgffpvaf Gflgnvcnipflgalfrrlqgtssmv*ktemsslnldhwlkgak REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1		ŀ	
GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEABEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1		[
MDSPLDSRYCALLLPLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEABEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1		1	
FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEABEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1	1		1
QLRKNQQLQRFIQWLKEABEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1			•
6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1		1	
IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	- <u></u> -			
HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	6185	791	44	
GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	ì			
REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1	1	1	
GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	J		1	1
	ł		1	
6186 569 238 VYGIDSSNTNTHGAEERNRKLKKHWKLCHAQSRLDVNGLALKMA				
	6186	569	238	VYGIDSSNTNTHGAEERNRKLKKHWKLCHAQSRLDVNGLALKMA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	Giucamic Acid, repnenylatanine, GeGlycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
			L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			KERKVKNKVKNKADTEEVFNNSPTNQEKMPTSAILPDFSGSVIS
	1		NIRNOMETLHSQPHQEENLCFENSFSLINLLPINAVEPTSSQQI
J	} .		PNRETSEANKERRKMTSKSSESNIYSPLTSFITADSELHDIIKD
			LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVCSVGCCYHLLSE
			EFENOHKERTQEKWGFPMCHYLKEERWCCGRNARMSACLALERV
			AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRHVGKIYSKCSSF
ı			LDYVRRSLKKLGLDESKLPEKIIMNYYEKYKPRMNELEAFNMLK
1			VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLFDPVKSPRCYA
	1		VIALKKQQ*FPLKQIIRCISL*DSAGCAEEVSVGDGGPALRDAP
		•	PSGSRVGSRYD
6187	1701	771	
""'	1,01	1/1	DAWGPETRLARILNPDSFIEPRPGRLPELEATRPHMEPKASCPA
1		:	AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDIPGLEVAVVTT
	,		ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDPVLHIDLRRWADL
Į			LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSKPLLFCPAMNT
1			AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGDEGLGAMAEVG
1			TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEWVQAKSVKMDV
!			GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPGLSFFQPGEAA
<u> </u>			A
6188	238	1534	KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHPSA+GPRWASW
			NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCMQEMG
j			NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYEKKKYMDRSLD
		• •	INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKMPQKKEDPQLP
			RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTLEKDLDLLASV
			PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEPGSKSEEIGKK
	·		QLSKDSILSLYGSQTPQMPTQAMFMAPAQMAYPTAYPSFPGVTP
Į.			PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGYMGGMQASMMG
	l i		VPNGMMTTQQAGYMAGMAAMPQTVYGVQPAQQLQWNLTQMTQQM
Ī			AGMNFYGANGMMNYGQSMSGGNEQAANQTLSPQMWK
6189	1297	793	LGEPLGDLCELIPGDVQQLQMGEVHPGTGAQGSAAQSVAGEVOL
1			TQLSHARQRPSCQGSQLIALDLOHMDISROPRWOHVOPVAROVO
İ	·		RAQQAQLAEGVAVHLWAGDAVVAEVELLQEVGGGKVFAANACDL
1		•	VVQDHEGAHAARQATGHALQRVIVQVRRVQPLEAL*RVPSGLPR
1			
1	<u> </u>		RVRAFMILHNQITGIGREDFATTYFLEELNLSYNRITSPQVHRD
1	·		AFRKLRLLRSLDLSGNRLHMLPPGLPRNVHVLKVKRNELAALAR
[GALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQ
l ·	,		LTEIPEGLPESLEYLYLQNNKISAVPANAFDSTPNLKGIFLRFN
1			KLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKE
61.00			EEEEDEVEEEETR
6190	66	1309	ILVGNVSFLLSFAEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQ
			GLHCETCKEGFYLNYTSGLCQPCDCSPHGALSIPCNSSGKCQCK
	ļ		VGVIGSICDRCQDGYYGFSKNGCLPCQCNNRSASCDALTGACLN
	}		CQENSKGNHCEECKEGFYQSPDATKECLRCPCSAVTSTGSCSIK
			SSELEPECDQCKDGYIGPNCNKCENGYYNFDSICRKCQCHGHVY
[PVKTPKICKPESGECINCLHNTTGFWCENCL*GYVHDLEGNCIK
1	1		KVILPTPEGSTILVSNASLTTSVPTPVINSTFTPTTLQTIFSVS
1	ļ		TSENSTSALADVSWTQFNIIILTVIIIVVVLLMGFVGAVYMYRE
] 1			YONRKLNAPFWTIELKEDNISFSSYHDSIPNADVSGLLEDDGNE
)	İ		VAPNGQLTLTTPIHNYKA
6191	1212	1511	VNLCHGGLLHLSTHHLGIKPSMH*LFFLMLSFPHLTPQQPKCPS
			MIDWIKKIWYIYTMEYYATIKRNEIMFFAGTWMEMEAIILSKLM
j (ļ	ODYMFSLISGS
6192	3	050	
6,34	ا د	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
			KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
	.	,	PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
			RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
<u> </u>			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
		to first	
	corresponding	•	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Į.	\=possible nucleotide insertion)
			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAOKRKSKW
			DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
		1	IVKKAKQ
6193	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
		1	KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
			PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
			RCSNHLODKIOKLYBRKIKEGMDMNYIIORKKEFRNPSIYEKLI
	İ		QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAOKIEMDKLEK
			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
		1	DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
			IVKKAKO
6194	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
V.274) 550	
			KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
			PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
		1	RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
	1		DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
			IVKKAKQ
6195	736	235	VANGLQSNMPKFYCDYCDTYLTHDSPSVRKTHCSGRKHKENVKD
		1	YYQKWMEEQAQSLIDKTTAAFQQGKIPPTPFSAPPPAGAMIPPP
		1	PSLPGPPRPGMMPAPHMGGPPMMPMMGPPPPGMMPVGPAPGMRP
		· ·	PMGGHMPMMPGPPMMRPPARPMMVPTRPGMTRPDR
<u> </u>	<u> </u>	<u> </u>	
6196	1512	623	KTGKRRSAAYVRNILDNAEOVISNLEARNIGPRLTPLLOEEDSH
6196	1512	623	KTGKRRSAAYVRNILDNAEQVISNLEARNLGPRLTPLLQEEDSH ORLLMGLMVSELKDHFLRHLOGVEKKKIEOMVLDYISKLLDLIC
6196	1512	623	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC
6196	1512	623	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL
6196	1512	623	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL
6196	1512	623	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVBTNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR
6196	1512	623	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVBTNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNBKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS
			QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVBTNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVBEAALKHTAMLLGL
6196	1512	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVBTNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVBEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG
			QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVBTNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVBEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRFRGFAYVQFEDVRDAEDALYNLNRKWVCG
			QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVBTNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVBEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG
			QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVBTNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVBEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRFRGFAYVQFEDVRDAEDALYNLNRKWVCG
			QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVBTNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVBEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRFRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS
			QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVBTNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ
			QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVBTNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRFRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS
			QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHYTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSTYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHYTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVBEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDPYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDPYTRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKPSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRNFGSRGSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKPSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPPEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRNFGSRGSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDDPLSSYINANYIRG
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKPSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRNFGSRGSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKPSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPPEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRNFGSRGSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDDPLSSYINANYIRG
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHYTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPPEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVBEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGNRRRSDSLKESRHRFSYSQSKSRSLPRRSTSARQ SRTPRNFGSRGRSRSKSLQKRSKSIGKSQSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDPLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREBS AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDPLDLDPVETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII
6197	111	1912	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSBRLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRAGGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKYYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE
6197	3	819	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTHLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSR YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREBS AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYLATQGPIVSTVADFWRWWQEHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA
6197	111	1912	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKBY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY
6197	111	1912	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDPYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKBY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN EKCTEYMPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV
6197	111	1912	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSSWGRNRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS YRHKNSW SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKBY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY

SEQ	Predicted	Predicted end	Lamino poid goment and
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	<u> </u>		FYDENDSKLFEQILKAEYEFDSPYWDDISDSAKDFIRNLMEKDP
			NKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKNFAKSKWRQ
ľ			AFNATAVVRHMRKLHLGSSLDSSNASVSSSLSLASQKDCASGTF
			HAL*
6200	702	96	LPEVPHSLRPRVKPHLCCAQPAVRVMARLPKLAVFDLDYTLWPF
1			WVDTHVDPPFHKSSDGTVRDRRGQDVRLYPEVPEVLKRLQSLGV
			PGAAASRTSEIEGANQLLELFDLFRYFVHREIYPGSKITHFERL
			QQKTGIPFSQMIFFDDERRNIVDVSKLGVTCIHIQNGMNLQTLS
-			QGLETFAKAQTGPLRSSLEESPFEA
6201	2809	2383	GQTPRVRWKMRRSLRAGKRRQTAGRKSKSPPKVPIVIQDDSLPA
ŀ			GPPPQIRILKRPTSNGVVSSPNSTSRPTLPVKSLAQREAEYAEA
			RKRILGSASPEEEQEKPILDRPTRISQPEDSRQPNNVIRQPLGP
			DGSQGFKQRR
6202	2	426	INADRAAVASSLLSRPTRKMAPQKDRKPKRSTWRFNLDLTHPVE
1			DGIFDSGNFEQFLREKVKVNGKTGNLGNVVHIERFKNKITVVSE
	ļ		KQFSKRYLKYLKKYLKKNNLRDWLRVVASDKETYELRYFQISQ
Ĺ			DEDESESED
6203	419	2550	RCPRPPATAGAAASRPDRSPPSGISGSEAAAGAGAAAAPASQHPA
1			TGTGAVQTEAMKQILGVIDKKLRNLEKKKGKLDDYQERMNKGER
			LNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTIKKTA
			RREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGV
1			PILSEEELSLLDEFYKLVDPERDMSLRLNEQYEHASIHLWDLLE
			GKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNHQNGLCEEEEAA
			SAPAVEDQVPEAEPEPAEEYTEQSEVESTRYVNRQFMAETQFTS
1			GEKEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQAD
			PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPM
			NPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVPLVSSTS
1			EGYTASQPLYQPSHATEQRPQKEPIDQIQATISLNTDQTTASSS
			LPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAPVP
1 1			PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG
	,		TYHGSPDQSHQVTGNHQQPPQQNTGFPRSNQPYYNSRGVSRGGS
			RGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAP
	49		RDYSGYQRDGYQQNFKRGSGQSGPRGAPRGRGGPPRPNRGMPQM
6204	2933	707	NTQQVN
0204	2333	787	CTHNLISLIGGRALIHFNRFLNLKIQEGEAHNIFCPAYDCFQLV
	•		PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV
1 1			RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWECLGEAHEP
1 1	Į.		CDCQTWKNWLQKITEMKPEELVGVSEAYEDAANCLWLLINSKPC
1 1	1		ANCKSPIQKNEGCNHMQCAKCKYDFCWICLEEWKKHSFVHWEVI
1	}		YRCTRYEVIQHVEEQSKBMTVEAEKKHKRFQELDRFMHYYTRFK NHEHSYQLEQRLLKTAKBKMEQLSRALKETEGGCPDTTFIEDAV
1			HVLLKTRRILKCSYPYGFFLEPKSTKKEIFELMQTDLEMVTEDL
			AQKVNRPYLRTPRHKIIKAACLVQQKRQEFLASVARGVAPADSP
1 1		i	EAPRRSFAGGTWDWEYLGFASPEEYAEFQYRRHRQRRRGDVHS
			LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS
] [İ	•	SLRDYTPASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA
			LDEETROFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE
] [į		LLELGDSLMRLGAENDPFSTDTLSSHPLSEARSDFCPSSSDPDS
] [l		AGQDPNINDNLLGNIMAWFHDMNPQSIALIPPATTEISADSQLP
1	1		CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI
	Į		PGGGKQHPQAW
6205		1200	RAHRGKMALEVGDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD
	-	1200	
			SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR KRQKCFNPPPKPEPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN
<u> </u>	j	ľ	QDAVATELGILGMEGTIDRSRQSETYNYLLAKKLRKESQEHTKD
			LDKELDEYMHGGKKMGSKEEENGOGHLKRKRPVKDRLGNRPEMN
LL	<u></u>		THE STATE OF THE S

	•		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
10.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	,	to first	L=Leucine, M=Methionine, N=Asparagine,
1	corresponding		
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
.	sequence		\=possible nucleotide insertion)
	sequence		YKGRYEITABDSQEKVADBISFRLQEPKKDLIARVVRIIGNKKA
1			IELLMETAEVEQNGGLFIMNGSRRRTPGGVFLNLLKNTPSISEE
Į.			
			QIKDIFYIENQKEYENKKAARKRRTQVLGKKMKQAIKSLNFQED
	i		DDTSRETFASDTNEALASLDESQEGHAEAKLEAEEAIEVDHSHD
1	}		LDIF
6206	10	1442	IISERRERSCLHLVCIRCSCDVVEMGSVLGLCSMASWIPCLCGS
0200	1	1	APCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQ
1		İ	LNKIPGFCENEKGVVPCNILVGYKAVYRLCFGLAMFYLLLSLLM
	,		
l .		1	IKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFTTVW
1		1	FYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKMEEGNSRCWYA
			ALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLC
	İ	!	VGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTWSAMTNEPE
1	1		TNCNPSLLSIIGYNTTSTVPKEGQSVQWWHAQGIIGLILFLLCV
1			FYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
1	i		RAVDNERDGVTYSYSFFHFMLFLASLYIMMTLTNWYRYEPSREM
i			KSQWTAVWVKISSSWIGIVLYVWTLVAPLVLTNRDFD
6207	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
1	l		GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY
1	1		SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA
	ĺ		SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEFVP
1			GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA
1	1		VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
1 .			
1	-		HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRFGILSNCN
į		l	HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVBE
	İ	į	KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
	1	ì	GRREEPQRQKVGTSSRYRAQRRNHFWELIEERENSNPFDNDEEE
1		1	VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
6208	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
0200	2324	1 11/1	GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY
i	ľ		SVVCKYFQRGYCIYGDRCRYEHSKPLKQBEATATELTTKSSLAA
1	1		
	l		SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEFVP
1			GOPYCGRTAPSCTEAPLOGSVTKEESEKEQTAVETKKQLCPYAA
1	1	· ·	VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
1		· ·	HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRFGILSNCN
1	1	}	HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVEE
1			KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
1			GRREEPOROKYGTSSRYRAORRNHFWELIBERENSNPFDNDEEE
1		1	
L		<u> </u>	VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
6209	1758	829	ERLCFPCMQSKIYSYMSPNKCSGMRFPLQEENSVTHHEVKCQGK
1		,	PLAGIYRKREEKRNAGNAVRSAMKSEEQKIKDARKGPLVPFPNQ
1			KSEAAEPPKTPPSSCDSTNAAIAKQALKKPIKGKQAPRKKAQGK
1	1	1	TOONRKLTDFYPVRRSSRKSKAELQSEERKRIDELIESGKEEGM
			KIDLIDGKGRGVIATKQFSRGDFVVEYHGDLIEITDAKKREALY
1			AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ
1			
		1	TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL
1	,	ł	KH
6210	3761	387	IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT
1			SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV
1			SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
	1		CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
		1	TANDOURING TUTO A L CORONA ENCONTRO DE CONTRO
1	1		IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG
1			SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG
1		Į.	ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK
			QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE
1			WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRL
1			LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL
1	1	I	TOY A CONGULATIVE OF CONGULATION A CHARACTURA A 1011 A 111

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	1	\=possible nucleotide insertion)
			FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV
1			GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV
			SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH
			SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD
	1	1	IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ
			HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
			RPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD
	İ		DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN
			GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE
1			ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
ĺ	1	1	ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
1			WITCDNKIRLQEGPTSCSGRVBIWHGGSWGTVCDDSWDLDDAQV
		ļ	VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCP
1			ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA
	•		VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR
	·		EMNSCLNADDLDLMNSSGGHSEPH
6211	3761	387	IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT
	1		SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV
1	1		SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
1			CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
	į į		IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG
	1		SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG
1 .			ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK
1	ŀ		QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE
1			WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRL
1	· ·		LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL
			FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV
İ			GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV
			SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH
1			SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD
			IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ
			HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
	:		RPTIPEESAVACIESGQLRLVNGGGRCAGRVBIYHEGSWGTICD
			DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN
	· [GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE
1 .	.		ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
	.		ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
			WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV
			VCQQLGCGPALKAFKEABFGQGTGPIWLNEVKCKGNESSLWDCP
i	1		ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA
			VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR EMNSCLNADDLDLMNSSGGHSEPH
6212	1	1134	
"""		7734	LKWBLRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR
I	}		RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL
!			GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
			QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI
			SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS
		İ	VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT
		ļ	DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY
			NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK
6213	-		GPSGPSGPSTSSTSKSSSGSGNPTRK
0213	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR
]			RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL
Ī	1		GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
1		1	- DENDE VINDERS VERDE VE
I		1	QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS

680	Decode at a	Decade and	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT
1			DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY
			NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK
	}		GPSGPSGPSTSSTSKSSSGSGNPTRK
6214	2	460	HELAPSAIRRAARLGLGPARWQSRAAAFYFVRGFRTGWSFVGWV
		,	VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRESKRFSAYN
i	<u> </u>		YRTYAVRRIRDAFRENKNVKDPVEIQTLVNKAKRDLGVIRRQVH
			IGOLYSTDKLIIENRDMPRT
6215	2	1849	FVAGGPRGSGSAAETMPEIRVTPLGAGODVGRSCILVSIAGKNV
"2"	"	1027	MLDCGMHMGFNDDRRFPDFSYITQNGRLTDFLDCVIISHFHLDH
1			CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIAVDKKGE
			ANFFTSQMIKDCMKKVVAVHLHQTVQVDDELEIKAYYAGHVLGA
			AMFFISQMIKDCMKKVVAVHENGIVQVDDEBEIKAIIAGHVEGA AMFQIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNLLITEST
1			YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGRAOELC
			ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTNOKIRKT
1	1		
1	i i		FVQRNMFEFKHIKAFDRAFADNPGPMVVFATPGMLHAGQSLQIF
1			RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRQVLEVK
1]		MOVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKMEFLKQ
			KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKREMAQGL
			LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHQLRFTC
	į į		RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSVTVESVL
<u> </u>			LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLPQAPS
6216	11	393	QTTRPEPRNSALRQSRSKMAVVGVSSVSRLLGRSRPQLGRPMSS
			GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGEHERPE
	ļ		FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDE
6217	9	1178	TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHDPKEPEQ
	l .		LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQTKRSRG
			FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA
	1]	HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDRQSGK
			KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS
			AGSQRGRGGGSGNFMGRGGNFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
			GGSRGSYGGGDGGYNGFGGDGGNYGGGPGYSSRGGYGGGGPGYG
	ļ		NOGGGYGGGGYDGYNEGGNFGGGNYGGGGNYNDFGNYSGOOGS
			NYGPMKGGSFGGRSSGSPYGGGYGSGGSGGYGSRRF
6218	1305	906	SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGVPVIKVA
			NDNAPEHALRPGFLSTFALATDOGSKLGLSKNKSIICYYNTYOV
			VOFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQVVEVS
6219	2	890	AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRPHQRPFL
0219	. 4	550	IGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVVILSQDRFYK
			VLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP
			TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF
1	1	[VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEFCLP
			TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG
			RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH
6220	227	764	EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN
		1	KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ
			ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK
1		{	LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ
			NVH
6221	98	916	RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP
			NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG
			AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMPDTLVKIYK
			YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE
}	1	1	AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI
			DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL
			LDLREKRK
L	<u> </u>		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6222	2	2116	MARELRALLLWGRRLRPLLRAPALAAVPGGKPILCPRRTTAQLG
	1	Į.	PRRNPAWSLQAGRLFSTQTAEDKEEPLHSIISSTESVQGSTSKH
J			EFQAETKKLLDIVARSLYSEKEVFIRELISNASDALEKLRHKLV
	1		SDGQALPEMEIHLQTNAEKGTITIQDTGIGMTQEELVSNLGTIA
			RSGSKAFLDALQNQAEASSKIIGQFGVGFYSAFMVADRVEVYSR
			SAAPGSLGYQWLSDGSGVFEIAEASGVRTGTKIIIHLKSDCKEF
			SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIWMMDPKDVRE
l	}		WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKPSM
1			FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSEDI
İ			PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDAEKYAKF
			FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTSLS
			EYASRMRAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLFCF
1.			EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPAAE
1			CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEMG
l			AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRAS
6223		715	EPGLAQLLVDQIYENAMIAAGLVDDPRAMVGRLNELLVKALERH
0223	3	715	DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGCY
			RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDSCYKLGAYYVTGK
			GGLTQDLKAAARCFLMACEKPGKKSIAACHNVGLLAHDGQVNRD
1			GQPDLGKARDYYTRACDGGYTSSCFNLSAMFLQGAPGFPKDMDL
			ACKYSMKACDLGHIWACANASRMYKLGDGVDKVEAKAEVLKNRA QQVHKEQQKGVQPLTFG
6224	1		
			I DOT COMPRISON TO THE PROPERTY OF THE PROPERT
		133	LTSCHPLATON DESCRIPTION OF A PROPERTY OF A P
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTABGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPPLCKVCGRGYTSKSYLTVHERTH
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTABGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPPLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNIGLAHQRQQQLQFSD QSFQSDTABGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPPLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGBKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTABGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDPSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPPLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEBKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTABGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFPNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEBKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPPRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEKPYGCREGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPPRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPPRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS
			LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHRRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGPILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQGSLRVSTGLSWLLSLPWRAQRIRAGRSYA
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGPILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNIGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRNSVVEIES SQGRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPPLCKVCGRGYTTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCQQFSWKRSLTRHHWRIHSKE KFFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNIGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRNSVVEIES SQGRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDESALLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPPLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGPILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNIGLAHQRQQQLQFSD QSFQSDTABGQEKEKSTKPMAFSSPPLRHAVSSRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPPLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGBKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEBKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGBKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGBAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTABGQEKEKSTKPMAFSSPPLRHAVSSRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGBKSYVCSVCG RGFSLKANLLRHQRTHSGEKPPLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGBKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEBKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGBKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSFQSDTABGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEBKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGBAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNIGLAHQRQQQLQFSD QSFQSDTABGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSEBKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMBGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGBAMWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNIGLAHQRQQQLQFSD QSFQSDTABGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGINDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQCQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPQPAQLSVQQQAAQPTRWV
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNIGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPPRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNIGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVYHKRIHSGEKPPRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAMWSTGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAPANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATLAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGSOAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNIGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRNSVVEIES SQGRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPPLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE KFFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGGTTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKAPKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPPPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDCNCGQSOAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPBLIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNIGLAHQRQQQLQFSD QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLFTCRECHQGFRDBSALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVYHKRIHSGEKPPRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAMWSTGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAPANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATLAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGSOAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK

			·
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1		residue of	
	amino acid		S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6228	47	1978	GRRCRRGAVMELAOEARELGCWAVEEMGVPVAARAPESTLRRL
			CLGOGADIWAYILOHVHSORTVKKIRGNLLWYGHQDSPQVRRKL
			ELEAAVTRLRAEIQELDQSLELMERDTEAQDTAMEQARQHTQDT
	į		
	i		QRRALLLRAQAGAMRRQQHTLRDPMQRLQNQLRRLQDMERKAKV
	1		DVTFGSLTSAALGLEPVVLRDVRTACTLRAQFLQNLLLPQAKRG
			SLPTPHDDHFGTSYQQWLSSVETLLTNHPPGHVLAALEHLAAER
			EAEIRSLCSGDGLGDTEISRPQAPDQSDSSQTLPSMVHLIQEGW
			RTVGVLVSQRSTLLKERQVLTQRLQGLVEEVERRVLGSSERQVL
1			ILGLRRCCLWTELKALHDQSQELQDAAGHRQLLLRELQAKQQRI
1			LHWRQLVEETQEQVRLLIKGNSASKTRLCRSPGEVLALVQRKVV
			PTFEAVAPOSRELLRCLEEEVRHLPHILLGTLLRHRPGELKPLP
1			TVLPSIHOLHPASPRGSSFIALSHKLGLPPGKASELLLPAAASL
1	1	j	<u> </u>
		1	RQDLLLLQDQRSLWCWDLLHMKTSLPPGLPTQELLQIQASQEKQ
1			QKENLGQALKRLEKLLKQALERIPELQGIVGDWWEQPGQAALSE
L	<u> </u>		ELCQGLSLPQWRLRWVQAQGALQKLCS
6229	1571	560	GPSLLGTRGTPNPARTLQIFFLIIGRRLTGRMAAVDDLQFEEFG
1	İ		NAATSLTANPDATTVNIEDPGETPKHQPGSPRGSGREEDDELLG
1			NDDSDKTELLAGQKKSSPFWTFEYYQTFFDVDTYQVFDRIKGSL
		1	LPIPGKNFVRLYIRSNPDLYGPFWICATLVFAIAISGNLSNFLI
i		ł	HLGEKTYHYVPEFRKVSIAATIIYAYAWLVPLALWGFLMWRNSK
1	[ŀ	VMNIVSYSFLEIVCVYGYSLFIYIPTAILWIIPHKAVRWILVMI
1			
1	}		ALGISGSLLAMTFWPAVREDNRRVALATIVTIVLLHMLLSVGCL
			AYFFDAPEMDHLPTTTATPNQTVAAAKSS
6230	1723	600	SKMSGRSGKKKMSKLSRSARAGVIFPVGRLMRYLKKGTFKYRIS
İ		l	VGAPVYMAAVIEYLAAEILELAGNAARDNKKARIAPRHILLAVA
1.			NDEELNQLLKGVTIASGGVLPRIHPELLAKKRGTKGKSETILSP
	į	i	PPEKRGRKATSGKKGGKKSKAAKPRTSKKSKPKDSDKEGTSNST
1	ļ		SEDGPGDGFTILSSKSLVLGQKLSLTQSDISHIGSMRVEGIVHP
1	į		TTAEIDLKEDIGKALEKAGGKEFLETVKELRKSOGPLEVAEAAV
1.	1		
1	ĺ	İ	SQSSGLAAKFVIHCHIPQWGSDKCEEQLEETIKNCLSAAEDKKL
			KSVAFPPFPSGRNCFPKQTAAQVTLKAISAHFDDSSASSLKNVY
			FLLFDSESIGIYVQEMAKLDAK
6231	149	870	LIFSSSTMDRSLRNVLVVSFGFLLLFTAYGGLQSLQSSLYSEEG
1	,		LGVTALSTLYGGMLLSSMFLPPLLIERLGCKGTIILSMCGYVAF
1		}	SVGNFFASWYTLIPTSILLGLGAAPLWSAQCTYLTITGNTHAEK
	1		AGKRGKDMVNQYFGIFFLIFQSSGVWGNLISSLVFGQTPSQETL
1	,		PEEQLTSCGASDCLMATTTTNSTQRPSQQLVYTLLGIYTGSGVL
	1		AVLMIAAFLOPIRDVQRESE
		1	LANGUAGE AND ACTION
6222	3670	1476	BUACHTMACEMICTA DI VA ACDECENDOCCI MI CA AL DEL PULT
6232	3679	1476	FVAGTTMAGFWVGTAPLVAAGRRGRWPPQQLMLSAALRTLKHVL
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKBFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR INGWAVECRVYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR INGWAVECRVYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG IQPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR INGWAVECRVYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR INGWAVECRVYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG IQPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKBFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR INGWAVECRVYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG IQPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV THNIALLREVIINSRFVKGDISTKFLSDVYPDGFKGHMLTKSEK
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKBFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR INGWAVECRVYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG IQPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV THNIALLREVIINSRFVKGDISTKFLSDVYPDGFKGHMLTKSEK NQLLAIASSLFVAFQLRAQHFQENSRMPVIKPDIANWELSVKLH DKVHTVVASNNGSVFSVEVDGSKLNVTSTWNLASPLLSVSVDGT
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNERESQIRRNQKVVEE APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVVSKKNFY FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR INGWAVECRVYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG IQPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV THNIALLREVIINSRFVKGDISTKFLSDVYPDGFKGHMLTKSEK NQLLAIASSLFVAFQLRAQHFQENSRMPVIKPDIANWELSVKLH DKVHTVVASNNGSVFSVEVDGSKLNVTSTWNLASPLLSVSVDGT QRTVQCLSREAGGNMSIQFLGTVYKVNILTRLAAELNKFMLEKV
6232	3679	1476	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR INGWAVECRVYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG IQPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV THNIALLREVIINSRFVKGDISTKFLSDVYPDGFKGHMLTKSEK NQLLAIASSLFVAFQLRAQHFQENSRMPVIKPDIANWELSVKLH DKVHTVVASNNGSVFSVEVDGSKLNVTSTWNLASPLLSVSVDGT QRTVQCLSREAGGNMSIQFLGTVYKVNILTRLAAELNKFMLEKV TEDTSSVLRSPMPGVVVAVSVKPGDAVAEGQEICVIEAMKMQNS
6232	3679	2654	YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNERESQIRRNQKVVEE APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVVSKKNFY FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR INGWAVECRVYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG IQPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV THNIALLREVIINSRFVKGDISTKFLSDVYPDGFKGHMLTKSEK NQLLAIASSLFVAFQLRAQHFQENSRMPVIKPDIANWELSVKLH DKVHTVVASNNGSVFSVEVDGSKLNVTSTWNLASPLLSVSVDGT QRTVQCLSREAGGNMSIQFLGTVYKVNILTRLAAELNKFMLEKV

050	Dundinted	T 5000 43 - 5 - 3 3	
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
	Bequence		LACSRTYFFGATHVPYLGGDSKLPKKTEOIRLLSOIYAAVIEAV
			LAGIACYAKTSSLTKAKEVAEOTLGSGLDSFELIPFKAALRSKM
		İ	TFHIHAVNNOGRIVPLDSEDSLSFVKTACMAVYDIPDLLGGNGC
		ĺ	LGSVVFSESFLTSQILVKEKDGTVTTETSSVVLTAAVPRFCSWL
			VEDNEVKLSEKTHQAVRGDESFLGTYLTGGEGAYLYSSNLOSWP
1	}		EEGNVHFFSSGLLFSHCRHGSIIISKDHMNSISFYDGDSTSTVA
			ALLIDFKSSLLPHLPVHFHGSSNFLMIALFPKSKIYOAFYSEVF
			SLWKQQDNSGISLKVIQEDGLSVEQKRLHSSAQKLFSALSQPAG
			EKRSSLKLLSAKLPELDWFLQHFAISSISQEPVMRTHLPVLLQQ
			AEINTTHRIESDKVIISIVTGLPGCHASELCAFLVTLHKECGRW
[MVYRQIMDSSECFHAAHFQRYLSSALEAQONRSAROSAYIRKKT
			RLLVVLQGYTDVIDVVQALQTHPDSNVKASFTIGAITACVEPMS
			CYMEHRFLFPKCLDQCSQGLVSNVVFTSHTTEQRHPLLVQLQSL
	,	,	IRAANPAAAFILAENGIVTRNEDIELILSENSFSSPEMLRSRYL
, ,	[MYPGWYEGKLNAGSVYPLMVQICVWFGRPLEKTRFVAKCKAIQS
	,		SIKPSPFSGNIYHILGKVKFSDSERTMEVCYNTLANSLSIMPVL
.			EGPTPPPDSKSVSQDSSGQQECYLVFIGCSLKEDSIKDWLRQSA
i l			KQKPQRKALKTRGMLTQQEIRSIHVKRHLEPLPAGYFYNGTQFV
]			NFFGDKTDFHPLMDQFMNDYVEEANREIEKYNQELEQQEYHDLF
1			ELKP
6234	1731	404	PRVREDMDHKSPGNKGSLVYAGIKSIVKSSLGMVESSRHNWSGL
1			DKQSDIQNLNEERILALQLCGWIKKGTDVDVGPFLNSLVQEGEW
1 1			ERAAAVALFNLDIRRAIQILNEGASSEKGDLNLNVVAMALSGYT
			DEKNSLWREMCSTLRLQLNNPYLCVMFAFLTSETGSYDGVLYEN
			KVAVRDRVAFACKFLSDTQLNRYIEKLTNEMKEAGNLEGILLTG
1	·		LTKDGVDLMESYVDRTGDVQTASYCMLQGSPLDVLKDERVQYWI
			ENYRNLLDAWRFWHKRAEFDIHRSKLDPSSKPLAQVFVSCNFCG
		,	KSISYSCSAVPHQGRGFSQYGVSGSPTKSKVTSCPGCRKPLPRC
1	·		ALCLINMGTPVSSCPGGTKSDEKVDLSKDKKLAQFNNWFTWCHN
			"CRHGGHAGHMLSWFRDHAECPVSACTCKCMQLDTTGNLVPAETV
			QP
6235	1"	571	EKRDHRLPSWPRAALKVPGRGGRVGTTPELAAGGIMATRNPPPQ
			DYESDDDSYEVLDLTEYARRHQWWNRVFGHSSGPMVEKYSVATQ
1 ' 1			IVMGGVTGWCAGFLFQKVGKLAATAVGGGFLLLQIASHSGYVQI
1			DWKRVEKDVNKAKRQIKKRANKAAPEINNLIEEATEFIKQNIVI
			SSGFVGGFLLGLAS
6236	1	703	WDQNKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF
1		•	NLKFAAKELSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE
1			NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK
1 . 1			SMDATLKTMNLEKISALMDKFEHQFETLDVQTQQMEDTMSSTTT
			LTTPQNQVDMLLQEMADEAGLDLNMELPQGQTGSVGTSVASAEQ
L 5337	240		DELSQRLARLRDQV
6237	312	720	PTAMAEEGIAAGGVMDVNTALQEVLKTALIHDGLARGIREAAKA
[]			LDKRQAHLCVLASNCDEPMYVKLVEALCAEHQINLIKVDDNKKL
1			GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK
 			CKK
6238	2	4666	EEVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI
.		'	CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLF
	!		YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE
]			TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP
;	ſ		KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL
1			•
			INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNLGIK
			INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNLGIK MKKKAKMAIVESDPEERNYKVPEYKTVISFHSKDQLNITLSKCG
			INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNLGIK MKKKAKMAIVESDPEEBNYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTEAATGSSADFVKDLAPFMILNSLGLTISVSPS
			INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNLGIK MKKKAKMAIVESDPEERNYKVPEYKTVISFHSKDQLNITLSKCG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
{	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
]	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
<u> </u>	Dequesto		DTVEGSKKVTIRSPVOIRNHFSVPLSVYEGDTLLGTASPENEFN
			IPLGSYRSFIFLKPEDENYOMCEGIDFEEIIKNDGALLKKKCRS
			KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL
ļ			RNLLPYKIAYYIEGIENSVFTLSEGHSAOICTAOLGKARLHLKL
			LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
			1949
1			YNTGQTVVAFHSPYWMVNKTGRMLQYKADGIHRKHPPNYKKPVL
			FSFQPNHFFNNNKVQLMVTDSELSNQFSIDTVGSHGAVKCKGLK
			MDYQVGVTIDLSSFNITRIVTFTPFYMIKNKSKYHISVAEEGND
		•	KWLSLDLEQCIPFWPEYASSKLLIQVERSEDPPKRIYFNKQENC
			ILLRLDNELGGIIAEVNLAEHSTVITFLDYHDGAATFLLINHTK
			NELVQYNQSSLSEIBDSLPPGKAVFYTWADPVGSRRLKWRCRKS
1			HGEVTQKDDMMMPIDLGEKTIYLVSFFEGLQRIILFTEDPRVFK
			VTYESEKAELAEQEIAVALQDVGISLVNNYTKQEVAYIGITSSD
]			VVWETKPKKKARWKPMSVKHTEKLEREFKEYTESSPSEDKVIQL
			DTNVPVRLTPTGHNMKILQPHVIALRRNYLPALKVEYNTSAHQS
			SFRIOIYRIOIONOIHGAVFPFVFYPVKPPKSVTMDSAPKPFTD
			VSIVMRSAGHSQISRIKYFKVLIQEMDLRLDLGFIYALTDLMTE
			AEVTENTEVELFHKDIEAFKEEYKTASLVDQSQVSLYEYFHISP
			IKLHLSVSLSSGREEAKDSKONGGLIPVHSLNLLLKSIGATLTD
}			VODVVFKLAFFELNYQFHTTSDLQSEVIRHYSKQAIKQMYVLIL
			GLDVLGNPFGLIREFSEGVEAFFYEPYQGAIQGPEEFVEGMALG
			LKALVGGAVGGLAGAASKITGAMAKGVAAMTMDEDYQQKRREAM
			DAALVGGAVGGLAGAASKIIGANAKGVAANIINDEDIQQKKEEAN
			I NY ADAGEDRA TERRACUAT NOCENIA TERRATURUM PROPERTA A CARACANA I
			NKQPAGFREGITRGGKGLVSGFVSGITGIVTKPIKGAQKGGAAG
			FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR
			FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD
			FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDESDLNH
6239	2108	634	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA
6239	2108	634	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEBSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL
6239	2108	634	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA
6239	2108	634	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEBSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL
6239	2108	634	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM
6239	2108	634	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI
6239	2108	634	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG
6239	2108	634	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL
6239	2108	634	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVERSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG TLGLITVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI
6239	2108	634	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVERSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVI SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI
6239	2108	634	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEBSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA
6239	2108	634	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVI SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL
9 30		e en NRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQITWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS	
6239	2108	1176	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEBSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQITWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF
9 30		e en RKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQITWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ	
9 30		e en NRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQITWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL	
9 30		e en GNRKVSVVRALRHAVPAG ILCIGLTVAVDSYFWRQITWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL	
9 30		e en NRKVSVVRALRHAVPAG ILCIGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP	
9 30		e en GNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQITWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS	
9 30		e en NRKVSVVRALRHAVPAG ILCIGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP	
9 30		e en LGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV	
9 30		e en GNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS	
6240	2202	1176	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEBSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVI SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV
6240	2202	1176	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEBSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPPLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERIIPYLLRRQIKDETLQAAVR
6240	2202	1176	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEBSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERIIPYLLRLQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ
6240	2202	1176	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEBSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERIIPYLLRLQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV
6240	2202	1176	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEBSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQITWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCTT RVEBLTFHLLEFPEGKGVAVKERIIPYLLRLQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP
6240	2202	1176	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEBSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQITWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCTT RVEBLTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM
6240	2202	1176	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVERSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVLAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILGLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGFGQPPLSSPTRGGVKKVSGVGGTTYEISV RNAEEKKRLSLQREKITARVSIDNRTRALVQALRRTTDPKLCIT RVEBLTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC
6240	2202	1176	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVERSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVLAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLFNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG TLCLGLTVAVDSYFWRQGTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV RNAEEKKRLSLQREKITARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD
6240	2202	1176	FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDESDLNH KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVERSFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVLAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILGLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGFGQPPLSSPTRGGVKKVSGVGGTTYEISV RNAEEKKRLSLQREKITARVSIDNRTRALVQALRRTTDPKLCIT RVEBLTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC

Seginning	SEQ	Predicted	Toward and	
Note	1 -		Predicted end	Amino acid segment containing signal peptide
Cortisponding Contresponding Contr				
L-Leucine, M-Methionine, N-Asparagine, britat amino acid residue of amino acid residue of amino acid sequence s	I.O.			Glutamic Acid, r=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid sequence sequence 198 1310 6242 198 1310 6844 1310 1310 6844 1310 1310 6844 1310	ì			H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of anino acid sequence anino acid sequence (PT/PCOphan, Y-PYCophan, Y-Wipcophan, Y-Stubknown, *-Stop Codon, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible possible deletion, /-possible possible deletion, /-possible possible deletion, /-possible possible deletion, /-possible possible possible deletion, /-possible possible deletion, /-possible possible deletion, /-possible possible possible possible possible deletion, /-possible nucleotide deletion, /-possible deletion, /-possible possible possible possible possible possible possible possible possible possible nucleotide deletion, /-possible deletion, /-pos				
residue of amino acid sequence	1			
amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion)	1)	
Sequence	ľ		ļ	
6242 198 1310 GHELPGARTISPBAAVCTARRYBGRSLAAFFRRAAFRRAVENGE SEDIDQMFSTLLGEMDLITQSLGVDTLPPPDPNPPRAEFNYSV GFOLWESIRALEDQDLDARADIVADISEARGRITQAGKESL NQHHASALQAS TEGARASIGVATVAARGIGVGFOLDPPPBAD VLDLELPPPPBEDS GEBERQAKADKIKLALEKURSAVKKUL VKVHMENDRSTSLAKUVBORQLADVDLDNIPKHTLOCHVONCLYB LYBELQIERFFEDHENVSVISOMTROTESKILFLEEKEKAVKVUVKVHMENDRSTSLAKUVBORQLADVDLDNIPKHTLOCHVONCLYB LYBELQIERFFEDHENVSVISOMTROTESKILFLEEKEKAVKVUVKVHMENDRSTSLAKUKSSLETVEKNAKOLKESLEVELLLGSGRKE KOVCSITKSFASENNGKI 6243 1509 614 REASKFSGCKNSBOSTCCCCPSTCMSRSSASCPRARMFPSSARDT TSRASSRRLACOPOTRAGASTISTAMIPANSAAROTRATCCGPA MGOAGAGAGAGRAGKGSELAGGOFGRAHAHPSLFREFWYRTOPPA MGOAGAGAGAGRAGKGSELAGGOFGRAHAHPSLFREFWYRTOPPA MGOAGAGAGAGRAGKGSEAGGOFGRAHAHPSLFREFWYRTOPPA SPFFFFFTANDPIK RYFFFFYDHISTSSIOPPPCHAFHPRDPPAGTKRQLILVELK GPPILAPILLSUFLISSMSCAVTPATRALPANNASTITTGCCRA MGOAGAGAGRAGKGSEAGGOFGRAHAHPSLFREFWYRTOPPA SPFFFTANDPIK RYFFFFYDHISTSSIOPPPCHAFHPRDPPAGTKRQLILVELK GPPILAPILLSUFLISSMSCAVTPASELLDOPVDFILAFFTANDPIK RYFFFFTANDPIK RYFFFFTANDPIK RYFFFFTANDPIK RYFFFFTANDPIK RYFFFFTANDPIK RYFFFTANDPIK RYFFFTANDPIK RYFFFTANDPIK RYFFFTANDPIK RYFFFTANDPIK RYFFFTANDPIK RYFFFTANDPIK RYFFFTANDPIK RYFFFTANDPIK RYFFFTANDPIK RYFFFTANDPIK RYFFTANDPIK RYFFFTANDPIK RYFFTANDP			sequence	
6242 196 1310 GHILDRAFTUSPRAAVCTARRPERSLAAPRRAPERSVEW SENDIOMYSTILLERMILLIQUESUNTLEPPRAEPRYSV GFROLNESLINALEDQUIDALANDLVADISEAGRITQAGKESLQ NGHASASIQASITSGAASIGVOTIVAARGISQYEDDLPPPADEPYSV VIVUHANDISTKSLAVDERQLARDVLONLERKHICOCKVONCHY VIVUHANDISTKSLAVOERQLARDVLONLERKHICOCKVONCHY IYEELQIERPFEDISEGEERAGKAGKIKLAEKKEKKEKKUK VIVUHANDISTKSLAVOERQLARDVLONLERKHICOCKVONCHY IYEELQIERPFEDISGGEERAGKAGKIKLAEKKERKVKKUV VIVUHANDISTKSLAVOERQLARDVLONLERKHICOCKVONCHY IYEELQIERPFEDISGGEERAGKAGKIKAEKKEKKERKVKILV VIVUHANDISTKSLAVOERQLARDVLONLERKHICOCKVONCHY IYEELQIERPFEDISGGEERAGKAGKIKAEKKEKKERKVKILV VIVUHANDISTKSLAVOERQLARDVLONLERKHICOCKVONCHY IYEELQIERPFEDISHAVENTADISTRATUSTRATICHEREKKAVE MOPONFTULDIRGKKESKETINEKNIAANAASTITTIGCOFF MOQAGAGGAGRIKOERGSPAAGGERGAHAHISPSLIPERERPROPPADH GSAAGAGGAGGAGRIKAHISPSLIPERERPROPPADH GSAAGAGGAGGAGGAGAGKESAAGGERAGGHAHHISPSLIPERERPROPPADH GYPAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG		boquence		
SSEDIOGNETILICIBNDLIATIGLEVOTILEPPDENDEPRASPENS GEKUINESLAILALEDOLDIALMANDLVADISBABOPTIQACKESLO NGHHASALIQASIFSCASILGVOTIVAATGISQYEDDIA PPPADP VILDIPLPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	6242	198	1310	
GFKILINESLANALEDQUIDAIAMADIVADISEARQRETIQAQKESIQ NQHRASALQAS IPSGASALSIVATIVNANTATIGSDEDIP PPRADD VLIDLPIPPPPEPLGOERERAQAKADKIKALBEKLKRAVYKKLV VKVHMTMSTEKSUMDERQIARDVLDNIPEKTHCDCNYDMCLYBE IYPELQIERFFEDHENVVEVIGDWTRDTERKILLEKEEKYAVY RIPQNFTLDURGKKRSEKTMERMAKNKESLLEVRLILQSGRKR ROVCSIFKS PASENNGKI 6243 1509 614 RSASERSGCWSRDSTCCCCPSTCWSRSSASCPRARWPSSAPAT TSRASSRELACOFQTRAGATRSTAMTANNSARDTKRATCCRA AGTPSPTTMTCLTDVPTGCAAVEPTARLPAAWASTITTGCCPA MGQAGAGAGRKSEAGGGGRAHHAIPSPLEPRPRVRTGCPAH MGQAGAGAGRKSEAGGGGRAHHAIPSPLEPRPRVRTGCPAH MGQAGAGAGRKSEAGGGGRAHHAIPSPLEPRPRVRTGCPAH MGCAGAGAGRAGKSEAGGGGRAHHAIPSPLEPRPRVRTGCPAH MGCAGAGAGRAGKSEAGGGGRAHHAIPSPLEPRPRVRTGCPAH MGCAGAGAGRAGKSEAGGGGRAHHAIPSPLEPRPRVRTGCPAH MGCAGAGAGAGKESLAGGGRAHHAIPSPLEPRPRVRTGCPAH MGCAGAGAGAGKESLAGGGRAHHAIPSPLEPRPRVRTGCPAH MGCAGAGAGAGKESLAGGGRAHHAIPSPLEPRPRVRTGCPAH MGCAGAGAGAGAGKESLAGGGRAHHAIPSPLEPRPRVRTGCPAH MGCAGAGAGAGAGKESLAGGGAGHAIPSPLEPRPRVRTGCPAH MGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	0212	150	1310	
NOMHASALQASIISGGAASLGYGTNVAATGISGYEDULPPPPADD VLUDLPIPPPPPEDEJGGEBERGAKADKIKLALBIKKARAVYKKU, VKVHNNDSTKSLMVDERQLARDVLJDNIPEKTHCDCNVDWCLYE IYPELGIERFEDHENVVEVLSBWTRDTERKLEREKKYAVY NNONPYLDNIRGKESSKETNEKONAKSKESLLEVRLILQSGKE KDVCSIFKSFASENGKI 6243 1509 614 RSASRFSGKSKSRDSTCCCCESTCWSRSSASCPRARWPPSSAPAT TSRASSRBLACGPGTRAGATTSTAMTRANSAARDTRATCGRA AGTPSPTTMCLTDVPTGCAAWPPTABLEAAMSTTTGGCPA MGQAGAGAGRAGKASEAGGGGGRAHHAHPSPLEREPRAVTPPAH RVFFFYQHLTFFSIQPOPPCHAPHPSDPPAGTKRQLILVPLK GPPILAPILSITTISRNSCYPFSRSILAGOWELFFRENAVDPLK RVFFFYQHLTFFSIQPOPPCHAPHPSDPPAGTKRQLILVPLK GPPILAPILSITTISRNSCYPFSRSILAGOWELFFRENAVDPLK RVFFFYQHLTFSSIQPOPPCHAPHPSDPPAGTKRQLILVPLK GPPILAPILSITTISRNSCYPFSRSILAGOWELFFRENAVDPLK RVFFFYQHLTFSSIQPOPPCHAPHPSDPAGTKRQLILVPLK GPPILAPILSITTISRNSCYPFSRSILAGOWENSYNOGSSELSK FWFFYGHLTFSSIGPTGANNSEERCKLKLQGKTMSLWSWNNGSSELSK FWFFFYGHLTFFSSIGPTGSPRSTERGSPLUTYNOGSVPULVENGL ENVANILEYNKELQAKVNILRRCLAELETEDGMGSSP 6245 81 1148 LSLRRAKYSFPGELISEFSWTDLNDNICKRYIKMITNIVILSII ICISLAFWIISMTASTYYGHLARISPSPWCHILJWILSMSS RLITTWRKVPVGFNGGVTVVGVVGVCNGAVPTILJWILSMSSI KKSLDHSGALGGLUVGFILTIANSSFTSLLMFFISSSKLTKK KGEVKKRLDSEYKEGGGRWVQVVCNGAVPTILSMSENGFVULVSNGG KKSLDHSGALGGLUVGFILTIANSSFTSLALPMSENGFULTYNGLABSFT WOLNSFTKKARHTAGKPILDNIAVNILFSVLIALLLIMIENGFO EIPVPFSKQYSASMYCLSLLAALACSAGTWASEVGPVLYSNGG RUTHTWREVPVGFNGGVTVVGVSSLLGGTFVGTAPFITOLIFY NDLDISAAPQHPILAPGGAACLLGSIVDSYLGATMOTTGLBSTG WUNNSFTKKARHTAGKPILDNIAVNILFSSLLALBITTVOGNVFHLLSNILATS HCCKSVILGNSPLOURFSLALPKGYNGHLSNILTLLAKLLLINIS SGEDGOMIRLDGCLLULTERSKYKKKSSPLDLLIFRNVCYS PANKEKILABRKVITVLAACLESSNQARGRIGAAALWALITNYQ KAKTALKSPSVCKRYDBASYLAKTYFNSEAMPAYLYKCCER PANKEKILABRKVITVLAACLESSNQARGRIGAAALWALITNYQ KAKTALKSPSVCKRYDBASYLAKTYFNSEAMPAYLYKCCER PANKEKILABRKVITVLAACLESSNQARGRIGAAALWALITNYQ KAKTALKSPSVCKRYDBASYLAKTYFNSEAMPAYLYKCCER PANKEKILABRKVITVLAACLESSNQARGRIGAAALWALITNYQ KAKTALKSPSVCKYRTDGASYLAKTYFNSEAMPAYLYKCCER PANKEKILABRKVITVLAACLESSNQARGRIGAAALWALITNYQ KAKTALKSPSVCCATARAWANAGAGLALLARLARGUNALAYTYLKCCER VGNILSVNAPPTYLKAPTWSEKRERRIGREPITUTAGCYCVTWACYOL ULPPPIGNAADPPTYLKAPTWSEKRERRI				
ULDLPPPPPELSQEEERAQARADKILALEKLÆRAVYKKUV VKVMNNDNSYLSMURDRUJDLIPKHLOCONVOMCLYS IYVELGJERFFEDHENVUSVLSDWTROTENKILELEKEKKAVP NNONPYLDINGKKESKETNEKMAKNKESLLEVRLILQSGKKE KDVCSIFKSFASENNGKI 1509 614 RESASFRECKERDSTRUCCCESTUSSESSASCPRARWEFSSARKE KDVCSIFKSFASENNGKI RESASRRIACGEGYTRAGASTRSTAMIRANISAARDTRRATCRSA ACTPSFITMTCLTDVPTGCAAVEPTAALEAAWASTITTGCCPA MGQAGAGBAGKESEAGGGFGAHHAIPSPLE REPRVRTGEPAH SPFFGSIDPSFELSMUSSAGVTGESFLLDEVDFLIFKTRTAGCAP REPREVRTFFYGHLTPFSIQPOPPECHAFHERDPAGTKRQLILVPLK GPPILAPILSLITHISTSOCPHAFHERDPAGTKRQLILVPLK GPPILAPILSLITHISTSOCPHAFHERDPAGTKRQLILVPLK GPPILAPILSLITHISTSOCPHAFHERDPAGTKRQLILVPLK GPPILAPILSLITHISTSOCPHAFHERDPAGTKRQLILVPLK GPPILAPILSLITHISTSOCPHAFHERDPAGTKRQLILVPLK GPPILAPILSLITHISTSOCHAFHERDSKYLDEAYE EMVALIENNELQAKVILLERGKKHQKKTMSISWINOPSELSK FTMPLFEANNLUVIMPSVAPQSLIPLWEGIFLKRMNSSKYLDEAYE EMVALIENNELQAKVILLERGLALETETEGAKSELDAYE EMVALIENNELQAKVILLERGLALETETEGAKSELDAYE EMVALIENNELQAKVILLERGLALETETGALALETETGAME FERVENFRONT SASSWANCISLILABLATS SPWENLESPULVILVSLIL ICSLAFWILIMTASTYYGHLAALESSAGVAREVPLINSSSLILMINGEGE EIFVPSKQVSASSWACISLILABLAGSAGGVAREVPLINSSSLILMINGEGE EIFVPSKQVSASSWACISLILABLAGSAGGVAREVPLINSSSLILMINGEGE EIFVPSKQVSASSWACISLILABLAGSAGGVAREVPLINSSSLILMINGEGE EIFVPSKQVSASSWACISLILABLAGSAGGVAREVPLINSVILLILLIPTAAGTW NUNDSTYNKARHITAGKVILDAHAINSSVILLALLIPTAAGTW PRG 6246 1177 359 SIMPHILMDDSIMQISLQLLCVYTANFPNGCSSLCWSSGGGHPV QAHRGAVNSSIMLCILKLASSMPLESSVILLALLIPTAAGTW PRG 6247 3 1678 NSRVERRIBLAGGLULLTERKSYKHKSSPLOWYPHLISNIALIS SGEDGOMILIRLINGGCLULLTERKSYKHKSSPLOWYPHLISNIALIS SGEDGOMILIRLINGGCLULLTERKSYKHKSSPLOWYPHLISNIALIS SGEDGOMILIRLINGGCLULLTERKSYKHKSSPLOWYPHLISNIALIS SGEDGOMILIRLINGGCLULLTERKSYKHKSPLOWYPHLISNIANSVILLINGGAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	1		
VKVHMINDSTKSIMUDERQLARDVIDLIKETHCHOCNUDWICLYE IYVELQIERFEDHENVYEULSDWTROTENKI LELEREKXAVE KDVCSITKS PASENNOKI 6243 1509 614 RSARFSGGWSRDSTCCCCPSTCWSRSASCPEARWFPSSAPAT TERASSRILACGPOTRAGASTRSTAMIRANSAARDTRATCRSA ACTPSPITMICLTDVPTGCAARDSTRSTAMIRANSAARDTRATCRSA ACTPSPITMICLTDVPTGCAARDSTRSTAMIRANSAARDTRATCRSA ACTPSPITMICLTDVPTGCAARDSTRSTAMIRANSAARDTRATCRSA ACTPSPITMICLTDVPTGCAARDSTRSTAMIRANSAARDTRATCRSA ACTPSPITMICLTDVPTGCAARDSTRSTAMIRANSAARDTRATCRSA ACTPSPITMICLTDVPTGCAARDSTRSTAMIRANSAARDTRATCRSA ACTPSPITMICLTDVPTGCAARDSTRSTAMIRANSAARDTRATCRSA ACTPSPITMICLTDVPTGCAARDSTRSTAMIRANSAARDTRATCRSA ACTPSPITMICLTDVPTGCAARDSTRSTAMIRANSAARDTRATCRSA ACTPSPITMICLTDVPTGCAARDSTRATGAARDSTRATCRSA SPITGSIDSPITMICRTSTRATCRSSALLUPLEL SPITGSIDSPICATION SPITCHTSPILDIPLIFTRAVPPIR RVFFFYCHITFFSIQPPPCHAPHPDPAGTKRQLILVPIR RVFFFYCHITFFSIQPPPCHAPHPDPAGTKRQLILVPIR RVFFFYCHITFFSIQPPPCHAPHPDPAGTKRQLILVPIR RVFFFYCHITFFSIQPPPCHAPHPDPAGTKRQLILVPIR RVFFFYCHITFFSIQPPPCHAPHPDPAGTKRQLILVPIR EPHAPASOFGTHLANNISERCKIKLOQKTRSLUSSWINQPSELSK PTHPLFEANLILVBSSALCHLUSSUSSELLESTUSSWINQPSELSK PTHPLFEANLILVBSSELCKIKLOQKTRSLUSSWINQPSELSK PTHPLFEANLILVBSSELCKIKLOQKTRSLUSSWINQPSELSK PTHPLFEANLILVBSSELCKIKLOQKTRSVILVBSILGSTV KKRSLDISGRGLVSFTILTINFISSKLITKN KGSVKKRLDSSVIKGATUSVVEVLILVBNIG KKRSLDISGRGLVSFTILTINFISSKLITKN KGSVKKRLDSSVIKGATHOKVVEVNOVVENOAVPILLINMIENGEN EIVPFSKQYSASMMCLSLLAALACSAGTWASSVOPULSKSSS RLLITTWRKEVPOTROGVTVVCUVSVSLLGGTTVATASVVEVUVLILVBINGENT MVUNSPTKKRHITAGKPILDNINVLTSSLLAGATGSSTCASSCGCHPV PRG 6246 1177 359 SIMPHILMDSIMQISJOLICVYTANPPNICSSLCWSSCGCHPV ONTHRAVSNSIMLCILKLASOMPLENTITVOMVYFMLLSNLAR BCCKGVILOSNSTLANFISLALDENGSNCHLSNLTTLILVBLILLIN SCEDGOMMIRLDGCLILLTENSYV KKSSPLDALLILINS SCEDGOMMIRLDGCLILLTENSYV KKKSSPLDALLILING KKKALLABENVITVLAACLESENQBAGRIGAAALWALITNYQ KAKTALKSPSVCKRYRDSASVLAKATYPNERSKRINAYLYKIKCLEN LVQLINSS SCEDGOMMIRLDGCLILVBAGRYGRRGRANGANALATILLINGS CONTAGENCAMINANICSCULTURATUSTOMACHILLINGS CONTAGENCAMINANICSCULTURATUSTOMACHILLINGS CONTAGENCAMINANICSCULTURATUSTOMACHILLINGS CONTAGENCAMINANICSCULTURATUSTOMACHILLINGS CONTAGENCAMINAN				1
1YPELGIERFFEHHENVEVLSDURTDTENKILFLEKEEKYAVU KNPONFYLDINGKKESKETRIKKINAKNKESLLEVRLILGSGRKE KDVCSIFKSFASENNKI 1509 614 RESARFSGGVERNSTTCCCCPSTCWSRSSASCPRARWPFSSAPAT TERASSRILACGPOTRAGAETRSTAMIRANSAARDTRRATCRSA AGTPSFTTMTCLTDUPTGCAAVEPTARLEAAAWASTITGCCA MGQAGGAGGAGGKGSEAGGGGGARHAHPSPEPLPEFRVRTGSPAH SPTPGSIDPSPELSWGSAGVTQSSPLLDPUPFLIFTRAVDPLR RVFFFFYGHLIFFSIODPO PCIAFIPFRDPAGTKROLILVPLK GPPILAPILSLTPILSRWGCVFPRSILAGGHIS 6244 2119 1745 FERMANSOGGFFIGANESERCKLKLQCKTMSLWSWVNQDSELSK GPPILAPILSLTPILSRWGCVFPRSILAGGHIS 6245 81 1148 LSLENRAKYSFFGELISLFSMTDLINDIKCKRYIKMITNIVILSLI LGISLAFWILIMTASTYYGNLRFISPWRWLSVVLVUSNGL KKRSLDHSGALGGLVUGFILTIMFSFFTSLMFFISSKKILDEAVE EWNNI LENNELQAKVNILRRQLABLETEDOMGSBR KKRSLDHSGALGGLVUGFILTIMFSFFTSLMFFISSKKITKN KGEVKKRLDESYKEGGORNWOVPCKGAWPTELALLYMIENGPS EIPVDFSKOYASSWMCLSLLAALACSAGNESVPULVSNGS KKRSLDHSGALGGLVUGFILTIMFSFFTSLMFFISSKKITKN KGEVKKRLDESYKSGORNWOVPCKGAWPTELALLYMIENGPS EIPVDFSKOYASSWMCLSLLAALACSAGNESVPULVSNGS RLITTWEKVPWGTNGGVTVVGLVSSLLGGTPVGTAYPITQLIPV NDLDISAPQWPIIAPGGLAGLLGSIVONAVUFFULAURINLAN HOCKGVIJKSKNFLOMFISLALALACSAGNATWYTVGLAVSTLUBLITAR FFTSLLAALSSPSKRRVDCAYSLLAKTFPNSCSLCWSSCGGPPV QATHRGAWSNSIMLCILKLASQWPLENTTVQQVTVIJULINIALS HOCKGVIJKSKNFLOMFISLALAPKGSMKILTIMILIMILAISIALS SGEDGQOMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCSS PANKPKILABKKVITVLAALALDESKONNAGAALWALIYMVQ KAKTALKSPSVKRRVDCAYSLAKKTFPNSEANPLNAYYLKCLEN LVQLINSS SGEDGGOMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCSS PANKPKILABKKVITVLAALALDESKONNAGAALWALIYMVQ KAKTALKSPSVKRRVDCAYSLAKKTFPNSEARHGPLDDTITLLMSVTV SIFAIGGLVGTILVKMIGKVLGRKHTLLANNGFATSAALMACS LOAGAFFELLIVGFFTTSKSERTHGFPLDDTITLIMSVTV SIFAIGGLVGTILVKMIGKVLGRKHTLLANNGFATSAALMACS LOAGAFFELLIVGFFTTSKSERTHGFTDDTTTLTLUBARDVTSSISPKETRGSLG OVTATFICIGVFTGGLAGLPELLGKSTWPPLEGVIVVPAVVOL LESPPIDRSPRYLILEKHRARAVKAFQTEARVSCBUEFUL GRPLLIGGGMGGFGFGTTTTTTTTLTCHAFWYPTSSIFPKERTRGGIMGLFGTTTTKVCVV SOPTHEMAMPOPELBENNEYRT FRAGNISAVTONFGBALDLCI LANVKGUNSRLWVLYKGVLKRLILLLYSPLFRKRTYKJE SOAFSKRNKAYPPEEKINSAVTORGSAVTONFGARLDLCI LANVKGUNSRLWVLYKGVLKRLILLLYSPLFRKRTYKJE SOAFSKRNKAYPPEEKINGFTTSKCVITTUKCVVP				1 to the second
KINPONFYLDINGKKESKETNEKMNAKNKESLLEVRLILQSGRKE KDVCSIFKSASENNKI. 6243 1509 614 RSASRFSGCWSRDSTCCCCPSTCWSRSSASCPRARWPPSGAPAT TSRASSRLACGPQTTAGABETRSTAMIRANSARDITRACTCSA ACTSPSTTMICLTUDVETGCAAVEPTARLPAAAWASTITTGCCAA MGQAGGBAGKGSEAGGGPGRAHHAHPSPLPKERPYRTGPPAH SPIPGSIDPSBLSWGSAGVOTQSBLLDDFDFLLFSTRAVDPLR RVFFFYQHLJFFSLOPQPPDCHAFPRDPPAGTKRQLILVPLK GPPILAPILSLTPILSRNSCYPPSRLAQGHIS 6244 2119 1745 FEHAYASQFGTFLGNNESERCKLKLQQKTWSLUSWVNQPSELSK FINPLEANNLVIWPSVAPQSLEUBGITLRWNGSSKLDEAYE BMVNIIENTKLQAKVNILRRQLABLETEGMOSSP 6245 81 1148 LSLRNAKYSFFQSLISLFSMTDLNDNICKRYIKMITNIVILSLI KKISLDHSGALGGLVGFILTIANFSFFTSLLMFILSSKLTKW KGEVKKRLDSEYYLEGGANVOVPCCHAPVVVPVLIVSNGL KKISLDHSGALGGLVGFILTIANFSFFTSLLMFILSSKLTKW KGEVKKRLDSEYYLEGGANVOVPCCHAPVVVPVLIVSNGL KKISLDHSGALGGLUVGFILTIANFSFFTSLLMFILSSKLTKW KGEVKKRLDSEYYLEGGANVOVPCCHAPVVVPVVIVSNGL KKISLDHSGALGGLUNGFILTIANFSFFTSLLMFILSSKLTKW KGEVKKRLDSEYYLEGGALGILSIVDSTVLGATMQTTGLDESTG MVNNSPTKKARHLAGKPILDNNAVNUFSSLUGATMQTTGLDESTG MVNNSPTKKARHLAGKPILDNNAVNLFSSVLIALLLPTAAWGFW PRG				
6243 1509 614 RSASRFSGENSKISTCCCPSTCMSRSSASCPRARMPPSSAPAT TSRASSFRILAGGPOTRAGAETRSTAMIRANSARDTRERATCRSA AGTPSPTIMTCLTDVPTGCAAVEPTARLPAANMASTITTGCCSA MGQAGAGGRKSSEAGGGGGRAHHAHPSEPLPKERRVETGSPAH SPTPGGIPSPELSMGSAGVTGSSPLDPVDFLIFFRAVDPLR RVFFFFYCHLTFFSLOPGPPCHAFHPREDFLKRQLILVPLK GPFILAPILSLTFILSRMGSAGVTGSSPLDPVDFLIFFRAVDPLR RVFFFYCHLTFFSLOPGPPCHAFHPREDFLKRQLILVPLK GPFILAPILSLTFILSRMGSCYFPSSLAGGHLS 6244 2119 1745 FEHAYASGGTFIGANISSERCKLKLQGKMLSWNNQPSELSK FTMPLEANNLVIWBVAPQSLPLMSGIFLRWRSSKYLDEAYE EMWNI IEVINKELQAKVNI LIRQQLAELETBACKSCHQCMSD 6245 81 1148 LSLRNAKYSFPQELISLFSWTDLNDNICKRYIKMITNIVILSLI ICISLAFHIISMTASTYYGNLRFISFMRDESVVYVLIVSNGL KKRSLDHSGALGGLVVGFILTIANFSFFTSLMFFLSSKLITKM KGEVKKRLDESYKSGGQRNWVQVPCHGAVPTELALLYNIENGGS EIPVDFSKGYSASMMCLSLLAALGASGAFUKDESVDFUSKSSS RLITTWEKVPUGTNGGVTVVGLVSSLLGGTTVGIAVFITOLIFV NDLDISAPQWPITAFGGLAGLLSI UDSVLGATMQYTGLDSTG MVVNSSTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAANGFW PRG 6246 1177 359 SLMFWILMDDSLMQISLQLLGVLVYTANFPNGCSSLCWSSCGQHFV QATHRGAVSNSIMLCLIKINASQMPLENTTVQQNVFMLLSNLALS HOCKGVIJKONFLQMFLSLALPKGONKHINNITLÜLKLLLINI SGEDGGQMILRLDGCLDLLTEMSKYKHKSSPLLPLIIFHNVCSS PANKPKILANEKVITVULAGLLESSNONAGRAALWALITNYQ KAKTALKSPSVKRRVDEAYSLAKKTPPNSEANFLNAYYLKCLEN LVQLLMSS 6247 3 1678 NSRVWGFWTEPSAGSLRFMARKQNRNSKELGLVPLTDDTSHAGF PGGRALLECDHLRSGVPGGRRKKOWSCSLLVASLAGAFGSSIL VGYNLSVUNPTYYKSTYRSSERTHGFUTVSSISFKBIRGSLG OVTATFICIGVFTGGLLGLPBLIGKRSTWPLEGVIVVPAVVCL LSLPFLDRSFTYLLEKKINGRAVLAGRVILSSISFKBIRGSLG OVTATFICIGVFTGGLLGLPBLIGKRSTWPVLEGVIVVPAVVCL LSLPFLORSPYLLLEKKINGRANARAFGATHATVSPKVEGVIL GRRFLLIGGFGLMGLFFGTTLTITLTCDHAPWPYLSIVGILLI IASFCSGGGIPPILTGGFFTGGSGRRASAYTONFGAALDLCI AASIRCCELUVIJSLKSGTLDAFTGVLCAVLYSNERMRRKPHIL ALKQVEQCLKRLKNMNLEGSIODLFELFSNENGATYONFGAALDLCI AAVIKECHLVIJSLKSGTLDAFTGVLCAVLYSNERMRRKPHIL ALKQVEQCLKRLKNMNLEGSIODLFELFSNENGALTVKCVVV SOPVVELVIMKVIGACKLLLEKPLDACCKTELLTVKHIGLLGEFII LNIJWVGLVSRLMVLYKGVLKRLILLLYSPLFGLIGVEAURQPM YKDDTFPSTITEFLGGPYFAFKKOMPIPSTRAGVINGLTKVCVVV SOPVVELVIMKVIGACKLLLLKLEDDCCKTFLLTVKHIGLLGEFII LNIJWVGLVSRLMVLYKGVLKRLILLLYSPLFFAKKTURCUP				
6243 1509 614 RSASRRICWSRDSTCCCESTUMBRSSASCPRARMPPSSAPAT TSRASSRRIACGPOTRAGAETRSTAMIRANSARDTRRATCRSA ACTSSTTMTCLTDVPTGCAAVEPTAALRAAWASTITTGCCPA MGQAGAGRARKGSEAGGGGGAHHAHPSSLPRERRVRTGPPAH SPTPGSIDDSSELSWGAGAVTGESBLUDPUDFLERTRATUDELR RVFFFFYOHLTFFSIQPOPPECHAFHPRDPPAGTRRQLILVPLK GPPILAPHISLSTPILSRASCYPRESRLOKUNGWHLS GPPILAPHISLSTPILSRASCYPRESRLOKUNGWHLS FEHAYASGGGFLGNESSECKLKUQKTMSLWSWNNOPSELSK FTNPLFEANNLVIWESVAPQSLPLWEGIFLRWRSSKYLDEAYE EMWNIENKELQAKVNILRRQLAELETEGOMGESP 6245 81 1148 LSLRNAKVSFPGELISLFSMTDLBDNICKRYIKMITNIVLISLI LGISLAFWIISMTASTYTOKNLRPISPWRWLFSVVYPULIVSNGL KKKSLDHSGALGGLVVGFLITTANFSFFTSLLMFFISSSKLTKW KGEVKRKLDSEYKEGGGRWVQVFTGAVELALLWHINGGG EIFVDFSKQYSASMMCLSLLAALACSAGDTWASEVCPVLSKSSC RLITTWEKVPVGRNGGVTVVGLVSSLLGGTFVGIAYFLTQLIFV NDLDISAPQWBILAFGGLAGLIGSIVDSYLGATMQYTCLDESTG MVVNSFTKARHLAGKPILDNANNLFSSVLIALLLPTAAWGFW PRG 6246 1177 359 SLMPWILMDDSLMGISGLLCVTTANFPNGCSSLCWSSCGGHPV QAHRGAVANSALMCLIKLASGMPLENTTVQGNVFMLLSHLALS HDCKGYJOKNSFTLONFLSLALPKGNKHLSNLTILWEKLLINTS SGEDGQOMIRLRLGCLLDLLTEMSKYKKSSPLLELLIHPHVCPS PANKKKILANSKYITULAACESENOMAGRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTFPNSEAMPLMYLKCLEN LVQLLNSS SGEDGGQMIRLRLGCLLDLLTEMSKYKKSSPLLDLIFHHVCPS PRGRRALLECHLUKSGVGGGRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNASTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV SIFAAGGIVCTLLVKMIGKVLGRHTLLANNGFASSLLALLHACS CLAGAFEMLIVGRFTMGIDGGVALSVLAVSLAGLAGFGSSFL YGYNLSVVNASTPYIKAFYNPSLESHEKIRGSLG QVTAIFICIGVFTGQLLGLPELLCKESTWPLTGGVIVPAVVQL LSLSPFLIDSPRYLLLEKHNEARAVAROTILKKARUSPEUEVL ASSRVGRSIRLVSVLSLLRAPYVRNQVVTVIVTNACYQLCGINA IMPYTNSIFIGKAGIPPARTYPYTTICTHAAPTSQTLVFAVVGLIELI GRRPLLIGGFGGMGLFFTLTTITLQDHAPWYPYLSIVGILAI IASFCSGRGGIPFILTGGFFGQSGRPAAFILAGTVNNLSNFAVG SQAFSKRKKAYPPEEKIDSAVTUĞKNGRP VYFNDTTFSGAGIPPARVIF TATATAGGINKGRPAVTVONFGAALDLCI AAVINGCLUKLLKMMLBGSIOQLFELFSNENDPLTTKVCVVP SQPVVELVLMKVUGAGKLLLBELDCCCKTFFLITVKHISTQEFT LILLWWGLVSRLWVLYKGGVLRRELILLLYPELPFENLEGVARTQOM YKRDTTFPSDITTFLGGVFTGAFTATTICTICTHGTTTAAGGINFUPHL ALKQVGGCCCKRLKNMBLBGSIOQLFFELFSNENDPLTTKVCVVP SQPVVELVLMKVUGAGKLLLLBELDCCCKTFFLITVKHISTGCFTI LILLWWGLVSRLWVLY				
TSRASSRLACGPOTRAGAETRSTAMIRANSARDTRRATCRSA AGTPSPTTMTCLTDVPTGCAAVBPTARLRAAAWASTITTGCCSA MGQAGGRAGKGSEAGGGGGRAHHAHPSPLPREPRUPTGPPAH SPTPGSIDPSPELSWGSAGVTQESPLLDPVDFLLPRTRAVDPLR RVFFFFYCHLFFFSIQPSPPCHAFPPDPAGTRGQLLVPLK GPPILAPILSITPTLSRWSCYPFRSRIAQGWHLS 6244 2119 1745 FEHAYASGGTFLGNNESERCKLKLQQKTHLLWRKSVLDEAYE FWANTIEVNLSVAPGSLFWEGIFLRWRSSKYLDEAYE EMWNIEVNLSVAPGSLFWEGIFLRWRSSKYLDEAYE EMWNIEVNLSVAPGSLFWEGIFLRWRSSKYLDEAYE EMWNIEVNLSVAPGSLFWEGIFLRWRSSKYLDEAYE EMWNIEVNLSVAPGSLFWEGIFLRWRSSKYLDEAYE EMWNIEVNLSVAPGSLFWEGIFLRWRSSKYLDEAYE EMWNIEVNLSVAPGSLFWEGIFLRWRSSKYLDEAYE EMWNIEVNLSVAPGSLFWEGIFLWRRSSKYLDEAYE EMWNIEVNLSVAPGSLFWEGIFLWRRSSKYLDEAYE EMWNIEVNLSVAPGSLFWEGIFLWRRSSKYLDEAYE KKSSLDHSGALGGLVVGTLATLRFISLWFSLSSSKLTKW KGEVKKRLDSEYKGGGGRWWQVPCNGAVPTELALLYMIENGPG EIFVDFSKGYSASWMCLSLLAALACSAGDTWASEGVFLKSSKLTKW KGEVKKRLDSEYKGEGGGRWWQVPCNGAVPTELALLYMIENGPG EIFVDFSKGYSASWMCLSLLAALACSAGDTWASEGVFLKSSKLTKW KGEVKKRLDSEYKGEGGGRWWQVFCNGAVPTELALLYMIENGPG EIFVDFSKGYSASWMCLSLLGGFFVGLAFLTJUFLIFV NDLDISAPQWBI LAFGGLAGLLGSIVDSYLGATMGYTGLDESTG MVNNSFTNKAHHAGKPILDNAVANLFSSVLIALLLPTAAWGFW PRG 6246 1177 359 SLWFWILMDDSLMQLSQLLCVYTANFFNGCSSLCWSSCGGPFV QATHRGAVSNSLMLCILKLASGMFLERHTTVQCMVFMLLSNLALS HCKKGVICKSNFFLONTLSLALPKGNNHLSNLTILMLKLLLNIS SGEDGGOMILLBOCGLULLTUMSKYKKSSPLLIPLLIFHNVCFS PANKKPILANSKVITVLAACLESENONAGRIGAAALWALTYNYO KARTALKSSPVKRVEDEAYSLAKKFFPNSEANFLAAYYIKCKLEN LVQLLNSS 6247 3 1678 NSRVWGFWTEPSAGSLEFMARKGNRINSKELGUVPLTDDTSHAGP PGGRALLECDHLRSSVFGGRRRKDWSSCLLVASLAGGFGSSFL YGYNLSVNNAFTFYIKAFYNESBERRRGRFIDDTUTLLMSVTV SIFAIGGIGTLIVKMIGVLIGKFTLLANNFGSLLWASLLAGS LQAGAFEMLIVGRFIMGTDGGALSVLPMYLSEIDFKEIRGGL QVTAIFICIGVFTGQLLGLBELLGKESTWPYLFGVIVVPAVVOL LSLPFLPDSPRYLLLEKHNEARAKAFGFTLGKAHVSGWEEVL ASSRVGRSIRLVSVLELLRAPYVKNQVVTVIVTMACQLCGLMA IWFYTNSIFFGKAGIPPAKIPTTLANGFYTLGKAHVSGWEEVL ASSRVGRSIRLVSVLELLRAPYVKNQVTVIVTMACQLCGLMA IMFYTNSIFFGKAGIPPAKIPTYNTSTETLAAYFSGLVIFEHL GRRPLLIGGFGLMGLFFGTLTTLTLQDHAPWYPLSIVGLIGL GRRPLLIGGFGLMGLFFGTLTTLTLQDHAPWYPLSIVGLIGL GRGPLLIGGFGLMGLFFGTLTTLTLDDHAPWYPLSIVGLIGL LALWWGLVSLWVLYKGVLGRKLLLYSPLOPAKGINFGRFFLOVV S	6243	1509	614 .	
AGTPSFTTMTCLTDVPTGCAAVBPTARLBAANABTITTGCCBA MGQAGAGGAGGGGGTGRAHLAHSSPLPREPRVETGP PAH SPTPGSIDPSPELSWGSAGVTQESPLLDFVDFLLFRTRAVDPLR RVFFFPYCHLFFFSIQPQPPPCHAFHRDPPAGTRQLILVPLK GPPILAPILSITPILSRWSCYFPRSRIAQWHLS 6244 2119 1745 FEHAYASQGGTFLGNNESSECKIKLQQKTWSLWSWNQPSELSK FTYPLFEARINLVIWBSVAPQSLPLWGGIFYLWNRSKYKYLDEAYE EMVNIIENKELQAKVNILRRQLAELETEDGMQSD 6245 81 1148 LSLRNAKVSFPQELISLFBMTDLDNICKRYIKMITNIVILSLI LGISLAFWIISMTASTYVGNLRFISPMLSSVVLVULYSNGL KKKSLDHSGALGGLVVGFLIATLANFSYFTSLLMFFLSSKLTKW KGEVKKRLDSEYKEGGQRWVQVPCNGAVPTELALLYMIENGPG EIPVDFSKQYSASWMCLSLLAALACSAGDTWASEVGPVLSKSSP RLITTMEKVPYGTNGGVTVVGLVSSLLGGTFVGLTAFLTQLIFV NDLDISAPQWFIIAFGCLAGLIGSIVDSYLGATMQYTTCDESTG MVVNSFTNKARHIAGKPILDNAVNLFSSVLIAALLCSAGOTWASEVGPVLSKSSP RLITTMEKVPYGTNGGVTVVGLVSSLLGGTFVGLTAFLTQLIFV NDLDISAPQWFIIAFGLGAGLIGSIVDSYLGATMQYTELDESTG MVVNSFTNKARHIAGKPILDNAVNLFSSVLIAALLLFAAWGFW PRG 6246 1177 359 SLWFWILMDSIMQISLQLLCVYTANFFNGCSSLCWSSCGQHPV QATHRGAVSNSIMLCILKLASQMFLENTTVQQNVFMLLSNLALS HOCKGVIGKSFFLQNFISLALPKGGNKHLSNLTTLMKLKLLINIS SGEDGQOMILBLIGGCLDLLTENSKYKKKSSPLLPLLIFHNVCPS PANKPKILANBKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRVDDAYSLAKKTPPNSEAMFLMAYYLKCLEN LVQLLNSS 6247 3 1678 NSRVWSPYTESSAGSLEFMARKQNRNSKELGLVPLTDDTSHAGP PGGRALLECHLRISGVPGGRRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPYIKAFYNESWERRHGRFJIPDTTLTLMSVTV SIFALGGLVGTLLVKNIGKVLGRERTHLANNGFAISAALLMACS LQAGFEMLIVGRFINGIDGGVALKSVLPWYLSEISPKEIRGSLG QVTAFFICIGFFTGGGLFPLLKSVLPPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKNBAARVARFOTFLKARVSQEVBEVL ABSRVQRSIRLVSVLELLRAPYVRQVVTUTMACVQLCGNA IMFYTNSIFFGKGGIPPILTGEFFTGGGGFTGGTETLAAVFSGLVIELL GRRPLLIGGGGMGLFFGTLTTTLIDDHAPWYPLSIVGILAI IASFCSGGGIPFILTGEFFTGGGGFTGGTGTLATVLYFULPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKNGRB 6248 56 1773 VPPRMWAAVPFGLEFWNRVEIFRGGMRSAVTVONPGAALDLCI AAVIKECHLVILSLKSQTDABATDVLCAVISNNNRNGRKPHL ALKOVEGCLKRLNNNLEGSIODLFERSNODPLTTKVCVVP SQPVELVLMKVLGACKLLLRLLDCCKTFLLTVKHIGLQEFII LNLWWGLVSRLWVLYKGVLRRALILLLYPELFGGLUEVARCUPAP				
MGOĀGĀGPĀGRKĢSĒAGĢĢĢRĀHHĀHPSELPREPRVETĢPĀH SPŢPĢSIDPS PELSWGSĀGVTĢSPLLDVPĻLLRTRAVDPLR RVFFFYĢHLTFFSIDPQPPPCHAFHPRDPPĀGTKRQLILVPĻK GPPILAPILSITPILSRWSCYFPRSRIAĢGWHLS FEHĀYASĢGFŢILGNWSESPKCIKLĀĢKILMSWWNQPSELSK FTRPLEFANNLVIMPSVAPQSLPLWEGIPLRWMRSSKYLDEAYE EMWINIEVIKKLDĀKVMILRGLĀBELEGMĢSP 6245 81 1148 LSLRNĀKYSFPĢELISLFSMTDLNDNICKRYIKMITNIVILSLI ICISLĀFWIISMTASTYYGNLERISPWRWLPSVVVVVLIVSNGL KKRSLDHSGALGĢLVVYGIVSTLLTANFSTELMFFILSSKILTW KGEVKKRLDSEYKSGGGRWNVQVFCNGAVPTELALIYMIENGĢG EIPVDFSKQYSASWMCISLLABALGASADTBLALIYMIENGĢG EIPVDFSKQYSASWMCISLLABALGASADTBLALIYMIENGĢG EIPVDFSKQYSASWMCISLLABALGASADTBLALIYMIENGĢG EIPVDFSKQYSASWMCISLLABALGASADTBLAULYBIRAVĢTUVNDLDISAĢQWPILAFGGLAGLLĪĢSIVDSYLGATMQYTCLDESTG MVUNSPTKRAHTLĀRGY ILDNAVANLPSSVLIALLEPTAMĢTW PRG 6246 1177 359 SLMPWILMDBLMQISLQLLCVYTANFPNGCSSLCWSSCGĢHÞV QATHRGAVSNSLMLCILKLASQMPLENTTVQQMVFMLLSNLALS HDCKSVIQKSNTĢNTSLALÞKGSNHCHISNIT TILKKLLLANIS SGEDGQQMILRIDGCLDLLTEMSYKKKSPLLPLLIFHVOYSS PANKKRILANSKVITVLAACLESENQWAQRIGAAALWALTYNYQ KAKTALKSPSVKRVDEAVSLAKKTPPNSSAMPILMAYYLKCLEN LVQLLINSS 6247 3 1678 NSRVWGFWTEPSAGSLRPMARKQNRNSKELGILVPLTDDTSHAGP PGGRALLECDHLRSGVPGGRRRKOWSCSLLVASLAGAGGSSFL YGYNLSVVNAPTPYIRAFYNSSWERRIGRFIDPDTILLMSVTV SIFAIGGUGTLIVKMIGKVLGRRHTLANNGPATSAALLMACS LQĀĢFEMLIVĢRFIMGIDGGALSVLPPMYLSRISPKEIRGSLG OVTATFICIGVPTGQLLGPLELIGKSTWPLFGGVIVVPAVVQL LSLPPIPDSPRYLLLEKHNEARAVKAPQTFLIGKAHVSQEVEEVI ASSRVQRSIRLIVSVLELLRAPYVKNQVVTVIVTMACVLCGLMA INFYTNSIFGKAGIPPSAHTYPTVTSTGTLAAVFSGVIJEHL GRRPLLIGGGGIMGLFFGTLTITLQDHAPMVPYLSIVGILBI INFYTNSIFGKAGIPPSAHTYPVTSTGTLAAVFSGVIJEHL GRRPLLIGGFGLMGLFFGGLORFRANKINSPAVG LLFPPIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRKKAYPPBEKIDSAVTDOKINGRS 1489CSGGGIPPILIGGEFQQGGRRRSNOPOLTKKVCVVP SQPVVELVLMKVLIGACKLLLRLDCCKTFLLTVKHIGLQEFII LALWWGLVSRLWVLYKGVLGRKLLLLYPLPFGLGVVAGQPBI LALWWGLVSRLWVLYKGVLGRKLLLLLYPLPFGLGVAGTQPMP YKDDTFTPSDITTFLGQOPFTEAFKKOWP 1AFPAMGINKLLINLIF	1	. 1		
SPPTGSIDESPBLSMGSAGVTQSSPLLDEVDFLIFERTRAVDPIR RVFFFFYQHLTFFSIQPQPPPCHAFHPRDPPAGTKRQLILVPLK GPPILAPILSITPILSKNSCYFFRSRIAGGMHLS 6244 2119 1745 FERAYASQFGTFLGRNESERCKLKLQQKTMSLWSMVNQPSELSK FTMPLFERANNLVIMPSVAPQGSLBUSTPLKNRSKSYKDEAYE EMVNILEYNKBLQAKVNILRRQLAELETEDGMQSSP 6245 81 1148 LSKNAKYSFPQELISLFSWTDLNDNICRYIKMITNIVILSLI ICISLAFWIISMTASTYYGNLRPISPWRUPSVVVVVLIVSNGL KKKSLDHSGALGGLVVGFILTIANFSFFTSLMFFLSSSKLTW KGEVKKRLDSEYKEGGGNNWQVDFGAVPTELALLWMIENGG EIPVDFSKQYSASWMCLSLLAALACSAGDTWASEVGPVLSKSSP RLITTWEKVPGTNAGGTVVVGLVSSLIGGTFVGTADFLOYLFV NDLDISAPQWFILAFGGLAGLLGSIJDSYLGATMQYTGLDESTG MVVNSPTNKARHIAGKFILDNNAVNLFSSVLIALLLPTAAWGFW PRG 6246 1177 359 SLWFWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVSNSIMLCILKLASQWFENTTVQONVFMLLSNLALS HCKGGYLGXSFFLONFISLALPRGGKKHLSNITLIKKLLLNIS SGEDGQOMILRIDGCLDLLTEMSKYKHKSSPLLPLLLFHNVCFS PANKPKILLANEKVITULAACLESERGKKHLSNITLIKKLLLNIS SGEDGQOMILRIDGCLDLLTEMSKYKHKSSPLLPLLLFHNVCFS PANKPKILLANEKVITULAACLESERGKKHLSNITLIKKLLLNIS SGEDGGOMILRIDGCLDLLTEMSKYKHKSSPLLPLLLTFHNVCFS PANKPKILLANEKVITULAACLESERGKHLSNITLIKKLLLNIS SGEDGGOMILRIDGCLDLLTEMSKYKHKSSPLLPLLLTFHNVCFS PANKPKILLANEKVITULAACLESERGKHLSNITLIKKLLLNIS SGEDGGOMILRIDGCLDLLTEMSKYKHKSSPLLPLLLTFHNVCFS PANKPKILLANEKVITULAACLESERGKHLSNITLIKKLLLNIS SGEDGGOMILRIDGCLDLLTEMSKYKHKSSPLLPLILLTFHNVCFS PANKPKILLANEKVITULAACLESERGKHSPLIPDTITHAGP PGGGRALLECDHLRSGGVGGGRRKOWSCSLLVASLAGAGSSFL VGYNLYNAPTPYLKAPYMSPARGPLDDTLTLLNSVTVU SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGPALSAALIMACS LQAGAFEMLIUGRFIMGIDGGVALSVLPMYLSSISPKERGSLG QVTAIFICIGFYTGGLUGLFELKSKSTWPLFGVIVVPAVVQL LSLPFLDSSPYLLLEKHPRARVKAFQTFLGKAHVSGEVEBVL ABSRVQRSIRLVSVLELLRAPYVRQVVTVIVTMACYQLCGINA IMPYINSIFGKAGIPPAKIPYTGTGTGTLTAATVLYFULGCHIAA INSTUNSERGGGGIPPILTITTTLQDBARWYTLSIVGLIAI GREPLLIGGFGGTPFILTTTLTLQDBARWYTLSIVGLIAI GREPLLIGGFGGDFPILTTTTLTQDPORGAADLCI AAVIKGCHLVILSLKSGTLDAFTDVLCAVILVSNENRRMGRHKHL ALKOVEGCLKELKNINLMEGSIODFELFSSNENDPITTKVCVVP SQPVVELVLMKVLGACVLLRLILLYPPIGLIQEVARIQRMP YKDFTFSDITEFLGGPYFEAFKKMPIAFAAKGINKLINLEPI LNLWWGILVSRLWVLKGAUVRKILLUYSPEGLLQEVARIQRMP YKDFTFSDITEFLGGPYFEAFKKMPIAFAAKG		j ·		,
RVPFFFYQHLTFFSIQPQPPCHAFHERDPAGTKRQLILVPLK GPPILAPILSLTPILSRNSCYFPRSRIAQGWHLS 6244 2119 1745 FEHAYASGFGTFLGNNESBERCKLKLQGKTMSLWSWVNQPSELSK FTHPLFEANNLVIMPSVAPQSLPLWEGIFLRNRSSKYLDEAYE EMVNILEYNKLQAKVNSLWSWVNQPSELSK FTHPLFEANNLVIMPSVAPQSLPLWEGIFLRNRSSKYLDEAYE EMVNILEYNKLQAKVNSLWILGRGLAETEDGOMGSEP 6245 81 1148 LSLRNAKYSFPQELISLFSWTDLNDNICKRYIKMITNIVILSLI ICISLAFWIISMTASTYYGHLRPISPWRALPSVVPPULIVSNGL KKRSLDHSGALGGLVGVGFILTIANFSFFTSLLMFFLSSKLTTW KGEVKKRLDSEYKEGGORNWOVPCRGAPTELALLYMIENGG EIPVDFSKQYSASWMCLSLLAALACSAGDTWASEVGPVLSKSSP RLITTMEKVPVGTNGGVTVVGLUSSLLGGTFVGLAYFLTQLIFV NDLDISAPQWBIIAPGGLAGLLGSIVDSYLGATMQYYTGLDESTG MVVNSPTNARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW PRG 6246 1177 359 SLMPWILMDDSLMQTSLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVSNSIMLCILKLASQMFLENTVOQMVFMLLSNLALS HDCKGVIQKSWFLQNFLSSLALPKGGNKHLSNLTILWIKLLLINTS SGEDGQOMILRLDGCLDLLTEMSKYKKSSPLLPLLIFHNVCFS PANKKYLLANSKVITVLAACLESENNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTPPNSEANPLNAYYLKCLEN LVQLLNS 6247 3 1678 NSRVWGPWTEPSAGSLRFMARKQNRNSKELGLVPLTDDTSHAGP PGGRALLECDHLRSGYPGERKOWSCSLLVASLAGAGSSFL YGYNLSVVNAPTPYIKAFYMESSERRHGRPLDPDTLTLLWSVTV SIFAIGGLWGTLIVKMIGKVLGKKHTLLANNGFAISAALLMACS LQGAFEMLJVGRFTMGIDGGVALLPWILGSHGSFALSALLMACS LQGAFEMLJVGRFTMGIDGGVALLPWILGHTSKAHVASQEVEEVL ASSRVGSRIRLVSVLELLRAPYVRQVVTVLYTMACQLGLNAA IMPYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFGGLVIELL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI 1ASFCSGFGGIPFILLTGEFPGQSQRPAAFILAGTVNNLSNPAVG LLFPFIQKSLDTYCFLVPATICTTGATVLYVLPETTNRTYAEI SQAFSKRWAYPPERKLDSAVTDGKINGRP 6248 56 1773 VPPPRMMAAVPFGLEFWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIRCCHLVLLSLKSGTLDAETDVLCAVINNINNRMGRHKPHL ALKQVEGCLRFLKNNNLESGIODLFFFISSNENDPLTTKVCVVP SQPVVELVLMKVLGACKILLRLDCCCTFFLLTVKHLGCDEFII LNLVWVGLVSRLWVLYKGVLKRLILLYPPIPGLIQEVARIOMP YFKDFTFSDITEFLGQPYFEAFRKKMPIAPAAKGINKLLNNLF PYRDFTFFSDITEFLGQPYFEAFRKKMPIAPAAKGINKLLNNLF				
6244 2119 1745 FEHAYASQFGTFLGNNESERCKLKLQQKTMSLWSWVNQPSELSK FTNPLFBARNLTIWBEVAPQSLPLWEGTFLMWRSSKYLDEAYE EMWNIETHKELQAKVNLTRRGLAELETECOMQESP 6245 81 1148 LSLRNAKYSFPQELTSLFSMTDLNDNICKRYIKMITMIYLSLI ICISLAFWIISMTASTYYGNLRFISPWRWLFSVVVPVLIVSNGL KKKSLDHSGALGGGLVVGFILTIAMFSFFTSLLHFTLSSSKLTUM KGEVKKRLDSEYKEGGRNWUQVFCNGAVPTELALLYMIENGFG EIFVDFSKGYSASWMCLSLLAGKAGDTWASERSUPPULSKSSP RLITTWEKVPVGTNGGVTVVGLVSSLLGGTFVGIAYFLTQLIFV NDLDISAPQWFILARGFLAGLIGSIVDSYLGATMQYTGLDESTG MVVNSTYNKARHACKFILDNAVNLFSSVLIALLLFTAAWGFW PRG 6246 1177 359 SLWPWILMDDSIMQISLQLLCVYTANFPNGCSSLCWSSCGQPV QATHRGAVSNSIMLCTLKLASGMFLENTTUQCNVFMLLSNLALS HDCKGYIQKSNFLQNFLGSLALPKGGNKHLSNLTILWIKLLINIS SGEDGOMILRIDGCLDLLTEMSKYKKHSSPLLPLDLIFFNVCFS PANKPXILANBKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN LVQLLNSS 6247 3 1678 NSRVWGPWTEPSAGSLRFMARKQNRNSKELGLVPLTDDTSHAGP PGFGRALLECDHLRSGVFGGRRKLDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPYIKAFYNESWERRIGRFIDDTLTLLWSVTV SIFAIGGLUGTLJUTWSHKELGLVPLTDDTSHAGP PGFGRALLECDHLRSGVFGGRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPYIKAFYNESWERRIGRFIDDTLTLLWSVTV SIFAIGGLUGTLJUKMIGKVLGRRHTLLANGFAISAALLMACS LDAGAFEMLIVORFITMGTDGGYALSVLPMYLSSISPKETRGSLG QVTAIFICIGGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL LSEPPIPDSPRYLLLEKHNERAVKAFOTTLIKAMSVEEVL ASSRVQRSIRLIVSVLELLRAPVVRNQVVTVIVTMACYQCCGINA IWFYTNSIFGKAGIPPAKIPYTNSTGGISTLAAVPSGLVIEHL GRRPLLIGGFFGMLFFFSTLTTUTLTUTVALYQLPEKNATYAEI SQAFFSKRNAVPPEREKIDSAGVTUCHTVARVLSNENGRAWGRUF LLFPFIQKSLDTYCFLVFATICTGATYLFVLPEKNATYAEI SQAFFSKRNAVPPEREKIDSAGVTUCHTVARVLSNENGRRHKHH GRRPLIGGFFFINNENGRHKHHL ALKQVGCLKRIKNNLEGSFIFFSSNENGRGPTTKVCVVP SQPVVELVLMKVLGACKLLBELLDCCKTFLLTVKHIGLGFFII LNLVWMULVSRWWLVSRLWKLIKLLLLPFFLLGFFFSNENGPTTKVCVVP SQPVVELVLMKVLGACKLLBELLDCCCKTFLLTVKHIGLGFFII LNLVWKHLGACKLLBELLDCCCKTFLLTVKHIGLGFFII LNLVWKHLGACKLLBELLDCCCKTFLLTVKHIGLGFFII LNLVWKHLSGRYBGVYFRSDAYTKLINKLLSFI GAPLFFFSNENGRHYDH LNLVWWLSWFRWHVYRKWLYKSVKKLINKLLHKLF)	j ,		RVFFFFYQHLTFFSIQPQPPPCHAFHPRDPPAGTKRQLILVPLK
FTNPLFEANNLVIWPSVAPQSLPLWEGIFLRWNRSSKYLDEAYE EMWNIIEYNKELQAKVNILRRQLAELETECHOMOSE9 6245 81 1148 1SLRNAKYSPOGELSIEFSMITDINNICKRYIKMITMIVILSIJ ICISLAFWIISMTASTYYGNLRPISPWRWLFSVVVPVLIVSNGL KKKSLDHSGALGGLVVGFILTIANFSFFSLLMFFILSSKLITKM KGEVKKRLDSEVKEGGQRNWVQVVGVNGAVPTELALLYMIENGFG EIPVDFSKQYSASWMCLSLLAALACSAGDTWASEVGPVLSKSSP RLITTWEKVPVGTNGGVTVUGLVSLLGGTFVGIAYFLTQLIFV NDLDISAPQWPIIAPGGLAGLLGSIVDSYLGATMQVTGLDESTG MVNNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLFTAAWGFW PRG 6246 1177 359 SLWPWILMDDSIMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVSNSIMLCILKIASQMPLENTTVQONVFMLLSNLALS HCKGVIOKSNFLQNFLSLALDKGRKHLSNLTILHWIKLLLHIS SGEDGQQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS PANKRKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTPSNSEANPINAYYLKCLEN LVQLLMSS 1678 NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP PGGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTITLIMSVTV SIFAIGGLVGTLVKMIGKVLGRKHTLLLANNGPAISAALLMACS LQAGAFEMLIVGRFTMGIDGGVALSVLPMYLSSISFKEIRGSLG QVTAIFICIGVFTGQLLGLPELLCKESTWPLFGVIVVPAVVGL LSLPPLDSPRYLLLEKHNERAKVFOTFLGKAHVSQEVEBVL AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGINA IWFYTNSIFGKAGIPPAKIPYVTTSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGIMGLIFFGTLTILTQDHAPWYPSISIGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNPAWG LLFPPIQKSLDTYCFLVFATICITGAIYLFVLPETKNRTYAEI SQAFSKRINKAYP PERKIDSAVTYDKHNRMKRHPHL AKQVQBCLKRIKNINDEGSIODJFELFSSNENQPLTTKVCVVP SQPVENLVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLOFFII LNLWWGLVSRLWVLYKGVLKRLLLLLEPLFGLLQEVARIQPMP YKDFTFPSDTIEFLGQVFEERKKWP IAFAAKGINKLLENLELF	1			
FTMPLFEANNLVIWPSVAPQSLPLWEGIFLRWNRSSKYLDEAYE EMVNI IEYNKELQAKVNILRQLAELTEDGMQESP 6245 81 1148 LSERNAKYSFPQELISLFSMTDLNDNICKRYIKMITNIVILSLI ICISLAFWI ISMTASTYYGNLRP 13 PHRMLPSVVVPVLIVSNGL KKKSLDHSGALGGLVVGFILTIANFSFTSLLMFFLSSSKLTKW KGEVKRKLDSEVKEGGQRNWVQVPCNGAVPTELALLYMIENGPG EIPVDFSKGYSASWMCLSLLAGALGSAGDTWASEVGPVLSKSSP RLITTHEKVPVETNGGVTVVGLUSSLLGGTFVGTAYPLTQLIFV NDLDISAPQWPIIAPGGLAGLLGSI VDSYLGATMQTTGLDESTG MVVNSPTNKARRIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW PRG 6246 1177 359 SLWFWILMDDSIMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVSNSIMLCILKLASQMFLENTTVQORVFMLLSNLALS HDCKGVIOKSNFLQNFLSLALDFGKNKLSNLTITLMKLLLINS SGEDGQOMILRIDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTPFNSEANPLNAYYIKCLEN LVQLLNSS NSRVWGPWTEPSAGSLRFMARKQNRNSKELGLVPLTDDTSHAGP PGGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPPPYIKAFYNESWERHGRIDDDTITLLWSVTV SIFALGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSBISPKEIRGSLG QVTAIFICIGVFTGQLLGLPBLLCKESTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLILEKHNERAVKPOTFLIGKAHVSGEWEVL ABSRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGINA IMFYTNSIFGKAGIPPAKIPYTTLTUQDHAPWYPSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNPAVG LFPPIQKSLDTYCFLVFATICITGAIYLTVTVLPETKNRTYAEI SQAFSKRIKAYP PEREKIDSAVTJOCHPARTYAEI SQAFSKRIKAYP PEREKIDSAVTJOKKNGRP 6248 56 1773 VPPPRMMAAVPPGLEPHWRVRTPRAGRRSAVTYONPGAALDLCI AAVIKECHLVILISLKSQTLDAETDVLCAVLYSNENRMGRRHKPHL ALKQVEQCLKRLKNNNLEGSIGDLYFELFSSNENQPLTTTKVCVVP SQPVELVLMKVLGACKLLIRLLDCCCKTFLLTVKHIGLGFTI LNLWWGLVSRLWVLYKGVUKRLILLYEPLFGLLQEVARIQPMP YKDFTFSDITEFLGQVFEEFKKNP IAFAAKGINKLLNLILF	6244	2119	1745	FEHAYASQFGTFLGNNESERCKLKLQQKTMSLWSWVNQPSELSK
SI	1			17
ICISLAFWIISMTASTYYGNLRPISPWRWLFSVVVPVLIVSMGL KKKSLDHSGALGGLVVGFILITIANFSFTSLLMFFILSSSKLTKW KGEVKRLDESPKEGGGRWOVPCKGAVPFELALLYMLENGPG EIPVDFSKQYSASWMCLSLLAALACSAGDTWASEVGPVLSKSSP RLITTWEKVPVGTNGGUTVVGLVSSLLGGTFVGIAYFLTQLIFV NDLDISAPQWBI LAFGGLAGLIGSIVDSYLGATMQYTGLDESTG MVVNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW PRG 6246 1177 359 SLWPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVSNSLMLCILKLASQMPLENTTVQMVFMLLSNLALS HDCKGYIQKSNFLQNFILSLALPKGGNKHLSNLTILWIKLLLMIS SGEDGQMTLRLDGCLDLLTERKYYHKSSPLLPLLIFHNVCFS PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKFPPNSEANPLNAYVIKCLEN LVQLINSS 6247 3 1678 NSRVWGPWTEPSAGSLRFMARKQNRNSKELGLVPLTDDTSHAGP PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASILAGAFGSSFL YGYNLSVVNAPPTYIKAPYNERRHRHDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGPAISAALLMACS LQAGAFEMLIVGRFINGIDGGVALSVLPWYLSEISPKEIRGSLG OVTAIPICTGVPTGQLLGLELKSSTMPYLFGGIVTEHAVYSGLVCEINA INFYTNSIFGKAGI PPAKL PYTLSTGGIETLAAVYSGLVCEINA INFYTNSIFGKAGI PPAKL PYTLSTGGIETLAAVYSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHARWPYPLSTUGILAI IASFCSGGGIPFILITGEFFQQSQPBAFILAGTVNWLSNFRAG LLFFTGSGGGMGFFGTLTITLTLQDHARWPYLSTUGILAI IASFCSGGGIPFILITGEFFQQSQPBAFILAGTVNWLSNFRAG SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMAAVPPGLBEWNRVR I FKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHRRMGRHKPHL ALKQVEQCLKRIKNNNLEGS I ODLFELFSSNENQPLITKVCCVVP SQPVVBLVLMKVLGACKLLLIRLLDCCCKTFLLTVKHLGLQEFII LNLVWGLVSRLWVLYKGVLKRUILLYPEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQEVFFEAFKKKMPIAPAAKGINKLLMKLF	1			EMVNIIEYNKELQAKVNILRRQLAELETEDGMQESP
KKKSLDHSGALGGLVVGFILTIANFSFFTSLIMFFLSSSKLTKW KGEVKRLDSEYREGGGRNWQVUFORAVPTELALLYMIENOPG EIEVDFSKQXSASMCLSLLAALACSAGTPGLALLYMIENOPG EIEVDFSKQXSASMCLSLLAALACSAGTPGLAYPLTQLIFV NDLDISAPQWPIIAFGGLASLLGSIVDSYLGATMQYTCLDESTG MVVNSPTNKARHIAGKPILDNNAUNLFSSVLIALLLPTAAWGFW PRG 6246 1177 359 SLWPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVSNSIMLCILKLASQMPLENTTVQQMVFMLLSNLALS HDCKGVIQKSNFLQNFLSLALPKGGNKHLSNLTLWLKLLANIS SGEDGQQMILRLDGCLDLLTEMSKYKKHSSPLLPLLIFHNVCFS PANKPKILANEKVITVLAACLESSNQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN LVQLLNSS 6247 3 1678 NSRVWGPWTEPSAGSLRFMARKQNRNSKELGLVPLTDDTSHAGP PGGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPFTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRRHTLLANNGPAISAALLMACS LQAGAFEMLVGRFIMGIDGGVALSVLPMYLSE ISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL LSLPFLDDSPRYLLLEKHNEARAVKAPCTFLGKAHVSGEVEEVL ASSRVQRSIRLVSVLELLRAPYVRNQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITITLTLDHAPWUPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNRAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKLDSAVTDGKINGRP 6248 56 1773 VPPPRMMAVPFGLEFMNRVEIPKGRIRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRRKPHL ALKQVEQCLKRLKNNMLEGS IQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQFFII LNLVMVGLVSRLWVLYKGVLKRLILLYPPLFGLLQEVARIQPMP YFKDFTFPSDITEFLEQVYFEAFKKKNP IAFAARGINKLLNKLF	6245	81	1148	LSLRNAKYSFPQELISLFSMTDLNDNICKRYIKMITNIVILSLI
KGEVKKRLDSEYKEGGQRNWUQVFCNGAVPTELALLYMIENGPG EIFVDFSKQYSASWMCLSLLAALACSAGITWASEVGPVLSKSSP RLITTMEKVPVGTNGGVTVVGLUSSLLGGTFVG1AYFLTQLIFV NDLDISAPQWPIIAFGGLAGLLGSIVDSYLGATMQYTGLDESTG MVVNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW PRG 6246 1177 359 SLWPWILMDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVSNSLMLCILKLASQMFLENTTVQQMVFMLLSNLALS HDCKGVJVQKSNFLQNFLSLALPKGGNKHLSNLTILWILLLMIS SGEDGQQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALITYNYQ KAKTALKSPSVKRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN LVQLLNSS 6247 3 1678 NSRVWGFWTEPSAGSLRFMARKQNNSKELGLVPLTDDTSHAGP PGPGRALLECDHLRSGVPGGRRKDWSCSLLVASLAGAFGSSFL VGYNLSVVNAPTFYIKAFYNESWERRHGPIDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLCKESTWPYLFGVIVVPAVVQL LSLPFLDDSPRYLLLEKHNEARAVKAFQTFLGKARVSQBVEBVL AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGINA IWFYTNSIFGKAGIPPAKRIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGFGGIPFILTGEFFQQSGRAAFIIAGTVNWLSNFAVG LLFPFIQKSGLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMMAVPPGLEFWNRVRIFKGRNESAVTVNPGAALDLCI AAVIKSCHLVILSLKSQTLDAETDVLCAVLYSNENRMGRRKPHL ALKQVEQCLKRLKNMNLEGSIQDLFEFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLIRLLDCCCKTFLLTVKHLGLQFFII LNLVMVGLVSRLWVLYKGVLKRILLLPEPLGLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKNPIAFARGIKNLLNKKP	ì			ICISLAFWIISMTASTYYGNLRPISPWRWLFSVVVPVLIVSNGL
EIPVDFSKQYSASWMCLSLLAALACSAGDTWASEVGPVLSKSSP RLITTMEKVPVGTNGSVTVVGLUSSLLGGTFVGLTAYFLTQLIFV NDLDISAPQWPI1ABGGLAGGLUSSLUSPLTQTAYFLTQLIFV MVUNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW PRG 6246 1177 359 SLWPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVSNSLMLCILKLASOMPLENTTVQQNVFMLLSNLALS HDCKGVIQKSNFLQNFLSLALPKGGNKHLSNLTILWLKLLLNIS SGEQQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTPPNSEANPLNAYYLKCLEN LVQLLNSS 6247 3 1678 NSRVWGPWTEPSAGSLRFMARKQNRNSKELGLVPLTDDTSHAGP PGFGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL YGGNLSVNNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGPAISAALLMACS LQAGAFEMLTVGRFIMGIDGGVALSVLPWYLSSISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLGKSSTWPYLFGVIVVPAVVQL LSLPFLPDSSRYLLLEKHNEARAVKAFQTPLGKHVSQEVEEVL ABSRVQRSIRLVSVLELLLRAPYVRWQVVTVIVTMACCQLCCLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQVILDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SOPVVBLVLMKVLGACKLLIKLLDCCCKTFLLTVKHIGLQEFII LNLWMGLVSRLWVLYKGULKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGGPYFEAFKKWPTAFAAKGINKLLNKLF	1			KKKSLDHSGALGGLVVGFILTIANFSFFTSLLMFFLSSSKLTKW
RLITTWEKVPVGTNGGVTVVGLVSSLLGGTFVGIAYFLTQLIFV NDLDISAPQWPI IAFGGLAGLIGSI VDSYLGATMQYTGLDESTG MVVNSPTNKARHIAGKP ILDNNAVNLFSSVLIALLLPTAAWGFW PRG 6246 1177 359 SLWPWILMDDSLMGISLQLLCVYTANFPNGCSSLCWSSCGGHPV QATHRGAVSNSLMLCILKLASQMPLENTTVQQMVFMLLSNLALS HDCKGVIQKSNFLQNFLSLALEKGRKKHLSNLTILWLKLLLNIS SGEDGQQMILRLDGCLDLLTEMSKYKKKSSPLLPLLIFHNVCFS PANKPKILANBKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTPPNSEANPLNAYYLKCLEN LVQLLNSS 1678 1678 NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP PGGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS LQAGAFFMLTVGRFTHGTDGGVALSVLPMYLSBISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL LSLPFIPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVEEVL AESRVQRSIRLVSVLELLARPYVRWQVVTVIVTMACYQLCGINA IMFYTMSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWYPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVPATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPDEKIDSAVTDGKINGRP GRPPLIGGFGLMSLFFGTLTSTYLFVLPETKNRTYAEI SQAFSKRNKAYPPDEKIDSAVTDGKINGRP AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNENNGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLILLILDCCCKTFLLITVKHIGLQEFII LNLWMGLVSRLWVLYKGULKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGGPYFEAFKKKMPIAFAAGINKLLNKLF	ĺ			KGEVKKRLDSEYKEGGQRNWVQVFCNGAVPTELALLYMIENGPG
NDLDISAPQWPIIAFGGLAGLLGSIVDSYLGATMQYTGLDESTG MVVNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW PRG 5246 1177 359 SLWPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVSNSIMLCILKLASQMPLENTTVQQMVFMLLSNLALS HDCKGVIQKSNFLQNFLSLALPKGGNKKHLSNLTILWLKLLLNIS SGEDGGQMILRLDGCLDLLTEMSKYKKKSPLLPLLIFHNVCFS PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN LVQLLNSS 6247 3 1678 NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP PGPGRALLECDHLRSGVPGGRRRDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALMACS LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG QVTAIFTCIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVEEVL ABSRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA IMFYTNSIFGKAGIPPAKIPYVRWQVVTVIVTMACYQLCGLNA IMFYTNSIFGKAGIPPAKIPYVRQVVTVIVTMSVSIVGILAI IASFCSGPGGIPFILTGEFFQQSGRPAAFILAGTVWMLSNFAVG LLFPPIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSIKSQTLDAETDVLCAVLYSNHNRMGRRKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVBLVIMKVLGACKLLLIKLLLYPDLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF	ļ			EIPVDFSKQYSASWMCLSLLAALACSAGDTWASEVGPVLSKSSP
MVVNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW PRG 6246 1177 359 SLWPWILMDDSIMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVSNSIMLCILKLASQMFLENTTVQQMVFMILSNLALS HDCKGVIQKSNFLQNFLSLALPKGGNKHLSNLTILWLKLLLNIS SGEDGQQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN LVQLLNSS 6247 3 1678 NGRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP PGGRALLECDHLRSGVPGGRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPYLKAFYNESWERRHGRPIDPDTITLLMSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS LQAGAFEMLIVGRFIMGIDGGVALSVLDPWILSEISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL LSLPPLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVEEVL ABSRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKTPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLPFGTLTITUTLQDHAPWYPLSIVGILAI IASFCSGPGGIPFILTGGFGTGTTTTUTLQDHAPWYPLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVWWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMAAVPPELEDWNRVRIPKAGNRSAVTVQNFGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEGCLKRLKNNNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVMKVLGACKLLILLYPLFFGLLQEVATQPMP YFKDFTFPSDITEPLGQPYFEAFKKKMPIAPAAKGINKLLNKLF	İ			RLITTWEKVPVGTNGGVTVVGLVSSLLGGTFVGIAYFLTQLIFV
6246 1177 359 SIMPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVSNSIMLCILKLASQMPLENTTVQQMVFMLLSNLALS HDCKGVIQKSNFLQNFLSLALPKGGNKHLSNLTILWLKLLLNIS SGEDGQQMILRILDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTPPNSEANPLNAYYLKCLEN LVQLLNSS 1678 NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP PGPGRALLECDHLRSGVFGRRRKDWSCSLLVASLAGAFGSSFL YGSNLSVVNAPTPYIKAFYNESWERRHGRPLDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG QVTAIFICIGVFTGQLIGLPELLGKESTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVEEVL AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA IMFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGIMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFGQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPRMMAAVPPGLEDSAVTDGKINGRP AVIKECHLVILSLKSQTLDAETDVLCAVLYSNINRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLIRLLDCCCKTFLLTVKHIGLQEFII LNILVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAARGINKLLINKLF				
6246 1177 359 SLWPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVSNSIMLCILKLASQMPLENTTVQQNVFMLLSNIALS HDCKGVIQKSNFLQNIESLALPKGGNKHLSNITILWLKLLINIS SGEDGQQMILRLDGCLDLLTEMSKYKHKSSPLLPPLLIFHNVCFS PANKPKILANBKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN LVQLLNSS 6247 3 1678 NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP PGGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGARGSSFL YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSBISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVEEVL AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGINA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLITITLDQHAPWVPYLSIUGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVPATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP VPPRMMAAVPPGLEPWNRVTFFKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEGCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLEDCCKTFLLTVKHLGLQEFII LINLWMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF				MVVNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW
QATHRGAVSNSIMLCILKLASQMPLENTTVQQMVFMLLSNLALS HDCKGVIQKSNFLQNFLSLALPKGGNKHLSNLTILWLKLLLNIS SGEDGQQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN LVQLLNSS 1678 NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSBISPKEIRGSLG OVTAIFICIGVFTGQLLGLPELLGKBSTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAPQTFLGKAHVSQEVEVL AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LINLVMVGLVSRLWVLYKGYLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF				
HDCKGVIQKSNFLQNFLSLALPKGGNKHLSNLTILWLKLLLNIS SGEDGQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFENVCFS PANKKILANBKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTPNSEANPLNAYYLKCLEN LVQLLNSS 1678 NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP PGPGRALLECDHLKSGVPGGRRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPYIKAFYNESWERRHGPIDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG OVTAIFICIGVFTGQLIGLPELLGKESTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVEEVL AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGFGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFFLFSSNENQPLTTKVCVVP SQPVVELVLMKVLLGACKLLLRLDCCCKTFLLTVKHLGLQEFII LNLWMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAPAAKGINKLLNKLF	6246	1177	359	
SGEDGQQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS PANKPKILANBKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN LVQLLNSS SSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISSALLMACS LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVEEVL AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWPYVISIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNPAVG LLFPFIQKSLDTYCFLVFATICITGAIYLVFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMMAAVPFGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHIGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYFPLFGLLGEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF				
PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN LVQLLNSS 1678 16			**	3
KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN LVQLLNSS 1678 1678 NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLGKBSTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAFQTPLGKAHVSQEVEEVL AESRVQRSIRLVSVLELLRAPYVVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLDCCCKTFLLTVKHIGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARRLQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF				
LVQLLNSS 1678 1773 17			•	
1678 NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVEEVL AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF			•	
PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVEEVL AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPPIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 1773 VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNNNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF				1 -
YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGPAISAALLMACS LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVBEVL AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF	6247	3	1678	
SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVEEVL AESRVQRSIRLVSVLEILRAPYVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHIGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF				
LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAFQTPLGKAHVSQEVEEVL AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPPIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMMAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHIGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF	1			1
QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAFQTPLGKAHVSQEVEEVL AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF				1.1
LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVEEVL AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF				1
AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHIGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF				- -
IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF				1
GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPPIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF				
IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF		1		
LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 6248 56 1773 VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF				
SQAFSKRNKAYPPEEKIDSAVTDGKINGRP 56 1773 VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF				
VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF	[]			l .
AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYPEAFKKKMPIAFAAKGINKLLNKLF	67/0		1773	
ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF	0248	56	1773	· · · · · · · · · · · · · · · · · · ·
SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF				1
LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYPEAFKKKMPIAFAAKGINKLLNKLF		1		1
YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF]	1		· ·
		,		1
TIME GO SKAP DE I TITUE TO KRAK OM KINA ÖMNA DIT GÖ BAKKAK AK		ļ		
	L			TIME COLUMN TIME TO THE TRANSPORT OF THE PROPERTY OF THE PROPE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	<u> </u>	\=possible nucleotide insertion)
			KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
			VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI
			FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
		1	ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
		1000	HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6249	56	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI
			AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
			ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
[SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII
			LNLVMVGLVSRLWVLYKGVLKRLILLYBPLFGLLQEVARIQPMP
			YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF
		1	LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGQPVKNKRVF
			KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
]	j	1	VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
			TSKHHLRORRSONKFLRRORKPORKLOSTLLREIOOFSOGTRKS
			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
			HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6250	232	1306	LAALHIMALPFRKDLEKYKDLDEDELLGNLSETELKOLETVLDD
0230	232	1300	LDPENALLPAGFROKNOTSKSTTGPFDREHLLSYLEKEALEHKD
			REDYVPYTGEKKGKIFIPKOKPVOTFTEEKVSLDPELEEALTSA
ļ			SDTELCDLAAILGMHNLITNTKFCNIMGSSNGVDQEHFSNVVKG
}			EKILPVFDEPPNPTNVEESLKRTKENDAHLVEVNLNNIKNIPIP
			TLKDFAKALETNTHVKCFSLAATRSNDPVATAFAEMLKVNKTLK
}			SLNVESNFITGVGILALIDALRDNETLAELKIDNOROOLGTAVE
			LEMAKMLEENTNILKFGYQFTQQGPRTRAANAITKNNDLVRKRR
			VBGDHO VBGDHO
6251	62	972	TPGSGPMSAWAAASLSRAAARCLLARGPGVRAAPPRDPRPSHPE
0202	02	1	PRGCGAAPGRTLHFTAAVPAGHNKWSKVRHIKGPKDVERSRIFS
			KLCLNIRLAVKEGGPNPEHNSNLANILEVCRSKHMPKSTIETAL
	•		KMBKSKDTYLLYEGRGPGGSSLLIEALSNSSHKCQADIRHILNK
			NGGVMAVGARHSFDKKGVIVVEVEDREKKAVNLERALEMAIEAG
]			AEDVKETEDEEERNVFKFICDASSLHQVRKKLDSLGLCSVSCAL
			EFIPNSKVOLAEPDLEQAAHLIQALSNHEDVIHVYDNIB
6252	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLOTKRKKPRRYWEE
J		1	ETVPTTAGASPGPPRNKKNRELRPORPKNAYILKKSRISKKPOV
		1	PKKPREWKNPESORGLSGAODPFPGPAPVPVEVVQKFCRIDKSR
		1	KLPHSKAKTRSRLEVABAEEEETSIKAARSELLLAEEPGFLEGE
			DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
			RHLAFGGRRGHVAALDWVTKKLMCBINVMEAVRDIRFLHSEALL
		}	AVAONRWLHIYDNOGIELHCIRRCDRVTRLEFLPFHFLLATASE
			TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
			TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
	}	1	KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
			GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
			SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPABLIC
		1	LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
			SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS
			ALDRFVR
6253	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
			ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
			PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
			KLPHSKAKTRSRLEVAEABEEETSIKAARSELLLAEEPGFLEGE
1]	DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
		1	RHLAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL

	·		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
			TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
			TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
			KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
ļ	}	}	GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
			SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPAELIC
ŀ			LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
			SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS
6254	155	1120	ALDREVR
0234	155	. 1139	HALGRRGGSQELSAAACGCFALRLRAPGSGRPALAPGAAAFAGL
			GGAPRFPPRGSAAGRTMLLKBYRICMPLTVDEYKIGQLYMISKH
			SHEQSDRGEGVEVVQNEPFEDPHHGNGQFTEKRVYLNSKLPSWA
	ŀ		RAVVPKIFYVTEKAWNYYPYTITEYTCSFLPKFSIHIETKYEDN
1	1.		KGSNDTIFDNEAKDVEREVCFIDIACDEIPERYYKESEDPKHFK
			SEKTGRGQLREGWRDSHQPIMCSYKLVTVKFEVWGLQTRVEQFV HKVVRDILLIGHRQAFAWVDEWYDMTMDDVREYEKNMHEQTNIK
			VCNQHSSPVDDIESHAOTST
6255	1	1444	PTRPQQELLVSLATVIFVASQKALSVESKAVIKQQLESVSNGWT
0233		7444	VYRIARQASRMGNHDMAKELYQSLLTQVASKHFYFWLNSLKEFS
1			HAEQCLTGLQEENYSSALSCIAESLKFYHKGIASLTAASTPLNP
			LSFQCEFVKLRIDLLQAFSQLICTCNSLKTSPPPAIATTIAMTL
			GNDLQRCGRISNQMKQSMEEFRSLASRYGDLYQASFDADSATLR
			NVELQQQSCLLISHAIEALILDPESASFQEYGSTGTAHADSEYE
l			RRMMSVYNHVLEEVESLNGKYTPVSYMHTACLCNAIIALLKVPL
			SFQRYFFQKLQSTSIKLALSPSPRNPAEPIAVQNNQOLALKVEG
	i		VVQHGSKPGLFRKIQSVCLNVSSTLQSKSGQDYKIPIDNMTNEM
Į.			EQRVEPHNDYFSTQFLLNFAILGTHNITVESSVKDANGIVWKTG
]	}		PRTTIFVKSLEDPYSQQIRLQQQQAQQPLQQQQQRNAYTRF
6256	1	1542	CRGAGAEPAANPRSPRSLVPSLESTSTSVPPAPGTMATDSWALA
-			VDEQEAAAESLSNLHLKEEKIKPDTNGAVVKTNANAEKTDEEEK
	į·		EDRAAQSLLNKLIRSNLVDNTNQVEVLQRDPNSPLYSVKSFEEL
			RLKPQLLQGVYAMGFNRPSKIQENALPLMLAEPPONLIAQSOSG
	1:		TGKTAAFVLAMLSQVEPANKYPQCLCLSPTYELALQTGKVIEQM
			GKFYPELKLAYAVRGNKLERGQKISEQIVIGTPGTVLDWCSKLK
	[FIDPKKIKVFVLDEADVMIATQGHQDQSIRIQRMLPRNCQMLLF
	·		SATFEDSVWKFAQKVVPDPNVIKLKREEETLDTIKQYYVLCSSR
	l' '		DEKFQALCNLYGAITIAQAMIFCHTRKTASWLAAELSKEGHQVA
	·		LLSGEMMVEQRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVV
			INFDLPVDKDGNPDNETYLHRIGRTGRFGKRGLAVNMVDSKHSM
			NILNRIQEHFNKKIERLDTDDLDEIEKIAN
6257	210	615	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE
	į l		NNIVKEELALLDGSNVVPKLLGPVLVKQELGEARATVGKRLDYI
			TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG
			KA
6258	210	615	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGROKLEAQLTE
		-	NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI
			TAEIKRYESQLRDLERQSBQQRETLAQLQQEFQRAQAAKAGAPG
			KA
6259	2	1540	ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV
			SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII
	[SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDOKRNAI
			NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK
	.		YNECGRIFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH
		ļ	QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD
			KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTQLRRAHT
	Í	•	GEKTFECGECGKTFWEKSNLTQHQRTHTGEKPYECTECGKAFCQ
			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
<u> </u>	sequence	<u> </u>	KPHLTNHQRTHTGEKPYECKQCGKTFCVKSNLTEHQRTHTGEKP
-			YECNACGKSFCHRSALTVHORTHTGEKPFICNECGKSFCVKSNL
		1	
	1	ļ	IVHQRTHTGEKPYKCNECGKTFCEKSALTKHQRTHTGEKPYECN
			ACGKTFSQRSVLTKHQRIHTRVKALSTS
6260	2081	1436	GTGPEIHACAHASARAPGSRAMALRELKVCLLGDTGVGKSSIVW
			RFVEDSFDPNINPTIGASFMTKTVQYQNELHKFLIWDTAGQERF
	1	1	RALAPMYYRGSAAAIIVYDITKEETFSTLKNWVKELRQHGPPNI
ļ	ļ	1	VVAIAGNKCDLIDVREVMERDAKDYADSIHAIFVETSAKNAINI
			NELFIEISRRIPSTDANLPSGGKGFKLRRQPSEPKRSCC
6261	3	1188	FWYRLGPGTRSRWPRRGSWAASLVPRGPSPAALVTSPCPPDPLR
001	1		SPACEPCRPDFAPRPALLLRSGPRSAPAVTGKPALKGQPGPWPG
	1		MAEVSIDOSKLPGVKEVCRDFAVLEDHTLAHSLQEQEIEHHLAS
			NVQRNRLVQHDLQVAKQLQEEDLKAQAQLQKRYKDLEQQDCEIA
			QEIQEKLAIEAERRRIQEKKDEDIARLLQEKELQEEKKRKKHFP
			EFPATRAYADSYYYEDGGMKPRVMKEAVSTPSRMAHRDQEWYDA
			EIARKLQEBELLATQVDMRAAQVAQDEEIARLLMAEEKKAYKKA
			KEREKSSLDKRKQDPEWKPKTAKAANSKSKESDEPHHSKNERPA
1			RPPPPIMTDGEDADYTHFTNQQSSTRHFSKSESSHKGFHYKH
6262	2	1759	PECHSQGLCSVHRPGKVPQARMSGLVLGQRDEPAGHRLSQEEIL
			GSTRLVSQGLEALRSBHQAVLQSLSQTIECLQQGGHEEGLVHEK
1			ARQLRRSMENIELGLSEAQVMLALASHLSTVESEKQKLRAQVRR
	•		LCOENOWLRDELAGTOORLORSEQAVAQLEEEKKHLEFLGQLRQ
			YDEDGHTSREKEGDATKDSLDDLFPNEEEEDPSNGLSRGQGATA
ľ			AOOGGYEIPARLRTLHNLVIQYAAQGRYEVAVPLCKQALEDLER
			TSGRGHPDVATMLNILALVYRDQNKYKEAAHLLNDALSIRESTL
		ì	GPDHPAVAATLNNLAVLYGKRGKYKEAEPLCQRALEIREKVLGT
			NHPDVAKQLNNLALLCQNQGKYEAVERYYQRALAIYEGQLGPDN
	,		PNVARTKNNLASCYLKQGKYAEARTLYKEILTRAHVQEFGSVDD
			DHKPIWMHAEEREEMSKSRHHEGGTPYAEYGGWYKACKVSSPTV
ļ			NTTLRNLGALYRROGKLEAAETLBECALRSRROGTDPISQTKVA
	.j	[ELLGESDGRRTSQEGPGDSVKFEGGEDASVAVEWSGDGSGTLQR
-		'	SGSLGKIRDVLRR
6263	1	2408	RELDSLADLPERIKPPYANGLSTSHLRSSSVEDVKLIISEGRPT
	_ '	}	IEVRRCSMPSVICEHTKQFQTISEESNQGSLLTVPGDTSPSPKP
			EVFSNVPERDLSNVSNIHSSFATSPTGASNSKYVSADRNLIKNT
		1	APVNTVMDSPVHLEPSSQVGVIQNKSWEMPVDRLETLSTRDFIC
]	1	PNSNIPDQESSLQSFCNSENKVLKENADFLSLRQTELPGNSCAQ
ļ			DPASFMPPQQPCSFPSQSLSDAESISKHMSLSYVANQEPGILQQ
l			KNAVQIISSALDTDNESTKDTENTFVLGDVQKTDAFVPVYSDST
]	1		
1			IQEASPNFEKAYTLPVLPSEKDFNGSDASTQLNTHYAFSKLTYK
		1	SSSGHEVENSTTDTQVISHEKENKLESLVLTHLSRCDSDLCEMN
			AGMPKGNLNEQDPKHCPESEKCLLSIEDEESQQSILSSLENHSQ
1			QSTQPEMHKYGQLVKVELEENAEDDKTENQIPQRMTRNKANTMA
	1		NQSKQILASCTLLSEKDSESSSPRGRIRLTEDDDPQIHHPRKRK
1		1	VSRVPQPVQVSPSLLQAKEKTQQSLAAIVDSLKLDEIQPYSSER
			ANPYFEYLHIRKKIEEKRKLLCSVIPQAPQYYDEYVTFNGSYLL
	1	1	DGNPLSKICIPTITPPPSLSDPLKELFRQQEVVRMKLRLQHSIE
		1	REKLIVSNEOEVLRVHYRAARTLANQTLPFSACTVLLDAEVYNV
		1	PLDSOSDDSKTSVRDRFNARQFMSWLQDVDDKFDKLKTCLLMRQ
1			OHEAAALNAVQRLEWQLKLQELDPATYKSISIYEIQEFYVPLVD
	1		~
			VNDDFELTPI
6264	143	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
	1		TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
	1		WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
ļ	1	1	SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
1	1		ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT

SEO	Predicted	Predicted end	I had a self a second s
1 -	i e	i .	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
1	1	-	
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		<u> </u>	SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
1 '	·		ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
			INAISRGDLPCMENAVLALAQIENSAAVOKAIAHYDOOMGOKVO
i			LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFOKKLAAOL
1			DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
1			
1	ŀ		YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
j			QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK
1		}	EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
1	ŀ		CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI .
6265	143	1960	KHRQENNALDMAPBIHMTGPMCLIENTNGELVANPEALKILSAI
			TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
1			WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
1			· ·
1	ļ.	٠,	SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
1			ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT
I			SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
1			ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
1	į		INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
			LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQL
	ļ		DKKRDDFCKONOEASSDRCSALLOVIFSPLEEEVKAGIYSKPGG
	l	i	YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
	ļ		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
			QTDQILTEKEKEIEVECVKABSAQASAKMVEEMQIKYQQMMEEK
İ	i .		EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
			CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE
1.	·		GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD
			ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF
1			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR
			GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN
1.50	ح في م الله الله		SINLGSPEOMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF
			LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH
			RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD
	·		PVYKVATWEKQIYTCCRDGLVRRYQLSDL
6267	3	622	LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK
		*	NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS
			RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA
			ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA
j ·		•	VASTSTSDGMLTLDLIQEEDPSPEEPTSLC
6268	160	1260	! · · · · · · · · · · · · · · · · · · ·
0200	160	1368	HRELCONLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV
			DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA
			PNSDIPEEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV
			LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE
			SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ
			KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK
	,		IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS
1		ļ ,	GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ
			· · · · · · · · · · · · · · · · · · ·
			SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR
			KKKQPTS
6269	2886	1449	HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL
			TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT
]			GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN
			FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR
i !			IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALSINP
[[1		~
	ĺ		TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLACHNY
j			WHWALYLIEKGEYEAALTIYDTHILPSLQANDAMLDVVDSCSML
]			YRLQMEGVSVGQRWQDVLPVARKHSRDHILLFNDAHFLMASLGA
I			HDPQTTQELLTTLRDASESPGENCQHLLARDVGLPLCQALVEAE

SEQ	Predicted	Predicted end	I have a self-company and the
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequence	\=possible nucleotide insertion)
-			DGNPDRVLELLLPIRYRIVQLGGSNAQRDVFNQLLIHAALNCTS
İ			SVHKNVARSLLMERDALKPNSPLTERLIRKAATVHLMO
6270	23	2086	SVTVTLGSEGDGRPPTYHLEEMEQEPQNGEPAEIKIIREAYKKA
]		2000	FLFVNKGLNTDELGQKEEAKNYYKQGIGHLLRGISISSKESEHT
			GPGWESARQMQQKMKETLQNVRTRLEILEKGLATSLQNDLQEVP
			KLYPEFPPKDMCBKLPEPQSFSSAPQHAEVNGNTSTPSAGAVAA
			PASLSLPSQSCPAEAPPAYTPQAAEGHYTVSYGTDSGEFSSVGE
			EFYRNHSQPPPLETLGLDADELILIPNGVQIFFVNPAGEVSAPS
			YPGYLRIVRFLDNSLDTVLNRPPGFLQVCDWLYPLVPDRSPVLK
1			CTAGAYMFPDTMLQAAGCFVGVVLSSELPEDDRELFEDLLROMS
		ļ	DLRLQANWNRAEEENEFQIPGRTRPSSDQLKEASGTDVKOLDOG
	•		NKDVRHKGKRGKRAKDTSSEEVNLSHIVPCEPVPREKPKELPEW
		1	SEKVAHNILSGASWVSWGLVKGAEITGKAIQKGASKLRERIQPE
		· ·	EKPVEVSPAVTKGLYIAKQATGGAAKVSQFLVDGVCTVANCVGK
			ELAPHVKKHGSKLVPESLKKDKDGKSPLDGAMVVAASSVQGFST
		1	VWQGLECAAKCIVNNVSAETVQTVRYKYGYNAGEATHHAVDSAV
•			NVGVTAYNINNIGIKAMVKKTATQTGHTLLEDYQIVDNSQRENQ
		Í	EGAANVNVRGEKDEQTKEVKEAKKKDK
6271	32	1058	GCGVKTAGMVGREKELSIHFVPGSCRLVEEEVNIPNRRVLVTGA
			TGLLGRAVHKEFQQNNWHAVGCGFRRARPKFEQVNLLDSNAVHH
1			IIHDFQPHVIVHCAAERRPDVVENQPDAASQLNVDASGNLAKEA
	+		AAVGAFLIYISSDYVFDGTNPPYREEDIPAPLNLYGKTKLDGEK
			AVLENNLGAAVLRIPILYGEVEKLEESAVTVMFDKVQFSNKSAN
			MDHWQQRFPTHVKDVATVCRQLAEKRMLDPSIKGTFHWSGNEQM
			TKYEMACAIADAFNLPSSHLRPITDSPVLGAQRPRNAQLDCSKL
		:	ETLGIGQRTPFRIGIKESLWPFLIDKRWRQTVFH
6272	1136	528	GAVMEDAAAPGRTEGVLERQGAPPAAGQGGALVELTPTPGGLAL
			VSPYHTHRAGDPLDLVALAEQVQKADEFIRANATNKLTVIAEQI
ĺ		. , , , , , , , ,	QHLQEQARKVLEDAHRDANLHHVACNIVKKPGNIYYLYKRESGQ
			QYFSIISPKEWGTSCPHDFLGAYKLQHDLSWTPYEDIEKQDAKI
7 60 70		<u>;</u>	SMMDTLLSQSVALPPCTEPNFQGLTH
6273			
	256	843	SCPRVSPECRSLGCQVMFSLPLNCSPDHIRRGSCWGRPQDLKIA
	25 6	643	SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV
		043	SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS
		043	SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME
6274			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT
6274	56	1142	SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT
6274			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL
6274			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKFVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQBYKKDPDRGYGAGVVTVFKKLLNPKCR
6274			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS
6274			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED
6274			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS
6274			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKFVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI
6274			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKFVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA
6274		1142	SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA QSLHRVFQKS
	56		SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA QSLHRVFQKS SRRGRARCLARGSRRPVPRPAKTMAFMVKTMVGGQLKNLTGSLG
	56	1142	SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA QSLHRVFQKS SRRGRARCLARGSRRPVPRPAKTMAFMVKTMVGGQLKNLTGSLG GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR
	56	1142	SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA QSLHRVFQKS SRRGRARCLARGSRRPVPRPAKTMAFMVKTMVGGQLKNLTGSLG GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI
	56	1142	SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA QSLHRVFQKS SRRGRARCLARGSRRPVPRPAKTMAFMVKTMVGGQLKNLTGSLG GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI EEDTEEEEEKASVLGQLASLPGLNLGSLKDKAQATLGDLKQSAE
	56	1142 565	SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSULGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA QSLHRVFQKS SRRGRACLARGSRRPVPRPAKTMAFMVKTMVGGQLKNLTGSLG GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI EEDTEEEEEKASVLGQLASLPGLNLGSLKDKAQATLGDLKQSAE KCHVM
6275	56 20	1142	SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQBYKKDPDRGYGAGVVTVFKKLLNPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGAILQALAVHLALGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA QSLHRVFQKS SRRGRACLARGSRRPVFRPAKTMAFMVKTMVGGQLKNLTGSLG GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI EEDTEEEEEKASVLGQLASLPGLNLGSLKDKAQATLGDLKQSAE KCHVM
6275	56 20	1142 565	SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQBYKKDPDRGYGAGVVTVFKKLLNPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGALLQALAVHLALQESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA QSLHRVFQKS SRRGRACLARGSRRPVPRPAKTMAFMVKTMVGGQLKNLTGSLG GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI EEDTEEEEEKASVLGQLASLPGLNLGSLKDKAQATLGDLKQSAE KCHVM TLLPLPPPLPDTEGMILLNTGLEGTVAENPVPIVHTPSGNILTLE SCLQQLATHPGHWGIHLQIAEPAALRPSLALLARLSSLGLLHWP
6275	56 20	1142 565	SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQBYKKDPDRGYGAGVVTVFKKLLMPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGAILQALAVHLALQGESSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA QSLHRVFQKS SRRGRACLARGSRRPVPRPAKTMAFMVKTMVGGQLKNLTGSLG GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI EEDTEEEEEKASVLGQLASLPGLNLGSLKDKAQATLGDLKQSAE KCHVM TLLPLPPPLPDTEGMILLNTGLEGTVAENPVPIVHTPSGNILTLE SCLQQLATHPGHWGIHLQIAEPAALRPSLALLARLSSLGLLHWP VWVGAKISHGSFSVPGHVAGRELLTAVAEVFPHVTVAPGWPBEV
6275	56 20	1142 565	SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQBYKKDPDRGYGAGVVTVFKKLLMPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA QSLHRVFQKS SRRGRARCLARGSRRPVPRPAKTMAFMVKTMVGGQLKNLTGSLG GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI EEDTEEEEEKASVLGQLASLPGLNLGSLKDKAQATLGDLKQSAE KCHVM TLLPLPPPLPDTEGMILLNTGLEGTVAENPVPIVHTPSGNILTLE SCLQQLATHPGHWGIHLQIAEPAALRPSLALLARLSSLGLLHWP VWVGAKISHGSFSVPGHVAGRELLTAVAEVFPHVTVAPGWPEEV LGSGYREQLLTDMLELCQGLWQPVSFQMQAMLLGHSTAGAIGRL
6275	56 20	1142 565	SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL LAKEAFDEVDMAHRFAQBYKKDPDRGYGAGVVTVFKKLLMPKCR DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS AQLTHASSLGYNGAILQALAVHLALQGESSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA QSLHRVFQKS SRRGRACLARGSRRPVPRPAKTMAFMVKTMVGGQLKNLTGSLG GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI EEDTEEEEEKASVLGQLASLPGLNLGSLKDKAQATLGDLKQSAE KCHVM TLLPLPPPLPDTEGMILLNTGLEGTVAENPVPIVHTPSGNILTLE SCLQQLATHPGHWGIHLQIAEPAALRPSLALLARLSSLGLLHWP VWVGAKISHGSFSVPGHVAGRELLTAVAEVFPHVTVAPGWPBEV

Sec	SEQ	Predicted	Predicted end	1 700/00
No: noclectide corresponding to first amino acid residue of amino acid sequence 6277 4600 2744 A600 2744 A600 2744 AFFERMINYSVERTIVEASSELIGUTIONICATION AFFERMINYSVERTIVEASSELIGUTIONICATIONICATION AFFERMINYSVERTIVEASSELIGUTIONICATION AFFERMINYSVERTIVEASSELIGUTIONICATIONICATION AFFERMINYSVERTIVEASSELIGUTIONICATIONICATION AFFERMINYSVERTIVEASSELIGUTIONICATIONICATION AFFERMINYSVERTIVEASSELIGUTIONICATIONICATION AFFERMINYSVERTIVEASSELIGUTIONICATIONICATIONICATION AFFERMINYSVERTIVEASSELIGUTIONICATIONICATIONICATIONICATION AFFERMINYSVERTIVEASSELIGUTIONICATIONICATIONICATIONICATIONICATION AFFERMINYSVERTIVEASSELIGUTIONICATI	_			Amino acid segment containing signal peptide
Costion Corresponding Cofired				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first anino acid residue of anino acid residue of anino acid residue of anino acid sequence se	1 2.0.			Glucamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid residue of amino acid sequence 6277 4600 2744 4600 2744 AFPENDIRE, Y=TYROSHER, X=UNKNOWN, *=Stop Coden, /=possible nucleotide deletion, Apossible nucleotide deletion, Apossible nucleotide insertion) Apossible nucleotide insertion TESCELIDAR/TYPENDERSINGUM/MINDRATEP/PUTNY LIMPRILYPEVILASWRITYRIMDLEGISTICHTVTIGKGISP TESCELIDAR/TYPUTPILASWRITYRIMDLEGISTICHTVTIGKGISP TESCELIDAR/TYPUTPILASWRITYRIMDLEGISTICHTVTIGKGISP TESCELIDAR/TYPUTPILASWRITYRIMDLEGISTICHTVTIGKGISP TESCELIDAR/TYPUTPILASWRITYRIMDLEGISTICHTVTIGKGISP TESCELIDAR/TYPUTPILASWRITYRIMDLEGISTICHTVTIGKGISP TESCELIDAR/TYPUTPILASWRITYRIMDLEGISTICHTVTIGKGISP TESCELIDAR/TYPUTPILASWRITYRIMDLEGISTICHTVTIGKGISP TESCELIDAR/TYPUTPILASWRITYRIMDLEGISTICHTVTIGKGISP TESCELIDAR/TYPUTPILASWRITYRIMSTYLASSRIVITIRG TESCELIDAR/TYPUTPILASWRITYRIMSTYLASSRIVITIRG TESCELIDAR/TYPUTPILASWRITTISTAMSTYLASSRIVITIRG TESCELIDAR/TYPUTPILASWRITTISTAMSTYLASSRIVITIRG NDAHIGNLINSKYSTERSILKVINGOSPHITTVEQNSVYKVLEVV RE 6278 3 823 LIFRIVILISIVYLINSVATERKRABKULVESGOYAVVETVILLI LIKYSTKYDAVFAGAMITHASISKICLGLIVHYTEVILASFRARIPERK RIVYSMYSRRAABEVSYTIMMITALSSRICLGLIVHYTEVILASFRARIPERK PVSSACPRAICKOMTREMERITICHLESSCOTORISTYROK PVSSACPRAICKOMTREMERITICHLESSCOTORISTYROK PVSSACPRAICKOMTREMERITICHLESSCOTORISTYROK ARIBERDAR/TYPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPERSNINADAR/GROUPEPPALMGTIL LIKSTARMPTTPVAKKRYSTOPE	l			A=Histidine, i=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence shadow of the typeophan, Y-T				P-Proline O-Clubonine, N-Asparagine,
residue of amino acid sequence 6277 4600 2744	l		residue of	S-Serine T-Thronine, K-Arginine,
amino acid sequence 6277 4600 2744 KRPRITERICLYSEYFITIVEDSPINGVWHINDKLTEYPLUV LKRRNLYBVILLANSPRITYKIDDSPINGVWHINDKLTEYPLUV LKRRNLYBVILLANSPRITYKIDDSPINGVWHINDKLTEYPLUV LKRRNLYBVILLANSPRITYKIDDSPINGVWHINDKLTEYPLUV LKRRNLYBVILLANSPRITYKIDDSPINGVWHINDKLTEYPLUV LKRSLILALCISNVPRIMENDKAPRITYTIGSGLSD TESCEGLOPACPYVALITIKUDINGAPRITYTIGSGLSD TESCEGLOPACPYVALITIKUDINGAPRITYTIGSGLSD TESCEGLOPACPYVALITIKUDINGAPRITYTIGSGLSD TESCEGLOPACPYVALITIKUDINGAPPTICTICHTIGSGLSD TESCEGLOPACPYVALITIKUDINGAPPTICTICHTIGSGLSD TESCEGLOPACPYVALITIKUDINGAPPTICTICHTIGSGLSD TESCEGLOPACPYVALITIKUDINGAPPTICTICHTIGSGLSD TESCEGLOPACPYVALITIKUDINGAPPTICTICHTIGSGLSD TESCEGLOPACPYVALITIKUDINGAPPTICTICHTIGSGLSD TESCEGLOPACPYVALITIKUDINGAPPTICTICHTIGSGLSD TESCEGLOPACPYVALITIKUDINGAPPTICTICHTIGSGLSD TESCEGLOPACPYVALITIKUS LANGTHVERGETAPTIVTOR TESCEGLOPACPYVALITIKUS LANGTHVERGETAPTIVTOR TESCEGLOPACPYVALITIKUS LANGTHVERGETAPTIVTOR TESCEGLOPACPYVALITIKUS LANGTHVERGETAPTIVTOR TESCEGLOPACPYVALITIKUS LANGTHVERGETAPTIVTOR TESCEGLOPACPYVALITIKUS LANGTHVERGETAPTIVTOR TESCEGLOPACPYVALITIKUS LANGTHVERGETAPTIVTOR TESCEGLOPACPYVALITIKUS LANGTHVERGETAPTIVTOR TESCEGLOPACP TESCEGLOPACPYVALITIKUS LANGTHVERGETAPTIVTOR TESCEGLOPACP TESCEGLOPACPYVALITIKUS LANGTHVERGETAPTIVTOR TESCEGLOPACP TESCEGLOPACPYVALITIKUS LANGTHVERGETAPTIVTOR TESCEGLOPACP TESCEGLOPACPYVALITIKUS LANGTHVERGETAPTIVTOR TESCEGLOPACP TESCEGLOPACPYVALITIKUS LANGTHVERGETAPTIVTOR TESCEGLOPACP TESCEGLOPACP TESCEGLOPACPACPATART TESCEGLOPACP TESCEGLOPACPACPATART TESCEGLOPACPACTART TESCEGLOPACP TESCEGLOPACPACPACPACPACP TESCEGLOPACPACPACPACPACPACPACPACPACPACPACPACPACP	į.			W-Troptophan V-Tempeine V-Value
Sequence	:			Codon (-possibleleahide deleti
A600 2744 MAPRTEMELTYSYPETIVEDPELNEVMENDELTEYPLUTE LARRHLYPSYLLASWRITYKIRDLIGITATION LARRHLYPSYLLASWRITYKIRDLIGITATION			Judgannes	\=nossible nucleotide incontion\
LKRFNLYPBVILASWRITTKIMPLIGIGTOKITVGIGGIGG TESCEGLGPBACTVAVITIINGKIMALFFIYGTYLGSRIGGI VTVLCFFFRINGECTRVMTPPLKESFSYPELVLOMLLVYTHISTER TKLYKGSLIALCISNYPFILMPGACPVLTUTGASRIVTGY TLYKKGSLIALCISNYPFILMPGACPVLTUTGASLIVTUTGY TLYKKGSLIALCISNYPFILMPGACPVLTUTGALEAVYVVGY TDICKLRKITYHMISLALCYVLMFGNSMLITSYYASSIVTIM HAMRIPLKINYPSELSHAVYQGCFRLGTVITLKYLTSKIFOLA NDAHIGNILMTSKFSYKDFDTLLYTCAARFDFMKKETFURTYKT LLLPVULGFFATVAKISLSMYGLAKACOTHVEKTEFPURTYKT HALQLLAYTALGILINRLUFLTFHCVMASLICSRQLFGDLIBN KVEPGATVFALLAMASIGGSANLOTAMATOKATICHTOWNIVGERBENLOGELIBN KVEYSKPDAVFAGAMPTMASVKLGALRFIVMFHYEDAGLRART KIVYSMYSRAARSKYRRELILKANYTYLLESECVENLOGELIBN KVEYSKYBRAARSKYRRELILKANYTYLLESECVENLOGELIBN KVEYSKYBRAARSKYRRELIKANYTYLLESECVENLOGELIBN KVEYSKYBRAARSKYRRELIKANYTYLLESECVENLOGELIBN KVEYSKYSTRAARSKYRRELIKANYTYLLESECVENLOGELIBN KVEYSKYBPAARSKYRRELIKANYTYLLESECVENLOGELIBN KUTSTKYDERAMASICSANLOGENTUTALVISCATERSKOCHLUNGA RALUVGKKTITTKMLASKRICLALVYTIVEURTHFARALPPKQ YSHLARIPHTKOVHOHIALEISARLUVATIMOSLFPKKLISKEVENLOKANA RASILBOKAN RASILBOKA	6277		2744	MAPPTEMOLVYCYPYTYPA DODI NOVIMINIDAL TENDI LITAM
TESCEGLGPACTYANIFILMCIMALIFITYGTYLSGSRIGGI VTVLCFFFRHEGETSWIPTIGESSPYPTYLLUTVILTYTHAGSRIGGI VTVLCFFRHEGETSWIPTIGESSPYPTYLLUTVILTYTHAGSRIGHTAGET TKLYRGSLIALCISNVFPMLPMQPAQPVLITQIASLFAVYVVOY IDICKLRKITYIMISLALCYSNVFPMLPMQPAQPVLITQIASLFAVYVVOY IDICKLRKITYIMISLALCYSNVFRHEMESSHATTAGSLIVANG ILAMKPHEKINVSELSHWIQGCFWLFGTVLLKYLTSKITGIA NDARHGUNLTSKFSYKOPTULKYLTSKITGIA NDARHGUNLTSKFSYKOPTULKYLTSKITGIA NDARHGUNLTSKFSYKOPTULKYLTSKITGIA HACQLIAYTAGILTMRIKAFTLPHTWCVMSLICSRQLEGGLIPG KVPGATUPATLAMSIGGSALGTQWIPTVGESNILDQGELIEW IKYSTYPDAVPGAMPTHASVYLJALRFIVMHPHTEDAGLART KUVSMYSRKAAEEVKREILKKWNYYLLESGWCVARGKFGCSW PEIMOVEDPANAGKTPLCALLVKOSKPHTTVFQNSVXVKUEVV KYSMYSRKAAEEVKREILKKWNYYLLESGWCVARGKFGCSW PEIMOVEDPANAGKTPLCALLVKOSKPHTTVFQNSVXVKUEVV KYSMYSRKAAEEVKREILKKWNYYLLESGWCVARGKFGCSW PEIMOVEDPANAGKTPLCALLLUKOSKPHTTVFQNSVXVKUEVV KYSMLRFPHTIKVDYHDLHALSSALLVALMDELDPKLISKYEVKA ALGOVIGLKTITTKMLAISSRCLQLIVWITPVIRAHFPERLEPRQ YVSSACFRNICKQMTKWHEAIPDLLPEGTOMLFLINASVLH LKKQLSHLNVINDGEQPONGLYDADVAFYTGHAGHASVLHI LKQLSHLNVINDGEQPONGLYDADVAPYTGHAGHASVLHIM MASIMEGKR 6279 127 1687 GGAMASDGARKOPMKRSNSKLFGSIGHVYGACHPFPDPLLIGGTL LRSTAKMPTTPVKAKRVSTFORFSSNSDANDAGSDDLDQKPREAR PPSPPSGDLRILWSVSSSHTSCPRESASDAAPLORSQGLPHSAT VTLGGTSDPSTITSSALISERRASRLDKYFGULAGVLAVA ASSLANSEVVERTANSVLANHSGGGRPTLORGOLLAVA ASSLANSEVVERTANSVLANHSGGGRPTLORGOLLAVA ASSLANSEVVERTANSVLANHSGGGRPTLORGOLLAVA ASSLANSEVVERTANSVLANHSGGRAPTLORGOLLAVA ASSLANSEVVERTANSVLANHSGGRAPTLORFONLORGENA VETIGGSDPSTITSSALISERRASLDKYFGULARGVLLAVA ENVIGSSBPORTHHIVOSACHAVATORGARMATHLARRY VTLGGTSDPSTITSSALISERRASLDKYFGULARGVLLAVA VTLGGTSDPSTITSSALISERRASLDKYFGULARRY VTLGGTSDPSTITSSALISERRASLDKYFGULARRY VTLGGTSDPSTITSSALISERRASRLOKFFGULARRY VTLGGTSDPSTITSSALISERRASRLOKFFGULARRY VTLGGTSDPSTITSSALISERRASRLOKFFGULARRY VTLGGTSDPSTITSSALISERRASRLOKFFGULARRY VTLGGTSDPSTITSSALISERRASRLOKFFGULARRY VTLGGTSDPSTITSSALISERRASRLOKFFGULARRY VTLGGTSDPSTITSSALISERRASRLOKFFGULARRY VTLGGTSDPSTITSSALISERRASRLOKFFGULARRY VTLGGTSDPSTITSSALISERRASRASRLOKFFGULARRY VTLGGTSDPSTITSSALISERRASRASRLOKFFGULARRY VTLGGTSDPSTITSSALISERRAS	i			I.KRENI.VPRVII.ASWVPIVTKIMDI.TGTOTKICKTERTCEGI.CD
TKLYROSLIALGICSNYPHENDEPGAPVILIGALISATEAVYVOY IDICKLERKITYIMISLIALCEPVIMEGRISMILITSYYASSILTIMG ILAKKHELKINVISELSHWIQGCORULFOTULKYLTASKITGIA NDAHIGNILITSKFFSYKOFTTILIYTCAABFOPMIKKETPLRYTKY LLIPVILIGEPALVERITSDMINVLAKOGTHVERHOPDIGELVY HALQLLAYTALGILIMIKLELFITPHICVMASLICSRQLFGWLPC KVIPGATUPAILANISLIGSANLOTOMINIVEFSHINFOGELEIEN IKYSTYSPAVARARTHANAKTEPLCHLIVKOSKPHITTVENSVYKULEVY HERVOLDANAKTEPLCHLIVKOSKPHITTVENSVYKULEVY KE 6278 3 823 ILFRIVILISLVYLLINSVATEERKPABVLIVEGQQYAVVGTVLLLI IRTILISYCQGVINTFSVYTIMITRISSILKYFNSRSCQLVIGAGA ALQVVGLKITTINIALSRSCLQLIVHYTPUTRISPRANLEPRAC PEVENACFRANLEKOMIKOHERI FOLLIPEGTOMELINASYKUL LKKQLSHINVINDGGPONGLVTADVAFYTGNLQAKKGLKDLDIN MASHERGKR 6279 127 1687 GGMASADDARKOFKKRSNSKLPGSIQHVYGAQHPFFDPLLHGTL LRSTARMPTTPVKAKRVSTYGEFSSNTSDANDAGGEDDBLLANA ABSLNSEVWERTANIVLRHSIGNGGRFTLOGGOSLLOKYRPEAB PPSPSGDLKINKSVSSSTISCDAESSDAAPLORSGSLPHSAT VILGTSIPSSTASKERRSKLDKKFGLLAGENTTOLEELER LSWSGIKFDVRIMMWKSTTOEFSSNTSDANDAGGEDDBLANA ABSLNSEVWERTANIVLRHSIGNGGRFTLOGGOFLQOKYRPEAB PPSPSGDLKINKSVSSSTISCDAESSDAAPLORSGSLPHSAT VILGTSIPSSTASSSALSERRSKLDKKFGLLAGENTTOLEELER LSWSGIKFDVRIMMWKLIGGVLPANDURRPATLORKOKYFAPI EHYTOSRIBDESTSSALSERRSKELDKKFGLLAGENTTOLEELER LSWSGIKFDVRIMMWKLIGGVLPANDURRPATLORKOKEYFAPI EHYTOSRIBDESTSSALSERRSKELDKKFGLLAGENTTOLEELER LSWSGIKFDVRIMMWKLIGGVLPANDURRPATLORKOKEYFAPI EHYTOSRIBDESTSHHLIVCAGGARANLOKYGESTHORYCHTOLEELER LSWSGIKFDVRIMMPWTDATPDTRELEFINSIKTRYELARGUGKKUMLE ELVSRIDGGVHRHILDGHENGLIGGODNITKGVKEME ELVSRIDGGVHRHILDGHENGLIGGODNITKGVENGER ELVSRIDGGVHRHILDGHENGLIGGNITTOLERRAA QKHSFPRAHLGRSSSAGGSGSGSGSGNTURFGENFELTER LWDNINAVSSSSAGGSGSGSGGSGRTURGENFELDER GROMSLADVATPLORKORDERTURGDDK MORRIGGRYNPPVDATPDTRELEFINSIKTQVELARGUGKRAA QKHSFPRAHLGRSSAGGSGSGSGGSGAGNALORGOSHTALD LRPDERRFRAYFSIAVSSGGREVLGGGDDAICKYGGRFREFSSIK BEMDVNAVAPADISSGLIFFGSGDAICHTGEDSHITYGCH JRPBERFSRR GMARSROATGONNOPYNGOVPKANKKKLIFGGSBINTYRGH PRIHAGCRBONNOPYNGOVPKANKKKLIFGGSBINTYRGH PRIHAGGGGFBGGFREFSSRRIGGGRTURGERFOR MORRIGGRYNPPVDATPDTRELEFINSIKHOVYGGFSKRKRSKS ROMGNILDAVFFDONNIFINSSSRGTIHTOTORGGFTANTAD GRAFGG			ł	TRSCEGIGDDACEVVAVIETI NGI MMAI DELVCEVI COODI COL
TRUJROSSLIALCISNUTPMILPROPAGPULTQIASIFAVIVUSY IDICKLERII YIMISIALGY-VIMPORSMILTSYYASSIVI IWA ILAMKPHIKINVSELSIWVIQQCFWLPGTVILKYLTSKI FOI A NDAHIGNILTSKYFSYKOPTULTYCARSPUSTPIRTYK LLIPVUJUGPVAJVRKI ISDMIGVLAKQQTHVRKHQFHGGLIV HALQLIAYTALGILIMRIKIFITPHKVVAGALICSRQIFGKIPC KVIPGAIVJAILAMSIQGSAMLOTTONIVCEFSINLPQGELIER KVISTKPDAVFAGAMPTMASVKLGALRPIVMHPYEDAGILARIT KIVYSKYSRARABEVKREILKKKNYYILLESGWVARSKPQCSM PEIMOUDDPANAGKTPLCNILLVKDSKPHTTVFQNSVKVLEVV KB 6278 3 923 ILFRIVILISIVVILINSVATEERKPAEVLIVEGQQYAVVFTULL IRILEYCQSUMDIFSVTTEMITALSDLKKYPNSRSCOLVIGAG ALOVVGLKTITTKNIALISSECLQLIVWITPVIRAHFERALDPKQ YSMLRHFHITTKNIALISSECLQLIVWITPVIRAHFERALDPKQ YSMLRHFHITTKNIVHDLARIS LGALVAINBOSLOPKLIKKYEVKA PVDSAGFRNICKQMTKOMERI PDILDEEQTQMMFUR IRASYKLH LKKQLSHINVINDGGQPONGLVTADVAP YTTGKICALKKGKUDLIN MABINEQXR MABINEQXR 6279 127 1687 GGAMASDDARKGPWKRSNSKLPGSIQHVYGQQHPPFDPLLHGTL LRSTAMPTTPVKAKRVSTGOFFSNISDAMDAGEDDDELLAMA ASSLNSEVVMETANRVLRNISGORGRPTUGROGLQCKPRPAE PPSPSGDLRIVKSVSSHITSCPASSASDAAPLORGSJEPHSAT VTLGGTSOPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELER LSWSGIPKPUFMWKLLSGVLPANTORPEATLORGCSPPATL EHYYDSRDEWIGDTYRCHDITDRYFFVVPICEYIEAEEVDTVUVS GVPAEVLCNIEADTYRCMSKLIDDIJDNYTPFVVPICEYIEAEEVDTVUVS GVPAEVLCNIEADTYRCMSKLIDDIJDNYTPFVVPICEYIEAEEVDTVUVS GVPAEVLCNIEADTYRCMSKLIDDIJDNYTPFVVPICEYIEAEEVDTVUVS GVPAEVLCNIEADTYRCMSKLIDDIJDNYTPFVVPICEYIEAEEVDTVUVS GVPAEVLCNIEADTYRCMSKLIDDIJDNYTPFVVPICEYIEAEEVDTVUVS GVPAEVLCNIEADTYRCMSKLIDDIJDNYTPFVVPICEYIEAEEVDTVUVS GVPAEVLCNIEADTYRCMSKLIDDIJDNYTPFVVPICEYIEAEEVDTVUVS GVPAEVLCNIEADTYRCMSKLIDDIJDNYTPFVVPICEYIEAEEVDTVUVS GVPAEVLCNIEADTYRCMSKLIDDIJDNYTPFVVPICEYIEAEEVDTVUVS GVPAEVLCNIEADTYRCMSKLIDDIJDNYTRYTPTVVSICHTALDLLARAYRIKKELELGRIGGERSEEEEEDE DUDLAQVLAYLLRRGQVPLVQGGAANLGFIQALTRIGGERNDRA WGGRISTYNDVATPTDOMPHLYSSRDYTHICNIYGEGDTHTALD LRPGRFAVFSILVSKGGGTMSKOODTTRILVCRYGGRIKKRSE EMMEASRQAATGOODTTRILVCRYGGSSIMTYRGH GVHHTLIRCCYRDVANFPEELEIPSEIKTVGGGSBIMTYRGH GVHHTLIRCCYRDVANFPEELEIPSEIKTVGEGGSBIMTYRGH GVHHTLIRCCYRDVANFPOELEIPSEIKTGGGGSBIMTYRGH PBSEECASAPAPVQOSTFFSSIMPICHTSCHGGSSIMTYRGH GVHHTLIRCCYRDVANFPOELEIPSEIKTGGG		•		VTVI.CFFFNHGECTRVMWTDDI.DEGEGVDEI.VI.OMI.I.VPUTI DA
DICKLIRKITYTHMISLALGFYLMFORSHLTSYLASSLYTIMG ILAMKPHILKINVSELSHUVJGGCFWLFGTVILKYLTSKIFGIA NDAHIGNLITSKFSSYROFDTILTYCAARFDPMKKSTPLAYTKT LLLPVUNGSYAVIVRIISMGVLARQGTWARHOFDEGELVY HAQQLLAYTALGILLMRKLFJTPMGVVASLICSRQLFGGLFG KVHPGAIVPALAAMSIGGSALQTQWNIVGEFSNLFQGELIEW IKYSTKPDAVFAGAMPTMASVYLGALRPIVMFPHYEDAGLRAXT KIVYSMYSRRAAREEVRRBLIKKNNYYILESGMVVARSKFGCSM PELMOVEDARJAAKSTQCGALLVKDSKPHTTVYGNSVYKVLEVV KB 6278 3 823 ILFRIVLISLVYLINSVATEERKPAEVLIVEGGQYAVVGTVLLL IRTILEYCQGVDNIPSVYTDMLTRLSDLKKYFNSRSCQLVLGGA ALQVVGLKITTINLAISSRCLGLIVWTYPUTAHFPERRLPPKQ YSMLRRFHHTTKNYMDHIABISAKIVALMDSLFPKLLSKYSVKA PVPSACFRANICKOMYKCHREJ FDLLIPEGTGTURINASVKILL LKKQLSHLNVINDGGPONGLVTADVAFYTGNLQALKGLKDLDLN MAELHEQKX ALSHENGKY GGMMABGBARROFMKENSKLDGSIQHVYGAQHPFPDFLLIGGTL LRSTAMMFTTYVAKRVSTTQEFESNTSDAMDAGGDDDELLMAA ALSLNSEVVMETANKVLRHRSGRGSPTLGGSGLQQKPREAR PFSPSSGDLRIVKSVSSSHTSCPAESASDAAPLGRSGSLPHSAT VILGSTSDPSTLSSSSALSERGSSLDKKFQLLAGFNTTLBELERR LSMSGIFKDVREMTWKLLGGVLPANVDRRPATLGRKQKFYFAFI EHNYDSRNDEVINDOTYPQHILDFRWSPEALLJCFNTUELELRR LSMSGIFKDVREMTWKLLGGVLPANVDRRPATLGRKQKFYFAFI EHNYDSRNDEVINDOTYPQHTLDFRWSPEALLJCFNTVLEELLAN SURGIFKDVRHWTWKLLGGVLPANVDRRPATLGRKQKFYFAFI EHNYDSRNDEVINDOTYPQHTLDFRWSPEALLJCFNTVLEELTR LSMSGIFKDVRHWTWKLLGGVLPANVDRRPATLGRKQKFYFAFI EHNYDSRNDEVINDOTYPQHTLDFRWSPEALLJCFNTVLEELTR LSMSGIFKDVRHWTWKLLGGVLPANVDRRPATLGRKCKFYFAFI EHNYDSRNDEVINDOTYPQHTLDFRWSPEALLJCFNTVLEELTR LWSGIFKFRHLNQCRGSFHHLVCAGAFIVKRKRELEERDFCCTUR OVDLAQVLAYLLRRGQVRLVQCGCAANLQFTGVKKVMLE ELVSRIDGQVHRHLDQHEVRYLQFAFRWNNILLMRRVPLGTTR LWGRSGYFFRHLNQCRGSSAGGSGGSGGRFGRGRGRRFEEEEEDE DVDLAQVLAYLLRRGQVRLVQCGCAANLQFTGNTLATRGDPK GGUHATLTRCFFFFRHSTRGQFTYSGCSTGKVVVYDLLSGHIVVK LTHRKACVRDDVARPDTESSTEDGSDATVSRTHGDDFTDS YSGRAFGGITSROQPVTSRGGDATKLMQYRGAFFORDPA WGREGGDATADAGNWFPTGCORNOTRRGDPKFSTRA GGUHATLTRCFFFFRHSTRGQFTYSGCSTGKVVVYDLLSGHIVVK LTHRKACVRDDVARPPEELETSSSMSTHTHCTTRCFRYGRFRFKFSR EMMEASRGAATGQNDVFRQQVPCVQGGAANLQFTQALLDSEEEDEDD PUDLAQULAYLLRRGQVRLVQGGAANLQFTQALLDSEEEDEDD DVDLAQULAYLLRGGQVRLVQGGAANLQFTQALLDSEEEDDFTALD HERDDVANAVBRPEEKTUSSSSTTTCTGCTGRTRFKFSTR ROVGRSVLDVAFFDOM	1			TKLYRGSLIALCISNVFFMLDWOFAOFYTLTOTASLFAVYVVCV
ILAMKPHFIKINVSELSIMVIQGCFMLFOTVILKYLTSKIFGIA NDAHIGNILTSKFFSKNDPULLYTCASEPKSTEIRYTKT LLLPVULVGFVATVRIISDMWGVLAKOOTHVRKHOPHGELVY HALQLLAYTAGILIMRKLEFLFHENCYMELCSBOLFGHLER KVHFGATVFAILAMSIQGANLOTQWNIVGEFSNLPQEELIEW IKYSTKPDAVFAGAMPTMASVKLSALRFIVMHYHEDGIRART KIVYSNYSRKAABEVKRELIKLKWYYYLLESGCVYKRKKPGCSM PEIMOVEDPANAGKTFLCNLLVKOSPHFTTVTGWSYKVLEVV KE 6278 3 823 ILERLVLLSUVLLNSVATEERKPABVLIVEGGQYAVVGTVLLI KRILEKYCGMDIFSVYTUMLTRISDLUKKYNSKSCQLVLGAG ALQVVGLKTITTKNIALSSRCLQLIVHYIPVTEAHFPARLPFKQ YSHLRFIDHIKNYHDHLEGISALVALMGEDKLLKKKVEVXA PVDSACFRNICKQMTKMMEAIFDLLPESOTOMLPLRINASYKLH LKKQLSHLNVINDGGPONGLVTADVAPYTONLQALKGHKOLDLN MAEIWEQXR 6279 127 1687 GGAMABGBARKOFWKRSNSKLPGSIQHYYGAQHPFFDPLLHGTL LKGLSHLNVINDGGPONGLVTADVAPYTONLQALKGHKOLDLN MAEIWEQXR GGAMABGBARKOFWKRSNSKLPGSIQHYYGAQHPFFDPLLHGTL LKGSTARMFTTPVKARKVSTFQFESSNTSDAWDAGGDDDELLAMA ABSLNSEVVMETANBVLENHSQRQGFPTLQEGGGQCQKPRPEAB PPSPSGGLHLKVSVSSESHTSCAPSASADLFRSQSLPHSAT VTLGGTSPPSTLSSSALSERRASRLDKFKQLLAGFNTDLELRR LSWSGIPFVPRTWKLKLSGYLPANVURFRLQRSQSLPHSAT VTLGGTSPPSTLSSSALSERRASRLDKFKQLLAGFNTDLELRR LSWSGIPFVPRTWKLKLSGYLPANVURFRLARGERGYGPLLDFL LFWANIRIPAGSVQGINUTVFFFVVPICTREREWDTVDVS GVPASVLCNLEADTVRCHSKLLDGIQDNYTFAQPGIQMKVRMLE ELVSRIDEQVHRILDQHSVRYLQFFRWMINNLARGPVBLCTIT LFWARIRIPAGSVQGINUTVFFFVVPICTEREBEDDTVDVS GVPASVLCNLEADTVRCHSKLLDGIQDONYTFAQPGIQMKVRMLE ELVSRIDEQVHRILDQHSVRYLQFGAFRWMNNLLARGVFLGCTIR LMDTYQSS PDGTSHFHLVVCAAFLVRMKRELBEKDFQELLLFL QNLPTAHWDDEDISLLLARAYELKFAFADADPNHYKK LKDTYGSS PDGTSHFHLVCAAFLVRMKRELBEKDFQECHTFLL GRUSHLDVALVATLLRRGQVLVQGGGAANLQFIQALDGFTRAA QKHSFFRNLHQRERGLCHRGSFSLEGGSRVISHFLPNLGFTTS YSGKAFGGIYSKGGIFMSACQODTIRLNCGYGGFRKKFKSIKA RDVGRSVLDVATPDQNHFLYSSMSDYHLCNIYGBGDFTTALD LRPDERRFAVFSIAVSSBORGHUKKAPGDSSLMTYRGH GVLHTLIRCRFSFTIBSTQQQFTYSGCSTGKVVVDLLGGFTVKS LTMHACVGNVSWHPFEKKYSSSMOMLKLKPGDSSLMTYRGH GVLHTLIRCRFSFTIBSTQQCFTYSGCSTGKVVVDLLGGFTVKS LTMHACVGNVSWHPFEKKYSKSSMOMLKLKPGDSSLMTYRGH GVLHTLIRCRFSFTIBSTQQCFTMSACQCAATLQFTQLDGRAAA QKHSFPRMLHQREGICHRSSSSIGGGRSVLGGANDGCLTVFDREGDRATALD LRPDERRFAVFSIAVSSDORRULGGGNADCCLTVFDREGDRATALD LRPDERRFAVFSIAVAFS	ŀ			IDICKLRKI I Y I HMT SI. ALCEVI MEGNSMI I TSVVA SSI VI TWG
NDAHIGNLITSKFFSYKOPDILLYTCABEPDFREKSTELRYTKT LLIEVVILVSYTAURI ILBUMWQLAKOVIRKOPDHOELUY HALQLIAYTALGI LINRIKLELIPEHCUMASI LOSSGLIGGULEC KVIPGAIVPALAMSI GOGANLOTOMI VGERSNIPOBELIEK KVIPGAIVPALAMSI GOGANLOTOMI VGERSNIPOBELIEK KVIPGAIVPALAMSI GOGANLOTOMI VGERSNIPOBELIEK KVIPGAIVPALAMSI GOGANLOTOMI VGERSNIPOBELIEK KVIPSAIVPALAMSI GOGANLOTOMI VGERSNIPOBELIEK KVIPSAIVPALAMSI GOGANLOTOMI VGERSNIPOBELIEK KVIPSAIVPALAMSI KILVSKYPYILEESKUVRARKOCOM PEIMDEDPARAKKTELLULVOSKOPITTUTOMI VORTOKITUTOMI VORTOKITUTOMI VITAKING PEIMDEUDPALAKAKTULOTUTOMI VANTOKITUTOMI VA	İ			ILAMKPHFLKINVSELSLWVIOGCFWLFGTVILKYLTSKIFGIA
LLLPVILNGFVAIURALGOTHVERHOPHOGELVY HALQCLAYTAGGILNRELETPHENCWALL CSRGUEGGLEC KVIPGGIVPALIGAMSIQGSANLQTQWNIVGEPSNLPQBELIEW IKYSTKPDAVPAGAMPTNASVKISALREIVNHHYLEDGURART KIYYSMYSRKAABEVKRELIKLKWNYYILEBSGVVAVGRYENGCSM PEIMDVEDPANAGKTPLCNLLVKDSPPHFTTVFQWSVKVLEVV KB 6278 3 823 ILFRLVLLSLVYLIMSVATEERKPARVLVEGQVAVGTVLLL KBILLEVQUDNIPSVTTMLTRLSDLLKYMSSYSCOLVLGAV ALQVVCLKTITTKNLALSSRCLQLIVHYIPVIRAHFPARLPPKQ YSMLRHFPHITKDYHHHAEISAKLVAIMDSLEPKLISKYEVKA PVPSACFRAICKQMTKMEAHFPILDLEPSGYOTMMPFRINASYKLH LKXQLSHLNVINDGGQGGVTTADVAFYTGNLQALKGEKKDLDLN MARIMEQKR 6279 127 1687 GGAMASDGARKQFWKSNSKLPGSTQHVYGQQUPPFDLHGTI. LRSTAMMFTTPVAKKYVSTFOFFENTSDANDAGGEDDDELLAMA AESLNSEVVMETANRVLRNHSQRQGRPTLQBGGGQKPRPBLHGTI. LRSTAMMFTTPVAKKYVSTFOFFENTSDANDAGGEDDDELLAMA AESLNSEVVMETANRVLRNHSQRQGRPTLQBGGGQKPRPBAE PFSPPSGDLRIVKSVSSSHTSCPARSASDAAPLQRSQRHSAL LSMSGIFPVDENTWIKLLSGYLPANVORRPATLQRKOKEYPAFI EHYYDSRNBEVHQDTYRGIHDIPPMSGPALGPNTULEEIRR LSMSGIFPVDENTWIKLLSGYLPANVORRPATLQRKOKEYPAFI EHYYDSRNBEVHQDTYRGIHDIPPMSGPAPOGIOMKVMLDE ELVSRIDBOVIRRILDQHEVRYLLDGFATRWMREILERDGPATCPELLIFL LDHTYQSEPDGFSHFLYVCAAFLUFWRKEILERDGPELLIFFL LOHDTYQSEPDGFSHFLYVCAAFLUFWRKEILERDGPELLIFFL LWDTYQSEPDGFSHFLYVCAAFLUFWRKEILERDGPELLIFFL LWDTYQSEPDGFSHFLYVCAAFLUFWRKEILERDGPELLIFFL LWDTYQSEPDGFSHFLYVCAAFLUFWRKEILERDGPELLIFFL LWDTYQSEPDGFSHFLYVCAAFLUFWRKEILERDGFLLDFFL SYSKAFCGIYSKDGQIFMSACQDGTIRLYDCRYGFFKYKSIKA ROKGSVLDVATFPGWHFLYSSMBDTHHCNIYGGGLANLGPTDFTDS YSQKAFCGIYSKDGQIFFMSACQDGTIRLYDCRYGFFKYKSIKA RVGRSVLDVATFPGWHFLYSSMBDTHHCNIYGGGFHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDRRQMRTLQ IBSHBDDVNAVAFADISSQILPSGEDSRCILVFFLORDHTALD LRPDERRFAVFSIAVSSDGPFILGENFILKTOVELATGQLGIRRAA QKHSFPRMLHQRERGLCHROSFSILEGGSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQVFTYSGCTGKVVVVLLISGGUTYACH GVLHTLIRCGFSFILISGGDSRVISHTLPNDLGFTDS YSQKAFCGIYSKDGQVFTYSGCTGRANDCLYVFDRGBDDFT ANGRIGDGTNYPDVATTPTGELEFNEIKTGVELATGQLGIRRAA QKHSFPRMLHQRERGLCHROSFSILEGGSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQUFTNSKODCTIRLYDCRYGFFRKYKSIKA RDVGWSULDVATTPDGMFLYSSMSDITHCNITGGLGRRTLQ CHHPLERFAVAFSIAVSBOREVLGSRNDCCTYFORGRRTLQ LRPDERRFAVFSIAVSBOREVLGSRND	-			NDAHIGNLLTSKFFSYKDFDTLLYTCAAEFDFMEKETPLRYTKT
HALGLIAYTAGILIMRIKUFLIPHICMMSLICERGILFENIEC KVIPGAIVPAILAMMS (IGSANLOTOMNIVGERSILPORELLIER IKYSTAPDAVPAGAMPIMASVKLSALRPIVMIHHYEDAGIRART KIVYSMYSKRKAEEVKRELIKLKUNYYILEESWVRKORGCSM PEIMDVEDPANAGKTPLCNILLVOGKRPHTTVPQNSVYKVLEVV KB 1 LIFRUVLLSLVYLLNSVATEERKPABVLIVEGQYAVVGTVLLL IRIILEYCQGVDNIPSVYTDMLTRILSDLLKYFNSRSCQULGAGA ALQVVGLKITTITNIALSSRCLQLIVHYTUVIAHHFEARLPPKO YSMLRHFDHITKDYHDHIABISAKLVAIMDSLEPKLIKKYEVKA PVESACPRINICKOMTWAMEATPILLEEDOTOMPFILRINASYKLH LKXQLSHLNVINDGGPQNGLVTADVAPYTONLQALKGIKOLDIN MASINEGXR 6279 127 1687 GGAMASDGARKYFKRSNSKLPGSIQHVYGAQHPPFDPLLHGTL LRSTARMPTTPVKAKRVSTPGFFSSNTSDANDAGSDDDBLLAWA ABSLNSEVVEMTANRVLENISGRQCRPTLGGFTQCKPPFEAR PPSPPSGDLRIVKSVSSSHTSCPARSASDAAPLQGSOSLPHSAT VTLGGTSDPSTLSSALSERRARILDRYKLGSNTOLEELBR LSWSGIPKPVENTTRVLLSCYLDAWVDRRPATLQRKQKEYPAFI EHYYDSRTDSVHQDTYRQHIDIPMSPRALILGRYKVETERRI LSWSGIPKPVENTRVLLSCYLDAWVDRRPATLQRKQKEYPAFI EHYYDSRTDSVHRILDGHEVAYLQFAFRWANNLMREVPLRCTIR LDDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCELLIFL LMDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCELLIFL LMDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCELLIFL LMDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCELLIFL LMDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCELLIFL LMDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCELLIFL LWDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCELLIFL LWDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCELLIFL LWDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCELLIFL LWDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCELLIFL LWDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCELLIFL LWDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCELLIFL LWDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCELLIFL LWDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCCTTR LWDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCELLIFL LWDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCCTTR LWDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCCTTR LWDTYGSSPDSTSHFHLYVCAAFLVRWRKSILEERDFCTTR TERPENTALTGRSSTSGGSGSCDDFGCLFRGAGLRRSEEEEEDE DVDLAQVLAAVLLERGOVELVOGGGAANLQFTOALDTGEDTTALD LRPDERRFAVFSIAVSSDGTSTSGSTGKVVVDLLSGHTVRGH GVLHTLIRCRFSPHSTGQCFTYSGCTGKVVVDLLSGHTVAG LESBEDDVNAVFATDSGCDFTTRLDCCTXVFDRENGETDDA URGLIGGTNYPPVDATPTTRELEENDELKTCHGLITGGLGLGRFSTA QKHSFPBMLHQREGCLCHRGSFSIGEGGRVISHFLPNDLGFTDS YGQKAFCGIYSK	1		1	LLLPVVLVGFVAIVRKIISDMWGVLAKOOTHVRKHOFDHGELVV
KVIHGAIVPAILAMMSIQGSANLOTQMNIUGEPSALPOEELIEM IKYSTKPDAVPAGAMPIMASVIGASILVINIPHYBORDGIRATT KILVSHYSHKAAEEVKRELIKLKVNYYILEESUCVRRSKPGCSM PEIMDVEDPANAGKTELCHLUKDSKPHFTTYFORSYKVLEVV KB 6278 3 923 ILFRUVLLSLVYLINSVATEERKPAEVLIVEGQGYAVVGTVULL IRTILESYCGVDNIPSYTDMITRISDLKYFNSRSCQLVLGAG ALQUVGLKTITTKNLALSSRCLQLIVHYIPUTRAFPEARLPPKQ YSMLRHFDHITKDYHHAIAEISALVALDHSPEAKLLPEKQU YSMLRHFDHITKDYHHAIAEISALVALDHSPEAKLLPEKYVKA PVPSACFRNICKQMTKMHRAIFDLLPEEQTGMLFIRINASYKLH LKKQLSHLNVINDGGPQNGLVTADVAFYTGNLQALKGLKOLDLN MABIMBQKR 6279 127 1687 GGAMASDGARRYWKRSNSKLPGSIQHYYGAQHPPFDPLLHGTL LKSTARMFTTPVKAKKYSTFOEFFSSNTSDAWDAGGDDBLLLAMA ABSLINSEVVMTTANRVLRNHSQRGRPTLQEOPGLQKPPPEAB PSPSPSGDLRLVKSVSSESHTSCPAESASDAAPLQRSQSLPHSAT VILGGTSDPSTLSSSALSERRASRLUKFKQLLAGFNTDLEELER LSWSGIPKPVEPHTWKLLGGVLPANVDREPATLQRKKEYPAFI ENTYDSRADEVHQDTTAQHTDIFRHSPALILQPKVTEIFRI LFINAIRHPAGGVVQGINDLVTPFFVVFICEYIBREDVTVVOX GVPAEVLCULTEADTYVGMSKLDGIGJONTYFAQGGIGMKVKMLE ELVSRIDEQVHRIHDQHBVRYLDGAFRWMMILLARBVPLRCTIR LWDTYGSSPDOFSHFBILVYCAAPLVRWKREILEEKDFQELLIFL QNLPTAHWDDEDISLLLEAVRKAFADAANNHKK ELWSTLDVATYLLERGGVERVLQGGGAANTLLARBVPLRCTIR LWDTYGSSPDOFSHFBILVYCAAPLVRWKREILEEKDFQELLIFL QNLPTAHWDDEDISLLLEAVRKAFADAANNHKK GWISFPRIMLORERGLCHRGSFSIGEBEEEEEED DVDLAQVLATYLRRGGVERVLQGGGAANTLGALGALBEENDRA MOGRIGORYMPPVDATPDTRELEFNEIKYQUELATQLGLRRAA QKHSFPRHHQBREGLCHRGSFSIGEDALTKUNSHTMEDDDPK PVGALAGHQOITFILSGTAATSHTURDFTUS SYSKAFCGIYSKGGQIFMSACODOTTRLYDCRYGRFRKFKSIKA RDVGMSVLDVATTPDQNHFYSSSBODTITLMDTREPSR EMMERSRQAATQONDYRHQQVFKAMRKLLEPGDSELMYKKG LYMHLKCRPSPIBISTORDATILISNSCQTITLMDTIRFSSR EMMERSRQAATQONDYRHQQVFKAMRKLLEPGDSLMTYRGH GVLHPLIRCFSPBIBSTORDQFTYSGESGDDFSECLPRRGGGIRRSEEEEEEDD DVDLAQVLATLLRRGGVELVGGGAANLQFTQALLDSEEENDRA WGRIGGORSNSSSASSGSGSGSGDFSEGLPRRGAGLRRSEEEEEEDD DVDLAQVLATLLRRGQVELVGGGGAANLQFTQALLDSEEENDRA WGRIGGORSNSSSASSGSGDFSEGLPRRGAGLRRSEEEEEEDD DVDLAQVLATLLRRGQVELVGGGGAANLQFTQALLDSEEENDRA WGRIGGRYBPPVDATPTRELEFNEIKTGVURLATTGGGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREERDDPK 6281 657 2515 ECCDCMSSSNSSSSGSGDFSEGLPRRGAGLRRSEEEEEEDD DVDLAQVLATLLRRGQVELVGGGAN			ŀ	HALQLLAYTALGILIMRLKLFLTPHMCVMASLICSROLFGWLFC
IKYSTKPDAVPAGAMPTMASVILLAELPIUNIPHYEDAGLRATT KIVYSMYSKRAAESVKRELIKLKUNTYTILEESWCVRRSKEGCSM PEIMDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSVYKVLEVV KE 6278 3 823 ILFRLVLLSLVYLINSVATEERKPAEVLIVEGQQYAVVGTVLLL IRIILEYCGGUDNTPSVTTDMITRLSDLKYYBRSSCGLUKGG ALQVVGLKTITTKNLALSSRCLGLIVFUTRAHFFEARLDPKQ YSMLRHFDHITKDYHDHIAEISAKLVAIMDSLPDKLLSKYEVKA PVPSACFRNICKQMTKMHEAIPDLIPEEGTQMLFLRINASYKLL LKKQLSHLNVINDGGCONGLVTADVAPTYGNLQALKGLKOLDLN MABINEQKR 6279 127 1687 GGAMASDGARKQFWKRSNSKLPGSIGHVYGAQHPPFDPLLHGTL LRSTSARMPTTPVKAKRVSTFOEFSSNTSDANDAGEDDELLAMA AESLNSEVVMETANRVLRNHSQRQRPTIQEGGGLQQKPRPEAE PSPPSEGDLRIVKSVSESHTSCABESSADAPLQRSQSIPHSAT VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPHJCRGQSFPBAB PSPPSEGDLRIVKSVSESHTSCABESSADAPLQRSQSIPHSAT VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPHJCRKGKEYFAFI EHYYDSRDDEVHGHUNGSVERLDGTLDVTPFFGVTEVTLGRVERAFT EHYYDSRDDEVHGHUNGSVERLDGTLDVTPFFGVTEVTLGRVERAFT EHYYDSRDDEVHGHUNGSVERLDGTLDVTPFFGVTEVTLGRVERAFT EHYYDSRDDEVHGHUNGSVERLDGTLDVTPFTQVTEVTLGVTEFRET LFFWARINFBASGVVGGINDLVTPFFFVETEVTLAGRVERAFTLGKKGKEYFAFI EHYYDSRDDEVHFHLDGHSVRYLDGTARWMNILLARRBYDLRCTIR LWDTTQSSPDDFSHFHLIVCAAFLIVKRYRETLEEKDFQELLIFL QNLPTAHMDDEDISLLLAEATRLKFAFADADNHYKK ELVSRIDEQVFRHILDGHSVRYLDGARVKRETLEEKDFQELLIFL QNLPTAHMDDEDISLLLAEATRLKFAFADADNHYKK 6280 857 2515 ECCDQMSGNSSSASGSGDSGEGGSVISHFLINDLGFTDS YSGKAFCGIYSKGGGTPFSSEGDSVISHFLINDLGFTDS YSGKAFCGIYSKGGGTPFSSEGDSVISHFLINDLGFTDS YSGKAFCGIYSKGGTFFSSSAGSGSVISHFLINDLGFTDS YSGKAFCGIYSKGGTFTDSSGDARVLISNSKOCTIKLMDIRFSSR EMMEASRQAATQONDVFRWQQVFKAWRKLLDFGDDFK PWGALAGHQDGTFTDSSGDARVLISNSKOCTIKLMDIRFSSR EMMEASRQAATQONDVFRWQVFKAWRKLLEDGSLMTYRGH GVHHTLIKCFFSFIHSTGTPKELFFFRITYGVELATGGLKRAA QKHSFPRMLHQERGICLGRSFSIGGGRSVISHFLENDLGFTDS YSGKAFCGIYSKDGGTRAACQQDOTTRLYDCCYCRFRFKKSIKA RDVGRSVLDVAFTPDDAHFTRELEFFRITYGVELATGGLKRAA QKHSFPRMLHQERGICTRRSGFSIGGGRSVISHFLENDLGFTDS YSGKAFCGIYSKDGGTRWAACQQDOTTRLYDCCYCRFRFKKSIKA RDVGRSVLDVAFTPDDAHFTRELEFFRITYGVELATGGLKRAA QKHSFPRMLHQERGGLTSSGGGSGGSGGRANLQFTQALLTRAL LRPDERRFAVFSILVSSWGGTFSLGGGRVISHFLENDLGFTDS YSGKAFCGIYSKDGGTRWAACQQDOTTRLYDCCKVORTTMEREDDFK LTHINGAUNDGRAACGGGGANGCLTYVDR		1	1	KVHPGAIVFAILAAMSIQGSANLQTQWNIVGEFSNLPQEELIEW
KIVYSNYSRKAAEEVKRELIKLKVNYYILEESWCYRSKEGCSM PEIMOUDDANAGKTPLCNLUVKDSKPHTTVFQNSVYKVLEVV KE 1 ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLL RIILEYCGGUNNPSVTTDMLTRLSDLLKYFNSRSCQLVLGAG ALQVVGLKTITTKNLALSSRCLQLIVHYIPVTRAHFEARIPPKQ YSNLRHFDHITKYYHHIALEISAKLVAIMDSLPPKLISKKEVKA PVPSACFRNICKGMTKMHRAI FDLLPEGTGMLFLRINASYKLH LKKOLSHLMVINDGGPQNGLVTADVAFYTGNLQALKGLKOLDLN MAEIWEGKR 6279 127 1687 GGAMASDGARKQFWKRSNSKLPGSIGHYYGAQHPPFDPLLHGTL LRSTARMFTTPVKAKRVSTFGEFSSNTSDAMDAGGDDDBLLAMA ABSLNSEVVMSTANRVLRNHSQRGRPTLQEGPGLQKPRPEAE PSPPSGDLRLVKSVSSESSTSCPAERSDADLQRSQSLPHSAT VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR LSWSGIPKPVRPWMTKLLSGYLPANVDREPATLQRKKEYPAFI EHYYDSRDDEVHGDTTRQIHDIFRRPEALILGPKKYETFERI LFIWAIRUPAGSVYQGINDLVTPFFVVFICEYIBREVDTVDVS GVPAEVLCNIEADTYWGNSKLDGIGJONTFFAGGIGMKYKNLE ELVSRIDEQVHRIHDGHRWRLLGFARRWNNLLHREWPLRCTIR LWDTYGSBPOGSHFHILVYCASPLJWRREILERKDPGELLLFL ONLPTAHDDEDISLLLABAYRLKFAFADAPNHYKK ELVSRIDEQVHRHINDGREGLGIRGSFSIGEORVISHEDENDRA WGGRIGDRYNPPVDATPDTRELEFNSIKTQVELATGJGLGRRAA WGRHSFRNHINGREGLGIRGSFSIGEORVISHELDRINGFTDS YSGKAFCGIYSKGGIFMSACODOTTRLVDCRYGRFRKKSIKA RDVGMSVLDVAFTPDONHFLYSSWSDYHICHIYGGDTHTALD LRPDERRFAVFSIAVSSGGRBENGARCCLYVFDREGMRRTLQ ISSHEDDUNAVAFADISSGILFSGGDDATLINSKQTIKLMDIRFSSR EGMEASRQAATQGNDVYRWQQVFKAWRKLLEDGDSIMTYRGH GUHNTLIKCFPSEIHSTORGPTYSGESCIPREGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVELVGGGAANLQFTQALLDSEEENDRA WGRIGJGRYNPPVDATPTRELEFNSIKTURUPALTVKKL LYNHKACVRDVSNHPPEEKIVSSWDGNIRHWQYRQAEYFQDDM PSSECCASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDGWGSRNSSSAGSGGFBEGEPREGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVILVGGGAANLQFTQALLDSEENDRA WGRIGJGGYMPPPVDATPTRELEFNIKTURUPALTORLICRRAA GKHSFPRMLHQRRGGLGIRGSFSLGEGSRVISHFLENDLGFTDS YSGKAFCGIYSKDGQIFMSACQDOTTRLYDCCYGLATGOLGLRAA GKHSFPRMLHQRRGGLGIRGSFSLGEGGRVISHFLENDLGFTDS YSGKAFCGIYSKDGQIFMSACQDOTTRLYDCCYGLATGOLGLRAA GKHSFPRMLHQRRGGLGIRGSFSLGEGGRVISHFLENDLGFTDS YSGKAFCGIYSKDGQIFMSACQDOTTRLYDCCYGLATGOLGLRAA GKHSFPRMLHQRRGGLGURGGSPTGLEGGRNGCLYVFDREGRRTLQ IESHEDDVNAVFAFDISGULFGGSDNGCLYVFDREGDDRRTLAD LRPDERRFAVFSIRVSBURGGLURGGFSUCHTALD LRPDERRFAVFSIRVSBURGGLURGGRANGCLYVFDREG				IKYSTKPDAVFAGAMPTMASVKLSALRPIVNHPHYEDAGLRART
PEIMDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSVYKVLEVV KB 6278 3 823 ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLL IRIILEYCQGUNIPSVTIDMLTRLSDLLKYFNSRSCQLVLGAG ALQVVCHKTITKNIALSSKCQLLVHYFVPIRAHPERLPPKQ YSMLRHFDHITKDYHDHIABISAKQLVHYFVPIRAHPERLPPKQ YSMLRHFDHITKDYHDHIABISAKQLVHYFVPIRAHPERLPPKQ YSMLRHFDHITKDYHDHIABISAKQLVHYFVPIRAHPERLPPKQ PVSACFGRNICKQMYKMHRAIPDLESOTQMLPLRINASYKLH LKKQLSHLAWINDGGPQNGLVTADVAPYTGNLQALKGLKDLDLN MABINEQKR 6279 127 1687 GGMMASDGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTL LRSTARMPTTPVKAKRVSTFGFESNTSDAMDAGEDDDBLLAMA ABSINSEVVMETANKVLRNISGNGROGPPTLQBGPGLQQKPP PRAB PPSPPSGDLRILVKSVSESHTSCPAESASDAAPLQRSQSLPHSAT VTLGGTSDPSTLSSSALSERBASRLDKKKQLLAGPNTDLEELRR LSWSGIPKVVPRMWKLLSSYLPAMVDRRPATLQRKQKSYPAFI EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALIQFKVTEIFRRI LFWARIPRASGYVGGINDLVTPFFVVVFICSYTEAREVDTVDVS GVPAEVLCNIERDTYWCMSKLLDGIDDNYTPAQGIQMKVKMLB ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNILLMREVPIRCTIR LWDTYQSSPDGFSHFHLYVCAAFLVRWKEILERKDFQELLLFL QNLPTHHUDDBDISLLLARAYLKFBAFADAPNHYKK LWDTYQSSPDGFSHFHLYVCAAFLVRWKEILERKDFQELLFRI AWDGKLGDRYNDPVDATPDTRELEFNEI KTQVELATGQLGLRRAA QKHSFFRHLHQRERGICHRGSFSIGEGSRVISHFLENDLGFTDS YSQKAFCGIYSKDQIFMSACQDOTIRLYDCRYGRFRKKSIKA RDVGMSVLDVAFTFDGMHFLYSSSWFILGTHCNYVTOLLSGHTVKK LINHACVRDVSNHPPEEKIVSSSWDGNLRLWQTKQABYFQDDM PRSECAAPAPVQOSSTPFSSPQ PVGALAGHQDGITFIDSKGDARYLISNSKQTIKWDLISHTVKGH GVLHTLLRCRFSPIHFTGQFTYTSGTKVVYVDLLSGHTVKK LINHKACVRDVSNHPPEEKIVSSSWDGNLRLWQTKQABYFQDDM PRSECAAPAPVQOSSTPFSSPQ PVGALAGHQDGITFIDSKGRARAGLGLYVDRECDRRATQG GVLHTLLRCRFSPIHFTGGQFTYSGTKVVYVDLLSGHTVKK LINHKACVRDVSNHPPEEKIVSSSWDGNLRLWQTKQABYFQDDM PRSECAAPAPVQOSSTPFSSPQ PVGALAGHQDRYNPDVAGRFSGLGGSSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQOQTIRLYDCRYGRFRKKSIKA RDVGRWSVLDVAFTPDGNHFLYSSSSDTHLORITGGLRAAA QKHSFPRNLHGGRRGLCHRGSFSIGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQOQTIRLYDCRYGRFRKKSIKA RDVGRWSVLDVAFTPDGNHFLYSSSDDTHCNIYGCRGRRRKKSIKA RDVGRWSVLDVAFTPDGNHFLYSSSDDTHCNIYGCRGRRRKKSIKA RDVGRWSVLDVAFTPDGNHFLYSSSDDTHCNIYDCRYGRFRKKSIKA RDVGRWSVLDVAFTPDGNHFLYSSSDDTHCNIYFGCDNRTLL LRSHBDDVNAVAFADISSGILFSGDDDAICKWDRTMGDDFK	1.		[KIVYSMYSRKAAEEVKRELIKLKVNYYILEESWCVRRSKPGCSM
RE				PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSVYKVLEVV
IRITLEYCGSUNIPSVTIMILALSSECLGUIVHYIPURAHFEARLPRO ALQVVGLKTITTKNIALSSECLGUIVHYIPURAHFEARLPRO YSMLERIPDHITKOVIDHTAEI SALVIAIMOSLEPBLLISKYEVKA PVDSACFRRICKQMYKMHEAI FDILIPEQTOMLFLINASYKLH LKKQLSHLNVINDGGPONGLVTADVAPYTONLQAKKGIKDLDLN MABIWBQKR 6279 127 1687 GGAMASDGARKOFWKSNSKLPGSIQHYYGAQHPPFDPLLHGTL LRSTARMPTTPVKAKRVSTFQEFSNTSDAWDAGBDDDELLAMA ABSLNSEVVMETANRVLRNHSQRQRPTLQEGPGLQQKPRPEAE PPSPPSGDLRIVKSVSSESHTSCPAESASDAPLQRSQSJHHSAT VTLGGTSDPSTLSSSALSERRASRLDKFKQLLAGPROTDLEELRR LSWSGIPKVVRPMTWKLLISGYLPANVDRRPATLQRKQKSYPAFI EHYVDSRNDEVHQDYTYQIHLDIPKYTEIFERI LFIWAIRHPASGYVQGINDLVTPFFVVFICEYLEAEEVDTTUVS GVPARVLCHIEADTYWCKSKLLDGIQDNYTAQPEIQKWKMLE ELVSRIDEQVHRHLDQHEVYRLOFAFRWINNLIMRRVPIRCTIR LWDTYQSEPDFSHSHLYVCAAFLVRWKKSILEEKDFQBLLLFL ONLPTHWDDEDISLLLAEPAYLAFADADAPHYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGGDPSGLPRRGAGLRRSEEEEEDDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WGRIGDRYNPPUDATPDTRELEPBIKTQVSLATGQIGLRRAA QKHSFFRNIHQRERGLCHRSSFSIGBOSRVISHFLPNDLGFTDS YSKARCGIYSKGOJIFNSACQDOTTRLYDCRYGRFKKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDBRRFAVFSIAVSSDGREVLGGANDCCIYVFDREGNRRTLQ ISSHBDUNANAFADISSQLIFSGDATCKWORRRTTREDDPK PVGALAGHQDGITFIDSKGDARXLISNSKODTIKLMDIRRFSSR EMMEASRQAATQQWWYRWARKKLLELPGDSSIMTYRGH GVLHTLIRCRFSPTHSTQQQFIXSGCSTGKVVVVDLLSGHIVKK LTNIHKACVRDVSWHPFEEKIVSSSBDGNIRLMQYRQABYPQDDM PSSECASAPAPVDGSSTFFSSGD FGSECASAPAPVDGSSTFFSSGD FGSECASAPAPVDGSSTFFSSGD VGRSGGAGARGCGIFNSACQGGANLCFTQLLGGLGRRAA QKHSFPRHLHQRERGLCHRGSFSLGEGSRVISHFLPNDLGFTDS YSGKAFCGIYSKGOQIFMSACQGGAANLCFTQLLGGLGRRAA QKHSPPRHLHQRERGLCHRGSFSLGEGSRVISHFLPNDLGFTDS YSGKAFCGIYSKGOQIFMSACQGGAANLCFTQLLLDGSEEEDDRA WGGRLGDRYNPPVDATTDTTELEFFEITTQUGLGLRRAA QKHSPPRHLHQRERGLCHRGSFSLGEGSRVISHFLPNDLGFTDS YSGKAFCGIYSKGOQIFMSACQOTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYYGGGDTHTALD LRPDERRFAVSILVASSGGREVLGGANDGCLYVPDRGNRRTLQ YSGKAFCGIYSKGOQIFMSACQOTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYYGGGDTHTALD LRPDERRFAVSILVSSGGREVLGGADDGCLYVPDRGNRRTLQ ISSHBDDVNAVAFADDISSGLIESGGDDAICKWWDRRTRWREDDDR				KE .
ALQVVGLKTITTKNLALSSRCLQLIVHYIEVIRAHPEARLPPKQ YSMLRHFDHITKOYHDHIAEISAKLVAIMDSLFDKLLSKYEVKA PVPSACFRNICKQMTKWHEAIFDLLPEEQTQMHFLRINASYKIH LKKQLSHLANVINDGGPQNGLVTADVAFYTGNLQALKGLKDLDLN MASIBWQKR 6279 127 1687 GGAMASDGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTL LRSTARMPTTPVKAKRVSTFGETESNTSDADAGBBDDGLLAMA ABSLNSEVVMETANRVLRHNSGGRPTLQEGGGLQOKPRPSAE PPSPPSGDLRLVKSVSESHTSCPAESASDAAPLQRSQSLPHSAT VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR LSWSGIPKPVRRMTMKLLSGYLPANVDRRPATLQRKQKEYPAFI EHYYDSRNDEVHQDTYRGIHDIPRMSPBALLLQPKVTEIFERI LSWSGIPKPVRRMTWKLLSGYLPANVDRRPATLQRKQKEYPAFI EHYYDSRNDEVHQDTYRGIHDIPRMSPBALLLQPKVTEIFERI LFIWATRIPASGYVGGINDLVTPFAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEVRYLQFARRWNNLMRREVPLRCTIR LWDTTQSSPDGFSHFHLYVCARAFLVRWKKSILEEKDFGELLIFL QNLPTTHWDGEDISLLLABAYRLKFAFADAPNHYKK ECCDQKMGSRNSSSAGSGSGDFSEGIPRGAGLRRSEEEEEDE DDVLAQVLAYLLRRQQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKYQVELAGQLIRRAA QKHSFPRHLHQRERGLCHRGSPSLGGSRVISHFDNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLDCRYGRFRFKFKSIKA RDVGMSVLDVAFTEDGMHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSGREVLGGANDCCLVYFDREQNRTLQ IESHBDDUNAVAFADISSQILFSGGDDAICKWWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARXLISNSKDTIKLWDIRRFSSR BCMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTINHKACVRDVSWHPPEKIVSSSWGQIRLNWQYRQASYFQDDM PRSECCASAPAPVQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGALRRSEEEEEEDE DUDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIXTQVELATGGLGRRAA QKHSFPRHLHQRERGURLVGGSGANNLOFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIXTQVELATGGLGRRAA QKHSFPRHLHQRERGURLVGGSGANNLOFIQALLDSEEEDED WDGRLGDRYNPPVDATPDTRELEFNEIXTQVELATGGLGRRAA QKHSFPRHLHQREGGLCHRGSFSLGGGDRYLSHTLPNDLGFTDS YSGKAFCGIYSKGOQIFMSACQOTIRLVDCRYGFRKFKSIKA RDVGMSVLDVAAFTPDGMHPLYSSWSDYIHICNIYGGGDTHTALD LRPDERRFRAVFSIAVSSOGREVLGGANDCLTVPDRGNRRTLQ IESHEDDVNAVAFADISSGILFSGGDDAICKWWRTTMREDDPR	6278	3	823	ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLL
YSMLRHFDHITKDYHDHLAEISAKLVAIMDSLPDKLLSKYEVKA PVPBACFRNICKQMTKMHEAIFDLLPEQTQMLFLRINASYKLH LKKQLSHLAVINDGGPQMGLVTADVAFYTONLQALKGIKDLDLN MABIMBQKR 6279 127 1687 GGMAASDGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTL LRSTAKMPTTPVKAKRVSTFQEFESNTSDAWDAGBDDDELLAMA ABSLNSEVVMETANRVLRNISQRQGRPTLQGGFGLQQKRPFBAE PSPPSGDLRLVKSVSSEHTSCTAPESASDAAPLQRSQSLPHSAT VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR LSWSGIPKVVRRMTWKLLSGYLPANVDRRPATLQRKQKSYPAFI ENYYDSRNDEVVJODYTYGIHDIPRMSPBALILQPKVTEIFERI LFIWATRHPASGYVQGINDLVTPFFVVFICEYIEAEEVDTVDVS GVPAEVLCNIEADTYWCMSKLLDGIQDNTTAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEVSYLDFAFRWINNLLMRREVPLRCTIR LWDTYGSEPDFFSHFHLYVCAAFLVXWRKEILEEKDFQELLLFL QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK UDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQIGLRRAA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQIGLRRAA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQIGLRRAA QKHSFPRHLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDOTTRLVDCRYGRFRKFKSIKA RDVGMSVLDVAFTPDGNHFLLYSSSDYTHICNIYGGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ ISSHEDDVNAVAFADISSQILFSGGDDAICKWWDRTMREDDPK GGMEASRQAATQQWWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GGVLHTLIRCGRSFFILBSKGDARLISNSKOYTVLLMDIRRFSSR EGMEASRQAATQQWWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GGVLHTLIRCGRSFFILBSKGDARLISNSKOYTVLLMDIRRFSSR EGMEASRQAATQQWWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCGRSFFILBSKGGQFITSGCTTSKVVVYDLLSGHTVKG LTNHKACVRDVSWHPPEEKIVSSTOKVVVYDLLSGHTVKGH GVLHTLIRCGRSFFILGSGGDAICKWWDRTMREDDPK CCCQKMSSRNSSSAGSGGDPSEGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVOGGAANLOFTQALLDGSEENDRA WDGRLGDRYNPPUDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQGSVLSHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDOTTRLVDCRYGRFRKFKSIKA RDVGMSVLDVAFTPDCNHHTLYSSWSDYTHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCTRYDRCDRFRKFKSIKA RDVGMSVLDVAFTPDCNHHTLYSSWSDYTHICNIYGEGDTHTALD LRPDERRFRAVFSIAVSSDGREVLGGANDGCTYVPDRGNRRTLQ 1ESHEDDVNAVAFADISSGILFSGGDDAICKWWRTRTRREDDPR				IRIILEYCQGVDNIPSVTTDMLTRLSDLLKYFNSRSCQLVLGAG
PVPSACFRITCKOMTKMHRAIFDLLPEEGTQMLFIRINASYKLH LKKQLSHLNVINDGGPQNGLVTADVAPYTGNLQALKGLKDLDLN MAEIWEQKR 6279 127 1687 GGMASDGARKOFWKRSNSKLPGSTQHYVGAQHPFDPLLHGTL LRSTARMPTPVKAKRVSTFQFESNTSDAWDAGBDDDELLAMA AESLNSEVVMETANRVLRNHSGRGGRPTLGEPGLQGKRPEAE PPSPPSGDLRLWKSVSESHTSCPASSABDAAPLGRSQSLPHSAT VTLGGTSDPSTLSSSALSERSABDAAPLGRSQSLPHSAT VTLGGTSDPSTLSSSALSERSABAAPLGRSQSLPHSAT LSWSGIPKDVRPMTWKLLSGYLPANVDRRPATLQRKQKEYPAFI EHYYDSRNDEVHQDTYRQTHIDIFRMSFBALILQPKVTEIFERI LFWAIRHPASGYVQGINDLVTFFFVVFICSYLBEEDDTDVDVS GVPAEVLCNIEADTYWCMSKLLDGIODNYTPAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR LMDTYGSEPGFSHFHLYVCAAFLVRWKKEILEEKDFÇELLLFL ONLPTAHWDDEDISLLLAEAYBLKFAFADAPNHYKK 6280 857 2515 ECCDCKMGSGRNSSAGSGGSDEGLPRRAGGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDGEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEITTQVELATGQIGLRRAA QKHSFFRNLHQRERGLCHRGSFSLGGGSRVISHLJENDLGFTDS YSGKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYHICNIYGBERDHRRTLQ IBSHEDDVNAVAFADISSQILFSGGDDAICXVWDRRTMREDDPK BGMEASRQAATQQNMDYRMQVPKKAWRKKLKJEGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFYSGSGTGKVVVYDLLSGHTVKK LTINHKACVRDVSWHPPEKLYUSSSWDGNLRLWQYRQABYPQDDM PESEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDFSGLDFRGGLERSEEEEEDE DVDLAQVLAYLIRRGQVPLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRHLHQREGSLCHRGSFSLGGGSRVISHFLIPNDLGFTDS YSGKAFCGIYSKUPGGFMSAGGGTFMSACGTRFKKFKSIKA RDVGWSVLDVAFTPDGWIFLYSSWDDYIRLINGTGRFKKFKSIKA RDVGWSVLDVAFTPDGWIFLYSSWDDYIRLINGTGRFKKFKSIKA RDVGWSVLDVAFTPDGWIFLYSSWDDYIRLINGTGRFKKFKSIKA RDVGWSVLDVAFTPDGWIFLYSSWDYIRLINGIGCHYFTREFKSIKA CRHSFPRHLHQREGSLCHRGSFSIGGGSRVISHFLIPNDLGFTDS YSGKAFCGIYSKUPGGFMSAGGGLYFYGRFKKFKSIKA RDVGWSVLDVAFTPDGWIFLYSSWDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGADDGCLYVFORFRKKRKSIKA RDVGWSVLDVAFTPDGWIFLYSSWDDYIRLINIYGERGREREEEEDDE LFCCDQKWGSTANDFTPGGBTHTALD LRPDERRFAVFSIAVSSSDGDAALCKWDRTMREDDPK				ALQVVGLKTITTKNLALSSRCLQLIVHYIPVIRAHFEARLPPKQ
LKKQLSHLNVINDGGPQNGLVTADVAPYTGNLQALKGLKDLDLN MAEIWEQKR GGMAAGGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTL LRSTAKMPTTPVKAKKVSTFQBFESNTSDAWDAGGDDELLAMA ABSLNSEVVMETANRVLRNHSQQGRPTLQEGPGLQQKPRPEAE PPSPPSGDLRLVKSVSESHTSCPAESASDAAPLQRSQSLPHSAT VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR LSWSGIPKFVWENTWKLLSGYLPANVDRRPATLQRKQKEYPAFI EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALILQPKVTEIFERI LFWAIRHPASGYVQGINDLVTFFFVVFICEYIBABEVDTVDVS GVPAFULCNIEADTTWCMSKLDGIODNYTPAPQEIQMKVKNLE ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR LWDTYQSBPDGFSHFHLVVCAAFLVRWKEILEEKDFQELLLFL ONLPTHWDDEDISLLLARAYRLFRAFADADNHYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WGGRLGDRYNPPVDATPDTRELFMENTLYQUELATGQLGLRRAA QKHSFFRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDDTIRLYDCRYGRFRKFKSIKA RDVGMSVLDVAFTPDNHFLYSSMSDYHHCNI KUGGTHTALD LKPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IBSHEDDVNAVAFADISSQ LIFSGGDDAICKVWDRRTMREDDPK EMMEASRQAATQQNBYDRQQVPKKAMKKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFTYSGCTSKVVVYDLLSGHIVKK LTINHRACVRDVSWHPFEEKIVSSSWDGNLRIMQYRQABFYGDDD PRSEECASAPAPVQOSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVBLVQGGGAANLQFIQALLDSGEENDRA WGGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSIGGRVISHFLENDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFKKFKSIKA RDVGMSVLDVAFTPOMHFLYSSSWDYHLTCNITYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ CKHSFPRMLHQRERGLCHRGSFSIGGRVISHFLENDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFKKFKSIKA RDVGMSVLDVAFTPOMHFLYSSSWDYHLTCNITYGGEGTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRTTLQ LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRTLQ LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRTLQ LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRTTLQ LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRTTLQ LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRTTLQ				YSMLRHFDHITKDYHDHIAEISAKLVAIMDSLFDKLLSKYEVKA
MASIWEÇKR				PVPSACFRNICKQMTKMHEAIFDLLPEEQTQMLFLRINASYKLH
6279 127 1687 GGAMASDGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTL LRSTARMPTTPVKAKRVSTTQEFESINSDAMDAGEDDDELLAMA AESLNSEVVWETANRVLKINISQRQGRPTLQEGGGLQQKPREAE PPSPPSGDLRLVKSVSESHTSCPAESASDAAPLQRSQSLPHSAT VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR LSWSGIPKPVRPTWKLLSGEVPANVDRRPATLQRKQKSYPAFI EHYDGSRDEWHQDTYRQIHIDIPRMSPEALILQPKVTEIFERI LPIWATRHPASGYVQGINDLVTFFFVVFICEYIEABEVDTVDVS GVPAEVLCNIEADTYWGMSKLLDGIQDNYTPAQPGIGWKVMLE ELVSRIDEQVHRHLDGHEVRYLQFAFRWMNNLLMREVPLRCTIR LWDTYQSEPDGFSHFHLYVCAAPLVRWKESILEEKDFQELLLFL QNLPTAHWDDEDISLLLAERYRKFAFADADNIYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRQQVRLVQGGGAANLQFIQALLDSEEENDRA WBGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGJGLGRRAA QKHSFFRMLHQRERGLCHRGSPSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRRFKKFSIKA RDVGMSVLDVATTPDCNHFLYSSWSDYIHLCNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISQILFSGDDAICKVWDRRTMREDDDK PVGALAGHQDGTTFIDSKGDARYLISNSNQQTIKLMDIRRFSSR EMMEASRQAATQQNWDYRMQQVPKKAMRKLKJPGDSSLMTYRGH GVLHTLIRCRFSPIHSTQQFIYSGCSTGKVVVYDLLSGHIVKK LINNHACVRDVSWHPPEERIVSSSWDGNLRLMQYRQABYPQDDM PBSEECASAPAPVPQSSTFFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDFSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRQCVRLVQGGGAANLGFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFREIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTTRLYDCRYGABFRKSIKA RDVGMSVLDVATPDCNHFLYSSWSDYHILCNIYGGGDTHTALD LRPDERRFAVFSIAVSSDGREVLIGGANDGCLYVFDREQNRRTLQ ZKSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTTRLYDCRYGRFRKRSIKA RDVGMSVLDVATPDCNHFLYSSWSDYHILCNIYGGGDTHTALD LRPDERRFAVFSIAVSSDGREVLIGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKWWDRRTMREDDDK	1			LKKQLSHLNVINDGGPQNGLVTADVAFYTGNLQALKGLKDLDLN
LRSTARMPTTPVKAKRVSTTQEFESNTSDAWDAGEDDELLAMA AESLNSEVVMETANRVLRNISQRGRPTLQEGGLQCKPREEAE PPSPFSGDLRLVKSVSESHTSCPAESASDAAPLQRSQSLPHSAT VTLGGTSDPSTLSSALSEREASRLDKFKQLLAGPNTDLEELRR LSWSGIPKPVRPMTWKLLSGYLPANVDRRPATLQRKQKEYPAFI EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALILQFKVTEIFERI LFTWAIRHPASGYVQGINDLVTPFFVVPICEYIEABEVDTYDVS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTPAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLHARRVPLRCTIR LMDTYQSEPDGFSHFHILYVCAAFLVRWKSLIEEKDPQELLLFL QNLPTAHWDDEDISLLLARAYRLKFAPADAPNHYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGGDPSEGLPRRGAGGLRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGANNLGFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGRRAA QKHSFFRMLHQRERGICHRGSFSLGGDSRVISHFLENDLGFTDS YSQKAFCGIYSKDGQIFMSACODOTIRLVDCRYGFRFKFSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDCCLYVFDREQNRRTLQ IBSHEDDVMAVAFADISGJLBSGGDDAICKVWDRRTMREDDPK BCMEASRQAATQQNNDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSFIHSTGQOFTYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEFFQDDM PESSECASAPAPVPQSTFFSSPG 6281 857 2515 ECCDQKMGSRNSSAGSGGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRQCVRLVQGGGANNLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFREIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEGGSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKWSIKA QKHSFPRMLHQRERGLCHRGSFSLGEGGRSVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKWSIKA RDVGMSVLDVAFTPDGNHFLYSSWSDYHICNIYDGRYGRFRKWSIKA RDVGMSVLDVAFTPDGNHFLYSSWSDYHICNIYDGRYGRFRKWSIKA RDVGMSVLDVAFTPDGNHFLYSSWSDYHICNIYDGRYGRFRKKSIKA RDVGMSVLDVAFTPDGNHFLYSSWSDYHICNIYDGRYGRFRKKSIKA RDVGMSVLDVAFTPDGNHFLYSSWSDYHICNIYDGRYGRFRKKSIKA RDVGMSVLDVAFTPDGNHFLYSSWSDYHICNIYDGRYGRFRKKSIKA RDVGMSVLDVAFTPDGNHFLYSSWSDYHICNIYDGRYGRFRKKSIKA RDVGMSVLDVAFTPDGNHFLYSSWSDYHICNIYDGRYGRFRKKSIKA RDVGMSVLDVAFTPDGNHFLYSSWSDYHICNIYDGRYGRFRKKSIKA LIRPBERDDNNAVAFADISSQILFSGGDDDAICKWWDRRTMREDDDK	6279	127		
AESLNSEVVMETANRVLRNHSQRQGRPTLQEGGLQQKPRPEAE PPSPPSGDLRLVKSVSESHTSCPAESASDAAPLQRSQSLHSAT VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR LSWSGIPKPVRPMTWKLLSGYLPANVDRRPATLQRKQKEYPAFI EHYYDSRNDEVHQDTYRQIHLDIPRMSPEALILQPKVTEIFERI LFIWAIRHPASGYVQGINDLVTPFFPVVPICEYIEABEVDTVDVS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEVRYLOFAFRWNNNLLMREVPLRCTIR LWDTYQSEPDGFSHFHLYVCAAFLVRWRKEILEEKDFQELLLFI QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYMPPVDATPDTRELEMEIKQVELATGOLGLRRAA QKHSFFRMLHQRERGLCHRGSFSLGEQSRVISHFLENDLGFTDS YSQKAFCGIYSKDGQIFMSACQDDTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDCCLYVFDREQNERTLQ IBSHEDDVNAVAFADISQILFSGGDDAICKWDRRTMREDDPK PVGALAGHQDGITFIDSKGDAICKWDRRTMREDDPK GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTMHKACVRDVSWHPFEEKIVSSWDGNLRLWQYRQAEYFQDDM PESSECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEENEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEOSVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVATPPDCNHFLYSSWSDYIHICNIYGGGDHTALD LRPDERRFAVFSIAVSSDGRVLGGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK TYSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVATPPDCNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGRVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK	62/3	127	1687	GGAMASDGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTL
PPSPFSGDLRIJVKSVSESHTSCPAESASDAPLQRSQSLPHSAT VTLGGTSDPSTLSSALERRASRLDKFKQLLAGPNTDLEELRR LSWSGIPKPVRPMTWKLLGGYLPANVDRRPATIQRKQKEYPAFI EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALILQPKVTEIFERI LPIWAIRHPASGYVQGINDLVTFFVVPICSYIEAEEVDTVDVS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTPAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR LMDTYQSEPDGFSHFHLYVCABFLVRWRKEILEEKDFQELLLFL QNLPTAHWDDEDISLLLARAYRLKFAFADAPNHYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFFRMLHQRERGLCHRGSFSLGEGSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYHLCNIYGEGDTHTALD LRPDERRFAVFSIAVSSGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKQTIKLWDIRFFSSR EGMEASRQAATQQMWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVDLLSGHIVKK LTNHKACVRDVSWHPFEEKIVSSSWBGNLRLWQYRQAEYFQDDM PESECASAPAPVPQSSTFFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGGLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLEEQSRVISHPLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGMSVLDVAFTPDGNHFLYSSWSDYIHLCNIYGGEGDTHTALD LRPDERFAVFSIAVSSGGREVLGGSRVISHPLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGMSVLDVAFTPDGNHFLYSSWSDYIHLCNIYGGEGDTHTALD LRPDERFAVFSIAVSSGGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVMAVAFADISSQILFSGGDDAICKWWDRRTMREDDPK				LRSTAKMPTTPVKAKRVSTFQEFESNTSDAWDAGBDDDELLAMA
VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR LSWSGIPKPVRPMTWKLLSGYLPANTURRPATLQRKQKEYFAFI EHYYDSRNDEVHQDYTRQIHIDIPRMSPEALILQRKQKEYFAFI LFIWAIRHPASGYVQGINDLVTPFFVVFICEYIBABEVDTVDVS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR LMDTYQSEPDGFSHFHLYVCAAFLVRWKELILEEKDFQELLLFL QNLPTAHWDDEDISLLLABAYRLKFAFADAPNHYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGSGDBEGGLPRGAGLRREBEEEEDE DVDLAQVLAYLLRAGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEGSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYTHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILESGGDDAICKVWDRRTMREDDDRK PVGALAGHQOGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQWWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPTHSTGQQFTYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQABYFQDDM PESSECASAPAPVPOSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDBSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQQLIGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHLCNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVMAVAFADISQLIFSGGDDAICKWWDRRTMREDDPK	1			RESIDENCE IN LUXUUS CONTROL CO
L SWSGIPKPVRPMTWKLLSGYLPANVDRRPATLQRKQKEYPAFI EHYYDSRNDEVHQDTTRQIHDIPRMSPEALILQPKVTEIFERI LFIWAIRHPASGYVQGINDLVTPFFVVFICEYIEABEVDTVDVS GVPAEVLCNIEADTYWCMSKLLDGIQDNTTFAQPGIQMKVKMLE ELVGRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR LWDTYQSEPDGFSHFHLYVCAAFLVRWRKEILEEKDFQELLLFI QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANCCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNNDYRWQQVPKKAWRLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQGFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSWDGNIRLWQYRQABYFQDDM PESEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQAILDSEEENDRA WDGRLGDRYMPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGTHTTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ LESHEDDVNAVAFADISSQILFSGGDDAICKWWDRTMREDDPK				VTI.CGTCDDCTI.CCCAI CEDEACDI DVEVOI I AGRICULTURA
EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALILQFKVTEIFERI LFIWAIRHPASGYVQGINDUTPFFFVVFICEYIEAEEVDTVUVS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTPAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEVRYLQFAFRWNNNLLMREVPLRCTIR LWDTYQSEPDGFSHFHLYVCAAFLVRWRKEILEEKDFQELLLFL QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGSGPDSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLVDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSWDGNLRLWQYRQAEYFQDDM PESSECASAPAPVPQSSTFFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKWWDRTMREDDPK	j			I.CWCGTDYDIDDMTWYI I CCVI DANIDDDDANI ODVOVENDADI
LETWAIRRIPASGYVQGINDLVTPFFVVFICEYIEAEEVDTVDVS GVPAEVLCNIEADTYWCMSKLIDGIQDNYTFAQPGIQMKVKMUE ELVSRIDEQVHRILDQHEVRYLQFAFRWMNNLIMREVFLRCTIR LWDTYQSEPDGFSHFHLYVCAAFLVRWKEILEEKDFÇELLLFL QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDB DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATTDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFGIYSKDGQIFMSACQDOTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHBDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYNWQVVPKKAWRKLKLPGDSSIMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PBSEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQCGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHS FPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMRRDDPK	ĺ	:		EHAADEMDEMHUDLADUTATUTEDMEDENTITI UDALMETEEDT
GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLMREVPLRCTIR LWDTYQSEPDGSHFHLYVCAAFLVRWKKEILEEKDFQELLLFL QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGGDPSEGLPRRGAGLRRSEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFFRNLHQRERGLCHRGSFSLGEQSRVISHFLENDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IBSHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PSSEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYTHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKWWDRRTMREDDPK		was transfer to the Mills	e e e e	LFIWAIRHPASGYVOGINDI.VTPFFVVRICEVIEAREVDTVDVC
ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR LWDTYQSEPDGFSHHHLYCAAFLVRWRKEILEEKDFQELLLFL QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRNLHQRERGLCHRGSFSLGEQSRVISHFLDNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYUCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDDK PVGALAGHQDGITFIDSKGDARYLISNSKQDTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVVDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESSECASAPAVPQSSTPFSSEQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVPDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK]	:		GVPAEVLCNIEADTYWCMSKIJDGTODNYTPAOPGTOMKVKMIR
LWDTYQSEPDGFSHFHLYVCAAFLVRWRKEILEEKDFQELLLFL QNLPTAHWDDDISLLLAEAYRLKFAFADAPNHYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTFDGNHFLYSSWSDYTHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDUNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRRFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGGGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK			6 '	ELVSRIDEOVHRHLDOHEVRYLOFAFRWMNNI, MREVPLRCTIP
QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK 6280 857 2515 ECCDQKMGSRNSSSAGGGGDSEGLPRRGAGLRRSEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDUNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK				LWDTYOSEPDGFSHFHLYVCAAFLVRWRKEILEEKDFOELLLFI.
6280 857 2515 ECCDQKMGSRNSSSAGSGSDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLENDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSWSDYTHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRUQYRQABYFQDDM PESEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVPDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK	L		٠	QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK
DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELFFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFKKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLFGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESSECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVLSHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK	6280	857	2515	ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEFEDR
WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDCQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAMRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKPKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK		;	,	DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIOALLDSEEENDRA
QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESSECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK	<u> </u>	·		WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA
YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESSECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK	[QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS
RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESEECASAPAPVPQSSTPFSSPQ ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK			·	YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA
IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESEECASAPAPVPQSSTPFSSPQ ECCDQKMGSRNSSSAGSGSGDPSEGLPRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK			•	RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESEECASAPAPVPQSSTPFSSPQ ECCDQKMGSRNSSSAGSGSGDPSEGLPRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK				LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ
EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM PBSEECASAPAPVPQSSTPFSSPQ ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK				IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK
GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM PBSEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGGSGDPSEGLPRRGAGLRRSEEBEEDDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK	}	ĺ	İ	PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR
LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSDPSEGLPRRGAGLRRSEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK				EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH
FESECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSDPSEGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK		. }	ŀ	GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK
6281 857 2515 ECCDQKMGSRNSSSAGGGGDPSEGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK		j		LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM
DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEBEEDDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEBEEDDE WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK	6201			
WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK	0281	857	2515	
QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK				DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA
YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK		!		WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA
RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK				QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS
LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK		1		YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA
IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK	İ	l		RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
1ESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR			Ì	
PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR				1ESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK
				PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR

SEQ	Predicted	Predicted end	1 Amine and germanh coult it
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
[amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Bequence	\=possible nucleotide insertion)
			EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH
			GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK
			LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM
			PESEECASAPAPVPQSSTPFSSPQ
6282	125	906	RMAACRALKAVLVDLSGTLHIEDAAVPGAQEALKRLRGASVIIR
			FVTNTTKESKQDLLERLRKLEFDISEDEIFTSLTAARSLLERKQ
			VRPMLLVDDRALPDFKGIQTSDPNAVVMGLAPEHFHYQILNQAF
		ļ	RLLLDGAPLIAIHKARYYKRKDGLALGPGPFVTALEYATDTKAT
			VVGKPEKTFFLEALRGTGCEPEEAVMIGDDCRDDVGGAODVGML
			GILVKTGKYRASDEEKINPPPYLTCESFPHAVDHILOHLL
6283	140	1043	LSLFGIHVMNPFWSMSTSSVRKRSEGEEKTLTGDVKTSPPRTAP
		1043	KKQLPSIPKNALPITKPTSPAPAAQSTNGTHASYGPFYLEYSLL
	1		AEFTLVVKQKLPGVYVQPSYRSALMWFGVIFIRHGLYQDGVFKF
		1	TVYIPDNYPDGDCPRLVFDIPVFHPLVDPTSGELDVKRAFAKWR
•			RNHNHIWQVLMYARRVFYKIDTASPLNPEAAVLYEKDIOLFKSK
			VVDSVKVCTARLFDQPKIEDPYAISFSPWNPSVHDEAREKMLTO
			KKKPEEQHNKSVHVAGLSWVKPGSVQPFSKEEKTVAT
6284	1	2879	RSVIPGSTISSRWPGLSRPRFMAAHEWDWFQREELIGQISDIRV
	_	2075	QNLQVERENVQKRTFTRWINLHLEKCNPPLEVKDLFVDIODGKI
			LMALLEVLSGRNLLHEYKSSSHRIFRLNNIAKALKFLEDSNVKL
•			VSIDAAEIADGNPSLVLGLIWNIILFFQIKELTGNLSRNSPSSS
		•	LAPGSGGTDSDSSFPPTPTAERSVAISVKDQRKAIKALLAWVQR
			KTRKYGVAVQDFAGSWRSGLAFLAVIKAIDPSLVDMKQALENST
. 3			RENLEKAFSIAQDALHIPRLLEPEDIMVDTPDEQSIMTYVAQFL
			ERFPELEAEDIFDSDKEVPIESTFVRIKETPSEQESKVFVLTEN
			GERTYTVNHETSHPPPSKVFVCDKPESMKEFRLDGVSSHALSDS
			STEFMHQIIDQVLQGGPGKTSDISEPSPESSILSSRKENGRSNS
			LPIKKTVHFEADTYKDPFCSKNLSLCFEGSPRVAKESLRQDGHV
			LAVEVAEEKEQKQESSKIPESSSDKVAGDIFLVEGTNNNSQSSS
er ara e	10 G		CNGALESTARHDEESHSLSPPGENTVMADSFQIKVNLMTVEALE
			EGDYFEAIPLKASKFNSDLIDFASTSQAFNKVPSPHETKPDEDA
•	٠.	,	EAFENHAEKLGKRSIKSAHKKKDSPEPQVKMDKHEPHQDSGEEA
			EGCPSAPEETPVDKKPEVHEKAKRKSTRPHYEEEGEDDDLQGVG
			EELSSSPPSSCVSLETLGSHSEEGLDFKPSPPLSKVSVIPHDLF
			YFPHYEVPLAAVLEAYVEDPEDLKNEEMDLEEPEGYMPDLDSRE
			EEADGSQSSSSSVPGESLPSASDQVLYLSRGGVGTTPASEPAP
			LAPHEDHQQRETKENDPMDSHQSQESPNLENIANPLEENVTKES
ŀ			ISSKKKEKRKHVDHVESSLFVAPGSVQSSDDLEEDSSDYSIPSR
			TSHSDSSIYLRRHTHRSSESDHFSLCSVEERSRSG
6285	2157	1331	SCKTENLLEMWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHH
-	- -		IDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIYVRYKOVH
			ALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVS
			GAVLTFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCG
İ			VSALSMLTCSSVLHSGNFGTDLEOKLHWNPEDKGYVLHMITTAA
			EWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYDTAPCPIN
			NERTRLLSRDI
6286	1619	276	KAGASCCGSANPYVSVGKSCVLLAMAQLQTRFYTDNKKYAVDDV
		2/0	
			PFSIPAASEIADLSNIINKLLKDKNEFHKHVEFDFLIKGQFLRM
			PLDKHMEMENISSEEVVEIEYVEKYTAPQPEQCMFHDDWISSIK
			GAEEWILTGSYDKTSRIWSLEGKSIMTIVGHTDVVKDVAWVKKD
	: ·		SLSCLLLSASMDQTILLWEWNVERNKVKALHCCRGHAGSVDSIA
			VDGSGTKFCSGSWDKMLKIWSTVPTDEEDEMEESTNRPRKKQKT
İ			EQLGLTRTPIVTLSGHMEAVSSVLWSDAEEICSASWDHTIRVWD
	1		VESGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRHIRLWDPRT
1	l		VPCCINCI CI mounoumoumaannumoor ragar partuur unn
			KDGSLVSLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDT RSCKAPLYDLAAHEDKVLSVDWTDTGLLLSGGADNKLYSYRYSP

Designing nucleotide location corresponding corresponding contion corresponding cofirst amino acid amino acid residue of amino acid sequence sequenc	SEO	Predicted	Predicted end					
No: nuclectide corresponding to first coffirst amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence corresponding corresponding company comp				Amino acid segment containing signal peptide				
Coctation Corresponding Co first amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence	J		1	Glutamic Acid P-Phonylalanina C-Clusina				
corresponding to first amino acid residue of residue of amino acid residue of amino acid sequence Sequ	5.07			W-Wishiding T-Toployeins W Loring				
to first amino acid residue of service of Paproline, Q-Gultamine, R-Arginine amino acid sequence seque				I-Leugine M-Methionine Mannagerine				
amino acid residue of amino acid sequence 8-287 278 1482				P-Proline O-Clubamine D-Arminine				
xesidue of amino acid sequence Codon, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide insertion TTSNYGA 1482				S-Serine T-Threenine W-Waline				
Sequence Codon, /-possible nucleotide deletion, -possible nucleotide insertion -possible nucleotide insertion -possible nucleotide insertion	:			W=Tryptophan, Y=Tyrosine, Y=Inknown *-Stop				
Apossible nuclectide insertion]	amino acid		Codon. /=possible nucleotide deletion				
TISHUGA	1	sequence	<u> </u>	\=possible nucleotide insertion)				
APAKLOVOKILCDLLLPENLKEGIKESSWSILCTTKRRPPDFIS VMESSGILKEPS PROSEET PEVTSBEVKGSILRRGAGAGSINSTE MARAEDCIKRYSSPYLSVGKSKVILKKKALSLBGDVIVVKEOGR MALKKQGETPNEVCMFSLAYDDIPEBLIDVSDEGSLCMRLFFE PVTTOGHS FCINCLERCLDHAPYCELCKSKVLADRRYCH OLDEBLIVKYLPDELSERKKIYDBETABLSHLTKNUPIFVCMA YPTVPCPLSWFPPTYMINTSICJTCTKYGKVSTONFORDY GCMUGIRNVHFLPDGRSVVDTVGGKRFRVLKRGMKOGYCTADIE YLEDV 6288 1 743 VTLYFCRGLVGNILLGASGMASGCKIGPSILNSDLANIGACIGR MIMDSGADYLHLDVMGHFFYPHTTGHFVVSELKKQLGQDFFFOM HMWSKREGWVKPMAVAGANOYTFHLRATRRPGALIKDIERKGM KVGLAIKPTSVEYLAPWANGIDMALIVMTVSGAIM RSEDPRSVINILRNVCSERAGKYRSLDR 6289 1 743 VTLYFCRGLVGNLLLGASGMASGCKIGPSILNSDLANIGACIGR HLDSGADVHLLIKRNVCSERAGKYRSLDR FVYHWLRTQFPSLDIEVDGGUPDTVHKCARAGANMIVSGAIM RSEDPRSVINILRNVCSERAGKYRSLDR KVGLAIKPTSVEYLAPWANGIDMALVMTVERPGGGKFMEDMM PKVHWLRTQFPSLDIEVDGGUPDTVHKCARAGANMIVSGAIM RSEDPRSVINILRNVCSERAGKYSLDR TAGWILGVYSTPSLDIEVDGGUPDTVHKCARAGANMIVSGAIM RSEDPRSVINILRNVCSERAGKYSLDR KVGLAIKPGTSVEYLAPWANGIDMALVMTVERPGGGGKFMEDMM PKVHWRRTQFPSLDIEVDGGUPDTVHKCARAGANMIVSGSAIM RSEDPRSVINILRNVCSERAGKSLDR TAGWILGVYSTPSLDIEVDGGUPDTVHKCARAGANMIVSGSAIM RSEDPRSVINILRNVCSERAGKSLDR TAGWILGVYSTPSLDIEVDGGUPDTVHKCARAGANMIVSGSAIM RSEDPRSVINILRNVCSERAGKSSLDR TAGWILGVYSTVAPPILACLEPFPLRRRRRRRRMISRYTTKRA VPOSLELKGITKHALMHEPPBKLEBISPTSDSHEKKITSKGSKS DITRESSFTSAJDTNSLSAFSTVTAGGISTEGSFSWGGKELD QNATEKVOTMTTATDBLLYEGKLSVHITSKJGECCOWTASTPHL RILGRQITTPSEGGKRJYTRSPTVAGGISTEGFRSVRSTFHQ GKKLHFSSSYAHKASSIAKSSSKCSMEDRENDSITFGHR GKKLHFSSSYAHKASSIAKSSSKCSMEDRENDSITFGHR GKKLHFSSSYAHKASSIAKSSRCSMEDRENDSITFGHR GKKLHFSSSYAHKASSIAKSSRCSMEDRENDSITFGHR GKKLHFSSSYAHKASSIAKSSRCSMEDRENDSITFGHR GKKLHFSSSYAHKASSIAKSSRCSMEDRENDSITFGHR GKKLHFSSSYAHKASSIAKSSRCSMEDRENDSITFGHR GKKLHFSSSYAHKASSIAKSSRCSMEDRENDSITFGLBGA RVPVAPDELSSFPTLGRNNLIPTGKGCRSTFFLORT GKKLHFSSSYAHKASSIAKSSRCSMEDRENDSITFGHR GKKLHFSSSYAHKASSIAKSSRCSMEDRENDSITFGHR GKKLHFSSSYAHKASSIAKSSRCTSMEDRENDSITFGHR GKKLHFSSSYAHKASSIAKSSRCTSMEDRENDSITFGHR GKRUPTSSSTRATHGR GERPHOLSTONTONTONTONTONTONTONTONTONTONTONTONTONT								
APAKLQVGKILCDILLIPENLEGILKSSINSSLPCTKINPPDPISS VMESGSLBEPS PKQSES I PEVTSEPVGSUIRAGOSGINTST MARABCLKRVSSEPVLSVQSKGVLLKRKISLLEGOVI VMEDGR NIKLKQGETPNEVCMPSLAYGOPI PEBLIDVSCLCMBLPPYC PVTTPCCHSPCKNCLERCLDHAPYCQHCKESLKWLADRERYCYT OLLSELIVELYLLDBLISERKKI TDERTAELSHLITMVPI FVCTNA IPTVPCPLHVFBPRYRLMIRRS I GTGTKGYGHCVSDTQNSFADY GCMLQIRNVHFLPDGRSVUDTVGGKRFRVLKRGMKGGYCTADIE THEOV 1 VTLYPCGRGLVGNILLIGASGMASGCKIGPSILMSDLANLGAECLR MLDSGADYLHLDVMDGHFVFNITTGGFPVESLEKQLGGODFFFM HMWSKPEGWVKPNAVAGANQYTFHLEATENGGALTU ERKOM KVGLAIKPGTSVEYLAPWANGJUDALLVMTYGGGCKFEGOKFMEDMA RSEDPRSVINLLRIVCSEBAGKRSLDR 6289 1 743 VTLYPCGGLVGNILLIGASGMASGCKIGPSILMSDLANLGAECLR MLDSGADYLHLDVWDGHFVFNITTGGFPVESLEKQLGGODFFFM HMWSKPEGWVKPNAVAGANQYTFHLEATENGGALTU ERKOM KVGLAIKPGTSVEYLAPWANGJUDALLVMTYGGGCKFMEDMA PRIJHLIRNVCSEBAGKRSLDR ASEDPRSVINLLRIVCSEBAGKRSLDR MADSGADYLHLDVWGHVFVFNITTGGFPVESLKQLIGGDFFFM HMWSKPEGWVKPNAVAGANGYTFHLEATENGGALTKOLERNOM KVGLAIKPGTSVEYLAPWANGJUDALLVMTYVEGFGGKFMEDMA PRIJHLIRVGSPSLAFAGNISTGERAGRERGRKRMISGKSL MEMBSGADYLHALDVWGHVFVFNITTGGFPVESLKQLIGGDFFFM HMYSKPEGWVKPNAVAGANGYTFHLEATENGGALTKOLERNOM KVGLAIKPGTSVEYLAPWANGJUDALLVMTYVEGGGKFMEDMA PRIJHLIRVGSPSLAFAGNISTGERSPSLKKOLGGOPFFDM HMYSKPEGWVKPNAVAGANGYTFHLEATENGGALTKOLGENOM KVGLAIKPGTSVEYLAPWANGJUDALLVMTYVEGGGKFMEDMA RSEDPRSVINLLRNVCSBAGKRSLDR RSEDPRSVINLLRNVCSBAGKRSLDR RSEDPRSVINLLRNVCSBAGKRSLDR RSEDPRSVINLLRNVCSBAGKRSLDR RSEDPRSVINLLRNVCSBAGKRSLDR RSEDPRSVINLLRNVCSBAGKRSLDR RSEDPRSVINLRNVCSBAGKRSLDR RSEDPRSVINLLRNVCSBAGKRSLDR RSEDPRSVINLRNVCSBAGKRSLDR RSEDPRSVINLRNVCSBAGKRSLDR RSEDPRSVINLRNVCSBAGKRSLDR RSEDPRSVINLRNVCSBAGKRSLDR RSEDPRSVINLRNVCSBAGKRSLTFORGRERGRERGRENSTFFGIR GKKLHFSSSYAHKASS IAKSSSYCSMEDRESSJCVSKGRSTFFGIR GKKLHFSSSYAHKASS IAKSSSYCSMEDRESSJCVSKGRSTFFGIR GKKLHFSSSYAHKASS IAKSSYCSMEDRESSJCVSKGRSTFFGIR GKKLHFSSSYAHKASS IAKSSYCSMEDRESSJCVSKGRSTFFGIR GKKLHFSSSYAHKASS IAKSSYCSMEDRESSICUS SPROTTSCGRVX GKKLHFSSSYAHKASS IAKSSYCSMEDRESSICUS SPROTTSCG GRENDSSKAGSAVVDENYQPQCRULTHISTSPSMAGAGCARSCGRUNDSTILLGVR PHOLOPARAGRAGA ARKASLD	6287	278	1482	MQFFFNFQIGLRSTSGKEKYSGDAGFLGDALOLFLOCLALDEDF				
VMERSQSLMEDS PKOGEET PEWTSEPVKGSLINRAGSAGSINSTE MARABECLIKYWSS SPVLSVORKGVLLKRALLIAGOVT VMEDGR NILKKOGETPNEVCMFSLAYGDI PEBLI DVSDBFGCSLCMRLIFEE PWTTPCGHS FCKNICLERCLIAHPYED LANDERYCSLCMRLIFEE PWTTPCGHS FCKNICLERCLIAHPYED LANDERYCSLAWRIFFE PWTTPCHSTER FCKNICLERCLIAHPYED LANDERYCSLAWRIFFE PWTTPCHSTER FCKNICLERCLIAHPYED LANDERYCSLAWRIFFE PWTTPCHSTER FCKNICLERCLIAHPYED LANDERYCSTAPAY STTVPCPLIVEER FKKKIYDEETAELSHLIKKNVPIFFCTNSFADY GCMLQIRN/WFIPLARDERYCHGKSEKOKGCSTATIES GCMLQIRN/WFIPLARDERYCHGKSEKOKGCSTATIES TULEVV TULEVV TULEVCH MLDSGAMASGCKIGFSILNSDLANLGAECLR MLDSGADYLHLDVMDGHFVPNITTGFFVVESLKKOLGGDFFDM HMWSKERGWVKPMAVAGNOYTHHLARTMORGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIDMALVMTVERPGGAGKFEDMM FEVHURITOFFSLDIEVCGVGPDTVHKCABAANNIVSGSAIM RSEDPRSVINLLRNVCSEAAGKRSLDR TULEVGKGUVCHNLLGANGAGGKGGCKIGPSILNSDLANLGAECLR MLDSGADYLHLDVMDGHFVPNITTGFFVVSSLKKOLGGDFFDM HMWSKERGWVKPMAVAGANCYTFHLEATENGALLIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVMTVERGGKATENGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVMTVERGGKATENGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVMTVERGGKATENGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVMTVERGGKATENGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVMTVERGGKATENGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVMTVERGGKATENGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVMTVERGGKATENGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVMTVERGGKATENGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVMTVERGGKATENGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVMTVERGGKATENGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVMTVERGGKATENGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVMTVERGGKATENGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVMTVERGGKATENGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVMTVERGGKATENGALIKDIERSCM KVGLAIKPGTSVEYLAPAMAIDIMALVATURGENTARTERGALIKDIERSCM LENGMANTATTATDELLIKEGKGRLSTSTATESS DFSKTTGGSTATATBETTARTSKYSESTLICHTENSVERTLIKGE KVFUADSINGAMAITATDELLIKEGRLSTSTRATESS TSSLSTTVGSTRATESSTATATSKYSGGSGRPVNTTTGGE PRAVYRLZGLIKGTVARGELIKATEKKGRLSTSTRATES PPAXYRLZGLISCALCNTTPVKSELLIMGTVALGEDEERGERGG GRKROLASKYLVERNOSTOLOGERGLERGKOTTONGALIKATILTINAV LILLSLALDPGCFGLDPGFTNDPFSTNEPP APIIPHSGSIEKAELHERVVERRENTARALPEGFF			1	APAKLQVQKILCDLLLPENLKEGLKESSWSSLPCTKNRPFDFHS				
MPAREDCLKRVSSEPVLSVOGKGULLKRISLIEGOVIVWEDGR NKLKKGGETPBVCVMFSLATVGDIFEBLIDVSCLCMLIFER PVTTPCGHSFCNCLERCLDHAPYCCPLCKSSLKRYLARDRYCYT OLLEELIVYLYLDELSERSKYLYDETAGLSLKTKNVPTFVCTMA YPTVPCPLHVFEPBYRTMTRSIGTOTKOFGMCVSDTONSFADY GCMCJINNVHFLPGGRSVVDTVGGKRFRVLKKGMCDGYCTADIE YLEDY 6288 1 743 VTILYFCGUVGNLLLGASGMASGCKIGFSILNSDLANLGAECLR MLDSGADVHLLDVWDGHFVPNITTGGHPVVSSLKKQLGGDFFFM HMWSKPEGWWKPMAVAGANGYTFHLEATENGGALIKDIERKGM. KVGLAIKPGTSVEVLAPWANGJUDALLVMTVSGKARAMIVSGSAIM RSEDPRSVILLRNVCSERAGKRSLDR RSEDPRSVILLRNVCSERAGKRSLDR RSEDPRSVILLRNVCSERAGKRSLDR RSEDPRSVILLLRNVCSERAGKRSLDR RSEDPRSVILLLRNVCSERAGKRSLDR RSEDPRSVILLLRNVCSERAGKRSLDR RSEDPRSVILLLRNVCSERAGKRSLDR RSEDPRSVILLLRNVCSERAGKRSLDR RSEDPRSVILLLRNVCSERAGKRSLDR RSEDPRSVILLLRNVCSERAGKRSLDR RSEDPRSVILLLRNVCSERAGKRSLDR RSEDPRSVILLLRNVCSERAGKRSLDR RKUGAIRFOTSFELDIE SVDGGUGPDTVHKCARGAGAMIVSGSAIM RSEDPRSVILLLRNVCSERAGKRSLDR RVGIAIRFOTSFELDIE SVDGGUGPDTVHKCARGAGAMIVSGSAIM RSEDPRSVILLLRNVCSERAGKRSLDR RVGIAIRFOTSFELDIE SVDGGUGPDTVHKARGAGAMIVSGSAIM RSEDPRSVILLLRNVCSERAGKRSLDR RVGIAIRFOTSFELDIE SVDGGUGPDTVHKARGAGAMIVSGSAIM RSEDPRSVILLLRNVCSERAGKRSLDR RVGIAIRFOTSFELDIE SVDGGUGPDTVHKARGAGAMIVSGSAIM RSEDPRSVILLRRNVCSERAGKRSLDR RVGIAIRFOTSFELDIE SVDGGUGPDTVHKARGAGAMITSGSKS DITRESSFTSADITTGGRSTSFEGSSFFRWGGELD QNATEKVQTMTTADBLLYEQKSAVATHSIQGEROSTIFGIR RKLHFSSSYAHKASS IAKSSSCSMERBERDS I TUSEGI IEEY LÄPPHDIE EGFFRKYSERAFRKKGLGVPPIGVKREDULAY VPDSVCKVUSCMEQLITSSHMEGFASDESNVAVTRDDESSSCV LSEHHPLULPSFOKDSTVATTSSPMSLCOASFTVKGMEDULAY VPDSVCKVUSCMEQLITSSHMEGFASDESNVAVTRDDESSSCV LSEHHPLULPSFOKDSTVATTSSPMSLCOASFTVATTPOPOCPST RSSSTTUGSFORMSTOFFILDT QYRRSCAVEYPHQARPORGSAGPQURKLLDEPTPREVERSULLEGE RVPVAPDSLSSPSPTDGGRSLDLOPTPREVERSULLEGE RROADSKYLDDOCREALLEDPTPREVERSULLEGEGG GERKROADSKYLDDOCREALLEDPTSTVEPVGFTHLDF RATTSFELDAGGEGGEGGEGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			VMEESQSLNEPSPKQSEEIPEVTSEPVKGSLNRAQSAQSINSTE				
PUTTECHSTCKNCLERCLDHAPYCPLCKESLKEVLADRRYCUT OLIEBLI VKLYDEDLISREKKI YIDEBTARLIKAWPI PYCTMA YPTVPCCHAVFERPRILMIRRS 1070TKQFGMCVSDTONSFADY GCMLQIRNVHFLPDGRSVVDTVGKKRFTVLKRGKOGYCTADIE YLEDV 6288 1 743 VILYPCRGLVGNLILGASGNASGCKIGFSILNSDLANLGAECLR MLDSGADYLHLDVMDGHVPNTTFGHPVVSLRKQLGQDPFFDM HMWSKBEQWXFPMAVAGANQYTFHLRATENPGALIKDIRENGH KWGLAINFOTSVEYLAPMAQICDMALWTFEPGFGGCKFMEDM PKVHMLRTOFFSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM SEEDPRSVINLLRANVCSEAAQKRSLDR 6289 1 743 VILYPCRGLVGNLLLGASGNASGCKIGFSILNSDLANLGAECLR MLDSGADYHLHDVHDGHVPNTTTFGHPVVSLRKQLGQDFFFDM HMWSKBEQWXFPMAVAGANQYTFHLRATENGALIKDIRENGM KWGLAINFOTSVEYLAPMANQIDMALWMTVERGFGGCKFMEDMM PKVHMLRTOFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM SEEDPRSVINLLRANVCSEAAQKRSLDR FVSHMLRTOFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPRSVINLRANVCSEAAQKRSLDR FVSHMLRTOFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRANCSEAAQKRSLDR FVSHMLRTOFPSLDIEVDGGVGPTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRANCSEAAQKRSLDR FVSHMLRTOFPSLDIEVDGGVGPTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRANCSEAAQKRSLDR FVSHMLRTOFPSLDIEVDGGVGPTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRANCSEAAQKRSLDR FVSHMLRTOFPSLDIEVDGAVGPTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRANCSEAAQKRSLDR FVSHMLRTOFPSLDIEVDGAVGPTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRANCSEAAQKRSLDR FVSHMLRTOFPSLDIEVDGAVGPTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRANCSEAAQKRSLDR FVSHMLRTOFSEAGARTORSUMSTANCSSAID RSEDRSVINLLRANCSEAAGKRSLDR FVSHMLRTOFFSLDIEVDGAVGFTLDGAVGRAMMINSTANCH RSCHAMMINGSAIM RSEDPRSVINLLRANCSEAAQKRSLDR RSCHAMMINGSAIMMINGSAIMMINGSAIM RSEDPRSVINLLPRUSCHGAVGAVGATUM PKVAMPSLANCH ARCHITECTUM RSCHAMMINGSAIMMINGSA	1		1	MPAREDCLKRVSSEPVLSVQEKGVLLKRKLSLLEQDVIVNEDGR				
OLLBELTYKYLPDELSERKKIYDDETABLEHLTKAVPIFOTCHMA YPTYPCELWFBEPRYRIKHIRSIOTGTGGWCSDTONSPADY GCMLQIRNVHFLPDGRSVVDTVGGKRFRVLKRGMKDGYCTADIE YLEDV 1 VILYPCGLVGNLILGASGNASGCKIGPSILNSDLANLGAECLR MLDSGADYHHLDVMDGHFVBNITFGHPVVESLRKGLGQDFFFDM HMWSKEPGWVKPMAVAGANQVTFHIERAFGALIKDIREKGM PKVHMLKTOPPSLDIE UPDGVGPDTVHKCAEAGANMIVSGSAIM RSEDDRSVINLIRNVCSEAAQKRSLDR 6289 1 743 VITLYPCRGLVGNLILGASGNASGCKIGPSILNSDLANLGAECLR MLDSGADYHHLDVMDGHFVBNITFGHPVVBSLRKGLGQDFFFDM HMWSKEPGWVKPMAVAGANQVTFHLBATENFGALIKDIRENGM KVGLAIKPGTSVEYLAPMANG IDMALWMTVEPGFGGCKFMEDMM RSEDDRSVINLIRNVCSEAAQKRSLDR 6280 1 743 VITLYPCRGLVGNLILGASGNASGCKIGFSILNSDLANLGAECLR MLDSGADYHHLDVMDGHFVBNITFGHPVVBSLRKGLGQDFFFDM HMWSKEPGWVKPMAVAGANQVTFHLBATENFGALIKDIRENGM KVGLAIKPGTSVEYLAPMANG IDMALWMTVEPGFGGCKFMEDM PKVHMLRTOFFSLDIEVDGGAVGPDTVHKCAEAGANMIVSGSAIM RSEDDRSVINLIRNVCSEAAQKRSLDR 6290 3 1856 TLGRWLLGVYETVAPTLACLFRFRLRRRRRRRMISRYTRKA VPGSLEIKGITKHALNHHPPPBKLEEISFTSDSIEKSTSOSKS DITRESSFTSADTONSISAFFSYTGAGISTEGSSDFSWGYGELD QNATEKVQTMFTATDELLVEQKLSVHTKSLQSECQOTASFPHL RILGRQIITPSEGTRLTYRSPSAVASSFTSYGGRENGENSIIVSEGIIEEY LÄPHTDILEBGFHCKKSE BAATEKKLALGPFYCVKBDVLLAY VPDSVMCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV LSEHLPLVLPREYGCKBUNLDFFTGARFYCKMEDNLLAY VPDSVMCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV LSEHLPLVLPREYGCKSUNLTFSITSMSNLCQASEHQPNVNDLLVHG MPLOPRINLSSFSSFTISHADKLADLDLOKLINGRGSTTENMWNRAVEFS TSSLSTTVQSTTRRNPPFRTHHPJSTSHSCAETFRSVESILLGD MPLOPRINLSSFSSFTISHADKLADLDLOKLANGRGSTTENMWPRAVEFS TSSLSTTVQSTTRRNPPFRTHHPJSTSHSCAETFRSVESILLDF PFAXYMRLGQLSCALCKTTVKSELMGTIVLISKQHREKVALEKG AKEASGGSSASSAPGAPGRGSAGPQLHGSTKSQSGGRPVSRTKQG PFAXYMRLGQLSCALCKTTVKSELLMGTIVLISKQHREKVALEKG AKEASGGSSASSAPGVKKAPDADDQDVKRAKATLVPQVQPST SAMTTHFFOKIGKFFTRATFSKFSGLSLLEDPEFSTEDPEFSTHPPK APILIPHSGSIERAE HERVEVRERRENTAEDEEGEEEEEGG GERKRQDASKPLSDAGCKEHSVSSSRFVTSSVLUPPSTYDPQK ARTIPHSGSIERAE HERVEVRERRENTAEDEEGEEEGG GERKRQDASKPLSDAGCKEHSVSSSRFVTSSVLUPPSTYDPDV APILIPHSGSIERAE HERVEVRERRENTAEDEEGERDD GERKRQDASKPLSDAGCKEHSVSSSRFVTSSVLUPPSTYDPDV APILIPHSGSIERAE HERVEVRERRENTAEDEFSTHPPS APILIPHSGSIERAE HERVEVRERRENTAEDEF			ĺ					
STITUTCPLHUTEBERTREMIRESIOTOTKOGGMCUSDTONSFADY GCMLQIENVHFLDGRSVUDTUGGKRFRVLKRGKDGYCTADIE YLEDV STEEDY ST	ŀ		,					
GCMLQIRNVHIPLDGRSVVDTVGGKRFRVLKRGMKDGYCTADIE VLEDV 1 VLEDV 1 VLEDV WILDSGADYLHLDVMDGHFVENITTGHEVVESLERGLGODFFFG MLDSGADYLHLDVMDGHFVENITTGHEVVESLERGLGODFFGG KVGLAIKFGTSVEYLAPMANQIDMALMMTVEBGFGGCKFMEDMM PKVHMLKTOFPSLDIEVDGGVGDFVHKCAERGANMTVSGSAIM RSEDPRSVINLLRNVCSERAQKRSLDR 743 VLTVPGELGVGNLLLGASGMASGCKIGFSILMSDLANLGAECLR MLDSGADYLHLDVMDGHFVENITTGHFVVESLRKGLGODFFDM HMWSKPEGWWXFMAVAGANGYTFHLEATEMFGGALIKDILRANLGAECLR MLDSGADYLHLDVMDGHFVENITTGHFVVESLRKGLGODFFDM HMWSKPEGWWXFMAVAGANGYTFHLEATEMFGGALIKDILRANLGAECLR KVGLAIKFGTSVEYLAPMANQIDMALVMFDGFGGGKFMEDMM PKVHMLKTOFFSLDIEVDGGVGPDTVHKCAERGANMIVSGSAIM RSEDPRSVINLLRNVCSERAQKSLDR 6290 3 1856 TLGRWLLGVYETVAFFLACLFFFELRERFRRRRFRISKYTKKA WPOSLELKGITKHALNHHPPPBKLEEISFTSDSHEKDTSSQKS DITRESSFTSADTGNSLAAFFSTTGAGISTEGSSDFSMGYGGLD ONATEKVQTMFTAIDELLYEGKLSVHTKSLGEECQWTASFPHL RILGRGITTFSSGYALYFRSPSAVASSTILOGENGSTIFGS GKKLHFSSSYAHKASSIAKSSSFCSMERDREDSITVSEGILES LÄPPHILDIBEGFHGKKSKAATHEKUKSPTLAPVAMKEDVLAY VFDSVMCKVVSCMEQLTRSHMEGFASDDESSVAVTRPDEBSSCV LSEHLPLVLDRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHM MPLQPRNLSLMDKLLDLDDLKLIMRPGSSTILSTRNNFNRAVEFS TSSLSTTVQSTRRRNPPPRTHHFISTSHSCETFRSVEEILRGA RVFVADPSLSSSPSTPTSSRNLLPPIGTABEWHSVTVGRORM PHGDSRRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTGSFLLDT QYRRSCAVEYPHQAPSLSSSPSTPTSSNLLPDFFSRFRRGE PFRKYMRLGQLSCALCKTPVKSELLMGCHVLIKGKHEKKVAELKG AKEAGGSSASSAPQSVKRRAPDADDQDVKRAKATLVPCVQPST SAMTTAFDKIGGET FRATTPS KYPGGLIDPFDEFEREEBEEGG GERRGDASKPLSDAGKEHSVSSSREVTSSVLPNDFFSTMPFK RKUDAPKDQMKEMDEFQKAMRQVNTISEAIVABEDEERGRIDRQ IGEIDEQIECYRRVEKLRNRQDSIKNKLKEILTIKELKKKEER ABSDBBGGLQLLSQDWKKGALL LICAMATYGAVKQRAAMITPFCYQIFPPALMMLVAITVLLYDM SLOWNCYRYINGRNSDVLVVTNSDNTVLLPPYDDATVNGA AKBPPPPTVSA 6293 2382 1035 FWEUCHDVYFIGWCAINSKILVPPRTHAKFTDMKGYLMKKL			į					
1		,		YPTVPCPLHVFEPRYRLMIRRSIQTGTKQFGMCVSDTQNSFADY				
1								
MLDSGADYLHLDVMGGHVVBTITGGHVVESLRKQLGQOPFFDM HMWSKPGQWXFMAVAGANGYTFHLEATENFEALIGDTRENGM KVGLAIKPGTSVEYLAPMANQIDMALWTVBEGFGGQKFMEDM PEVHWLRTGPPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRNUCSEAAQKRSLD 6289 1 743 VTLYPCRGLVGNLLLGASGMASGCKIGFSILNSDLANLGAECLR MLDSGADYLHLDVMDGHFVPNITTGHFVVESLRGLGODPFFDM KVGLAIKPGTSVEYLAPMANQIDMALWTVBEGFGGQKFMEDMM PKVWINLKTOPPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRNUCSEAAQKRSLDR 6290 3 1856 TLGRWLIGVYETVAPHANQIDMALWTVSBGGGGKFMEDMM RYCWINLKTOPPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRNUCSEAAQKRSLDR 6290 4 TLGRWLIGVYETVAPTLACLFFRPRIRRRRRRRMISRYTRKA VPQSLELKGITKHALNHHPPBHKLEISFTSDSHEKUTSSOSKS DITRESSFTSADTGMSLSAFPSYTGAGISTEGSSDFSWGYGELD ONATEKVQTMFTAIDELIFSKUSLYBLGBECQWTASSPHL RILGRQIITPSRGYRLYPRSPSAVSASYETTLSOBRDSTIPGIR GKKLHFSSSYAHKASSIAKSSPCSMRRDEDSIIVSEGFIGEV LÄFPHIDIEGFHGKKSEAATEKQKLGVPPTAFFYCMKEDVLAY VFDSVMCKVVSCMCQLTTSSHMEGFASDDESSMVATERDSEBSSI GKKLHFSSSYAHKASSIAKSSPCSMRRDEDSIIVSEGTIEEY LÄFPHIDIEGFHGKKSEAATEKQKLGVPPTAFFYCMKEDVLAY VFDSVMCKVVSCMCQLTTSSHMEGFASDDESSMVATERDSEBST TSSLSTYVGSTRRNIPPPRTHHEISTSHSCAETPRSVEEILEGA RVPVAPDSLGSSPJPPLSRNNLLPPIGTAEVEHVSTVGPQRQMK PHGDSSRAQSAVVEPPYQCPPSRLLLLDFFFRPNTIOSFILDT GYRRSCAVAVEPHQAPPGRGSAGPQLUGSTKSQGGRPVSRTRQG PHGDSSRAQSAVVEPPYQCPPSRLLLDFFFRPNTIOSFILDT QYRRSCAVEYPHQARPGRGSAGPQLUGSTKSQGGRPVSRTRQG PFAXVRLGQLSCALCNTPVKSRLLMQTHVLIGKQHREKVARLKG AKEASQGSSASAPQSVKRKAPDADDQDVKRAKKATLVPQVQPST SAMTTHFDKIGKEFIRATPSKPSIGSLLPOYEDEEEEEEEEEGG GERKRGDASKPLISDAQCKEHSVSSSREVTSSVLIPNDFFSTMPFN RKVDAPKDQMKEMDEFQKAMRQVNTISSATVAREDEGGRLDRQ IGEIDEGI CYRRVEKLRNQDEIKNKLKEILTIKELQKKEEN ADSDDBGELQDLLSQDMRVKGALL LICAMATYGAVKQRAAMITPFCVQIFPFDADANCITAIAISLIMI LICAMATYGAYKQRAAMITPFCVQIFPFDADANCITAIAISLIMI LICAMATYGAYKQRAAMITPFCVQIFPFDADANCITAIAISLIMI LICAMATYGAYKQRAAMITPFCVQIFPFDADANCITAIAISLIMI LICAMATYGAYKQRAAMITPFTCVQIFFTPADATVNAA AKBPPPPVVSA 6293 2382 1035 FWCTLGTVDVHFIGWCAINSKILVPPRTHAKFTDMKGYLMKKL	6288	1	7/12					
HMMVSKPEGWWKPMAVAGANQTTFHLRATENPGALIKDITENGEM KVGLAIKPGTSVEYLAPWANQIDMIAUTVEYPEGGGKFMEDMM PKVHWLRTQFPSLDIEVDGVGPDTVHKCAEAGANNIVSGSAIM RSEDPRSVINLLENVCSEAAQKRSLDR 743 VTLTYCRGLVGNLLLGAGSMASGCKIGFSILMSDLANLGAECLR MLDSGADYLHLDWADGHFVPNTTFGHPVVSSLKQLGQDPFPDM HMMVSKPEGWWKPMAVAGANQYTFHLEATENPGALIKDIRENGM KVGLAIKPGTSVEYLAPWANQIDMALWATVEPGFGGKRMEDMM PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANNIVSGSAIM RSEDPRSVINLLENVCSEAAQKRSLDR 6290 3 1856 TLGRRLLGVVETVAPPLACLEPPELRRERRERRISRYTKAA VPQSLELKGITKHALNHHPPPEKLEEISPTSDSHEKDTSSGKS DITRESSFTSADTGNSLSAFPSYTJAGGISTEGSSDFSWGYGELD QNATEKVQTMFTAIDELLYEQKLSVHTMSLQBECQCWTASFPHL RILGRQITTPSEGVERLYPRSPSAVSTTLAGGERGDTIFGGIR GKKLHFSSSVAHKASSIAKSSSFCSMERDREDSIIVSGIIESY LÄPPHIDIEBGFHGKKSEAATEKQKLGVPJAPFYCMKEDDLAY VPDSVWCKVVSCWEQLTRSHWBGFASDDESNVAVTRPDSESSCV LSELHPLVLPRVPQSKVLYITSNPMSLCQARRQPNVNNLHVHG MPLOPRINLSIMDKLLDLDKLLIMPRGSSTILGTRNMPNRAVEFS TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA RVVAPDSLSSPSPTPLERNNLLPPIGTAREWHSTVCPGQRMK PHGDSSRAGSAVVDEPNYQQPCERLLLPDFFPRPMTTYSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKKQSGGRPVSRTRQG PHGDSSRAGSAVVDEPNYQGPCERLLLPDFFPRPMTTYSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKKSGSGRPVSRTRQG PFRYNNLGJSCALCNTPVKSELLULPKGRREKVARLKG AKEASGASSASSAPGSVKKARPDDOWKRAKATLVPQVQPST SAMTTNEDKIIGKEFTRATPSKPSGLSLLLPDFEREEBEEBEGD GERKRGDASKPLSDAGCKEHVSSSREVTSSVLPNDFFSTNPPK AKEAGGSASSASAPGAGKHEVSSSSREVTSSVLPNDFFSTNPPK RVDAPBGSIEKAEIHEKVVBRRENTAEALPEGFFDDPEVDARV RKVDAPRDQMDKEWDEFÇKAMRQVNTISEAIVAEEDEEGRILDRQ GERKRGDASKPLSDAGCKEHVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVBRRENTAEALPEGFFDDPEVDARV RKVDAPRDQMDKEWDEFCKAMRQVNTISEAIVAEEDEEGRILDRQ GERKRGDASKPLSDAGCKEHVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVBRRENTAEALPEGFFDDPEVDARV RKVDAPRDQWDKWBEFCKAMRQVNTISEAIVAEEDEEGRILDRQ GERKRGDASKPLSDAGCKEHVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVBRRENTAEALPEGFFDDPEVDARV RKVDAPRTRFYSNSCCLCCHVRTGTILLGWYLIINAVV LLILLSSALADPPQTYSASSELGGGFFFFMDDAMMCIAIAISLLMI LICAMATYGAYRQRAAWIIPFFCVOIEDFAMMLVAITVLITYN SIGNYTRGLPPPPPFYRDDVMSVMPTCLVLIILIPSILLTFKGV LICAMATYGAYRQRAAWIIPFFCVOIEDFAMMLVAITVLITYN SIGNYTRGLPPPPPTYSAA		· -	/ 73	MIDSGADVI.HI.DVMDGHEVIDNITTEGUDVGESI BYOT CORRESPONDENCE				
KVGLAIRPGTSVEYLAPWANQIDMALWHTVEPGFGGQKFMEDMM PEVHILARTOPPSIDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPRSVIMLLENVCSEAQKRSLDR 743 VTLYPCRGLVGNLLLGASGMASGCKIGFSILMSDLANLGAECLR MLDSGADYLHLDWUDGHFVPNITFGHPVUSSLKRQLGOPPFDM HMWSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM KVGLAIRPGTSVEYLAPWANQIDMALWHTVEPGFGGQKFMEDMM PRVSWILMENTOPPSIDIEVDGGVGPDTVHKCAEAGANNIVSGSAIM RSEDPRSVINLLENVCSEAAQKRSLDR 6290 3 1856 TLGRWLLGVYETVAPTLACLFRPRLRRRRRRRRMISRYTKA VPQSLELKGITKHALMHHPPPEKLEEISPTSDEHERDTSSQSKS DITRESSFTSADTGNSLSAFFSYTDAGISTFGSSDPSWGYGELD QNATEKVQTMFTAIDELLYEOKLSVHTKSLQEECQWTASFPHL RILGRQIITPSEGYRLYPRSPSAVSASYETTLSQERDSTIPGIR GKKLHFSSSYAKKASIAKSSFCSMKRDBESIIVSRGILERY LÄPPHIDIEBGFHGKKSEAATEKQKLGYPPIAPFYGMKEDVLAY VPDSVMCKVVSCMEQLTRSHWBGFASDDESNIVVTEPDSESSCV LSELHPLVLPRVPOSKVLVITSNIPMSLCQASRRQPNVDLLVHG MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRWPRRAVEFS TSSLSYTVQSTRRRNPPPRTTHPISTSHSCAETPRSVEEILRGA RVFVAPPDSLSSSPSTPLSRNNLLPPIGTAEVENSYTVGPRGNK PHGDSSRAQSAVDENTVQOPCERLLLPDFFPPPTTTGSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGRPVSRTRQG PAFAYNRLGGLSCALCNTPVKSELLMQTHVLGKGHEKVALKG AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAMTINFDKLGKEFIRATPSKPSGLSLLDPYEDEEEREEBEEGD GERKRGDASKPLSDAGGKBEVSVSEYTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHERVVERRENTAEALPEGFFDDBEUDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVABEDEEGRLEDRQ IGEIDEQIECYRRVEKLRNRQDEINNLKSILTILELQKKEECH ADSDBGSELQDLLSQDMRVKGALL LICHMATYGAYKQRAAMIIPFFCVQIFDFALMMJVAITVLIYPN SIGEYIRQLPPMFPFYSNSCCLCLOFVRTGTILLGVWYLLTINAVV LLILLSALADPDQVNFSSSELGGDFFFMDDAMMCTATAISLLMI LICAMATYGAYKQRAAMIIPFFCVQIFDFALMMJVAITVLIYPN SIGEYIRQLPPMFPYSDNSCUCLOFVRTGTILLGVWYLLTINAVV LLILLSALADPDQVNFSSSELGGDFFFMDDAMMCTATAISLLMI LICAMATYGAYKQRAAMIIPFFCVQIFDFALMMJVAITVLIYPN SIGEYIRQLPPMFPYSDNSCUCLOFVRTGTILLGVWYLLTINAVV LLILLSALADPDQVNFSSSELGGDFFFMDDAMMCTATAISLLMI LICAMATYGAYKQRAAMIIPFFCVQIFDFALMMJVAITVLIYPN SIGEYIRQLPPMFPYRDDVMSVMPTCLVLIILIFISILLTPKGY LISCVMCVRYTINGRNSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA		1		HMMVSKPEOWVKPMAVAGANOVTEHT.RATENDEAT.TENTERVON				
PRVHILITOFPSILDIEUDGGUGPDTUKCAEAGANMIVSGSAIM RSEDPRSVINILIRNYCSEAAQKRSLDR 1 743 VTLYPCRGLVGNLLIGASGRAGGKIGPSILNSDLANLGAECLR MLDSGADYLHLDVMDGHFVPN1TTGHFVVSLIRKQLGGDFFDM HMMVSKEDGWVKPMAVAGANGYTHLEATENPGALIKDIRRNGM KVGLAIKPGTSVEVLAPMANQIDMALUMTVEPGFGGQKFMEDMM PKVHWLRTOFPSLDIEUDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPRSVINILIRNVCSEAAQKRSLDR 6290 3 1856 TLGRWLLGVYETVAPTLACLFPFPLRRRRRRRRMISRYTRKA VPQSLELKGITKHALNHHPPPENLERISPYSDSHEKDTSSQSKS DITRESSFTSADTGNSLSAFPSYTGAGISTEGSSDFSWGYGELD QNATEKVQTMFTAIDELLYEQKLSVHTKSLGEECQGWTASFPHL RILGRQIITPSEGFWLYPRSPSAVSASYETTLSQREDSTIFGIR GKKLHFSSSYAHRASSIAKSSSCSWERDEEDSIIVSEGILEEY LÄPPHIDIEGGFHKKSEAATHRGSSTLSTRIWPRAAVES GKKLHFSSSYAHRASSIAKSSSCOMERDEEDSIIVSEGILEEY LÄPPHIDIEGGFHKKSEAATHRGSSTLISTRIWPRAAVES TSSLSYTVQSTRRRNPPPSTEGSSTLTSTRIWPRAAVES TSSLSYTVQSTRRRNPPPSTEGSSTLTSTRIWPRAAVES TSSLSYTVQSTRRRNPPPRTHPISTSHSCASTPRSVEEILRGA RVPVADPSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK PHGDSSRAQSAVVDENNYQOPERKLLLEPFFRPNTTQSFLLDT QYRRSCAVEYPHQARPGRGSAGFQLHGSTKSQSGGRPVSRTRQG PFAKYNALPGLSCALCNTPVKSELLWQTHVUGKQHREKVAELKS AKEASGGSSASSAPQSVKREAPDADDQDVKRAKATLVPQVQPST SAMTTNPDKIGKEFIRATPSKPSGSLSLLPDVEDEEBEEBEEG GERKRGDASKPLSDAQGKEBEYSKENTSSWLPDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKGDAGKEBYSKENTSSWLPDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKGDMKWVAPWTRFYSNSCCLCCHVRTGTILLGVWYLITINAVV LLILLSSLADPDQTNFSSSELGGDFEFMDDANMCIALAISLIMI LICMATYGAYKQRAAWIIPFFCYQIFPALMMUVAITVLIYPN SIGBSTRQLFPRPSYNSCCLCCHVRTGTILLGVWYLITINAVV LLILLASALADPDQTNFSSSELGGDFEFMDDANMCIALAISLIMI LICMATTGAYKQRAAWIIPFFCYQIFPALMMUVAITVLIYPN SIGBSTRQLPPRPSYNSCCLCCHVRTGTILLGVWYLITINAVV LLILLASALADPDQTNFSSSELGGDFEFMDDANMCIALAILSLIMI LICMATGAYKQRAAWIIPFTCOLLIILLISIILLTFKGY LISCVUNCYRYINGRNSSDVLVYVTSNDTTVLLIPPDDATVNGA AKEPPPPYVSA AKEPPPPYVSA FWCTLGTVDVHFIGWCAINSKILVPPRTHAKFTDWKGYLMKRL				KVGLAIKPGTSVEYLAPWANOIDMALVMTVRDGEGGOKEMEDMM				
RSEDPRSVINILIRNVCSEAAQKRSLDR VTLYPCRGLVGNLLIGASGMASGCKIGFSILNSDLANLGAECLR MLDSGADYLHLIDVMDGHFVPNITTGHPVVBSLRKQLGQDPFFDM HMWYSKPEQWYKPMAVAGANQYTFHLEATHPGALIKDIRENGM KVGLAIRPGTSVEYLAPMANQIDMALVMTVBPGPGQKFMEDMM PKVHWLRTQFPSLDIEVDGGVGPDTVHKCARAGANMIVSGSAIM RSEDPRSVINILRNVCSEAAQKRSLDR 6290 3 1856 TIGGRULGVYBTVAPTLACLPFPPLRRRRRRRRMISRYTRKA VPQSLELKGITKHALNHHPPPBKLEEISPTSDSHEKDTSSQSKS DITRESSFTSADTGNSLSAFPSYTGEBECOGWTASFPHL RILGRQIITPSEGGRLYPRSPSAVSASYSTILSQBRDSTIFGIR GKKLHFSSSYAHARSSIAKSSSFCSMERDEEDS ITVSEGILEEY LÄPPHIDIEBGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY VPDSVWCKVVSCMEQLTRSHWEFFASDEDSNVAVTRPDSESSCV VPDSVWCKVVSCMEQLTRSHWEFFASDESNVAVTRPDSESSCV VPDSVWCKVVSCMEQLTRSHWEFFASDESNVAVTRPDSESSCV VPDSVWCKVVSCMEQLTRSHWEFFASDESNVAVTRPDSESSCV VPDSVWCKVVSCMEQLTRSHWEFFASDESNVAVTRPDSESSCV VPDSVWCKVVSCMEQLTRSHWEFFASDESNVAVTRPDSESSCV VPDSVWCKVVSCMEQLTRSHWEFFASDESNVAVTRPDSESSCV VPDSVWCKVVSCMEQLTRSHWEFFASDESNVAVTRPDSESSCV VPDSVWCKVVSCMEQLTRSHWEFFASDESNVAVTRPDSESSCV VPDSVWCKVVSCMEQLTRSHWEFFASDESNVAVTRPDSESSCV VPDSVWCKVVSCMEQLTRSHWEFFASDESNVAVTRPDSESSCV VPDSVWCKVVSCMEQLTRSHWEFFASDESNVAVTRPDSESSCV VPDSVWCKVVSCMEQLTRSHWEFFASDESNVAVTRPDSESSCV VPDSVWCKVVSCMEQLTRSHWEFFASDESSTLUTH MPLQPRNLSLMDKLLDDBKLARPGSTILSTRWPPRRAVEFS TSSLSYTVQSTRRRNPPRSVEETLINGA RVPVAPDSLSSPSPTLLSRNNLLPFIGTAEVHVSTVGPQRMK PHGDSSRAQSAVVDEPNYQQPQBRLLLPPFFRPNTTIGSFLLDT QYRRSCAVEYPHQARPGRGSAGGPUSKTSVGSGRPVSRTRQE RVPVAPPSLSSPSPTLLSRNNLLPFIGTAEVHVSFLLWGRAFKRIES SAMTTNFDKLIGGLSCALCNTTPVKSELLWQTHVLGKQHREKVARLKS AKEASQGSSASSAPQSVKRKAPDADDQDVRAKATLVPQVQPST SAMTTNFDKLIGGLSCALCNTTPVKSELLWQTHVLGKQHREKVARLKG GERRGDASKPLSDAQKEMESVSSSEEVTSSVLURDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAELPGGFFDDPEVDARV RVDDAPRDQMDKEWDEFFCRMRQVNTISRALVBEDEEGRLDRQ GERRGDASKPLSDAQKEWSSVSSSEVTSSVLURDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAELPGGFFDDPEVDARV RVDDAPRDQMDKFFTFFSNSGCLCCHVFTGTILLGVWYLITNAVV LLILLSALADPDQYNFSSSELGGDFFFMDDANMCIALISLLMI LICMATTGAYKQRAMIIPFFCYQIFPALMMLVAITVLIYPN SIGBYIRQLPPPNFYFYSNAGCLCCHVFTOTILLGVWYLITNAVV LISCVMNCTRYINGRNSSDVLVYVTSNDTTVLLIPPJDDATVNGA LISCVMNCTRYINGRNSSDVLVYVTSNDTTVLLIPPJDDATVN	1							
MLDSGADYIHLDVMDGHFVPRITFGHPVVBSLRKQLGQDPFFDM HMVSKPRQWVKPMAVAGGNQYTFHLEATENFGALIKDIRENGM KVGLAIKPGTSVEYLAPMANQIDMALVMTVBGFGGQKFMEDMM PKVHNLRTOFPSLDIEVDGGVGPDTVHKCABAGANMIVSGSAIM RSEDPRSVINLLRANVCSBAAQKRSLDR 6290 3 1856 TLGRMLLGVYBTVAPTLACLFRPRLRRRRRRRRRISRYTRKA VPQSLELKGITKHALNHHPPPBKLBEIGFTSDSHEKDTSSQSKS DITRESSFTSADTGNSLSAFPSYTGAGISTEGSDFSWGYGGLD QNATEKVQTMTTALDELLYBCKLSVHTKSLGEECQQWTASFPHL RILGRQIITPSEGYRLYPRSPSAVSASYETTLSGERDSTIFGIR GKKLHFSSSYAHKASSIAKSSFCSMERDREDSIIVSGRDSTIFGIR GKKLHFSSSYAHKASSIAKSSFCSMERDREDSIIVSGRDSTIFGIR LAPDHIDIEGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY VPDSVWCKVVSCMEQLITRSHWEGFASDDESNVAVTRDSESSCV LSELHPLVLPRVPQSKVLYITSNDMSLCQASRHQPNVNDLLVHG MPLQPRILSIAMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA RVPVAPDSLSSPSTPDLSRNNLLPPIGTAEVEHVSTTGPGRQMK PHGDSSRAQSAVVDEPNYQQPQERLILLDFFFPRNTTQSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGRPVSRTRQG P 6291 1732 602 LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSKRIES FFAKYNRLGQLSCALCNTPYKSELLWOTHVLGKGHREKVAELKG AKEASQGSSASSAPQSVKRKAPDADQDVKRAKATLVPQVQPST SAWTTNFDKLIGKEFIRATPSKPSGLSLLMPTHPLGEBEBEBEBEEG GERKGDASKPLSDAQCKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKABIHEKVVERRRNTABALPEGFFDDPEDDARY RKVDAPROQMDKEMDEFQKAMRQVNTISEAIVABEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKBLQKKBEEN ADSDDBGELQDLLSQDWRVKGALL LICMMATYGAYKQRAAMIIPFFCVGIEPPALNMLVAITVLIYPN LILLLSALADPDQYNFSSSELGGDFFFMDDANMCIAIAISLLMI LICMMATYGAYKQRAAMIIPFFCVGIEPPALNMLVAITVLIYPN SIQEYIRQLPPMPYYRODAWSVPBTCLVLILLIFFISITIFKGY LICCMMCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVUPPFGWCAINSKILVPPRTHAKFTDWKGYLMKRL	1							
MLDSGADYLHLDVMDGHFVPNTTFGHPVVBSLRKQLGODPFFDM HMWVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM KWGLAIRFGTSVEYLAPMANQIDMALWTVYBFGFGGGKPMEDMM PKVHMLRTQFPSLDIEVDGGVGPDTVHKCABAGAMMIVSGSAIM RSEDPRSVINLIRMVCSEAAQKRSLDR 6290 3 1856 TLGRWLLGVYETVAPTLACLFRFRLRRRRRRRRRRSTRYTKA VPQSLELKGITKHALNHHPPPBKLEEIGPTGDSHEKDTSSGSKS DITRESSFTSADTORSLSAFSYTGAGISTEGSSDFSWGYGELD QNATEKVQTMFTAIDELLYEQKLSVHTKSLQEECQQWTASFPHL RILGRQIITPSEGYRALYRRSPSAVSASYETTLSQERDSTIFGIR GKKHHFSSSYAHKASSIAKSSFCSMFRDBEBSIIVSEGILEV LÄFPHIDIEBGFHGKKSEAATEKQELGYPTAPFYCMKEDVLAY VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV LSELHPLVLPRVPQSKVLYITSNDMSLCQASRHQPNVNDLLVHG MPLQPRILSLMDKLLDLDDKLLMRFGSSTILSTRNWPNRAVEFS TSSLSYTVQSTRRNPPPFRTHJFSTSHSCAETPRSVEEILRGA RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPGRQMK PHGDSRRAQSAVVDEPBYQQPQERLLLEDFFFPRNTTQSTLLDT QYRRSCAVETPHQARPGRGSAGPQLHGSTKSQSGRPVSRTRQG P 6291 1732 602 IVAKMASSASATPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFARYNELGGLSCALCNTPVKSELLWGTHVLGKGHREKVAELKS AKEASQGSSASSAPQSVKRKAPDADDDVKRAKATLVPQVQPST SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEGD GERKRGDASKPLSDAQCKEHSVSSSREVTSSVLENNDFFSTNPK APIIPHSGSIEKABIHEKVVERRENTABALPEGFFDDPEVDARV RVVDAPKDQMDKENDEFGKAMRQVNTISEALVAEEDEEGLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDBGELQDLLSQDWRVKGALL LICMMATYGAYKQRAAMIIPFFCVGIFDFALNNLVAITVLIYPN LLILLSALADPDQYNFSSSELGGDFEFMDDANNCIAIAISLLMI LICMMATYGAYKQRAAMIIPFFCVGIFDFALNNLVAITVLIYPN SIQEYIRQLPPMPYYBOAWSVNPTCLVLILLIFISITLIFKGY LICMMATYGAYKQRAAMIIPFFCVGIFDFALNNLVAITVLIYPN SIQEYIRQLPPMPYYBOAWSVNPTCLVLILLIFISITLIFKGY LICCMMCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVVPPFTHAKKFTDWKGYLMKKL	6289	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR				
KVGLAİKPGTSVEYLAPWANQIDMALVMTVEPGGGQKFMEDMM PKVHWLRTQFPSLDI EVDGGVPDTVHKCAEAGAMMIVSGSAİM RSEDPRSVINLLRNVCSEAAQKRSLDR TIGRWLLGVYETVAPTLACLPRPRLRRRRRRRRMISRYTRKA VPQSLELKGITKHALNHHPPPBKLEBISPTSDEHEKDTSSQSKS DITRESSFTSADTGNSLSAFPSVTGAGISTEGSSDFSWGYGELD QNATEKVQTMFTAIDELLYEQKLSVHTKSLQEECQQWTASFPHL RILGRQIITPSEGYRLYPRSPSAVASASYETTLSQERDSTIFGIR GKKLHFSSSYAKKASS IAKSSSFCSMERDEBGI IVSEGILEEY LÄPPHIDIEGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTREDSESSCV LSECHHPLVLPRVPQSKVLYITSRPMSLCQASRRQPNVDDLLVHG MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS TSSLSYTVQSTRRRNPPPRTLHFISTHSCAETFRSVEEILLRGA RVPVAPDSLSSPSPTPLSRNNLLPPIGTAFVEHVSTVEPQRQMK PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT QYRRSCAVEYPHQARPGRGSAGFQLHGSTKSQSGGRPVSRTRGG P 6291 1732 602 LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFARYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASAPQSKKAPDADDQDWKRAKATLVPQVQPST SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEEGD GERKRGDASKPLSDAQGKSHSVSSSEVTSSVLPNDFFSTNPK APIIPHGSGISKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEALVAEEDEEGRLDRQ IGEIDEQIECTRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELDLLSQDMVKGALL 6292 1835 1142 TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLTINAVV LLILLSALADPDQVNFSSSELGGDFFFMDDANNCIAIATSLLMI LICAMATYGAYKQRAAWII PFFCYQIFDPALMMLVAITVLIYPN SIGEYIRQLPNPFPYRDDVMSVNPTCLVLIILLFISILLTFKGY LISCVMNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLCTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL	1	1		MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM				
PKVHNLRTOFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRNVCSEAAGKRSLDR 1856 TLGWLLGVYETVAPTLACLFRPRERRRRRRRRRRSTRTKRA VPQSLELKGITKHALMHHPPPBKLEEISPTSDSHEKDTSSQSKS DITRESSFTSADTGNSLSAFPSYTGAGISTEGSSDFSWGVGELD QNATEKVQTMFTAIDELLVEQKLSVHTKSLQEECQOWTASFPHL RILGRQITTPSEGYRLYPRSPSAVSASYETTLSQERDSTIFGIR GKKLHFSSSYAHKASSIAKSSPCSMERDEEDSIIVSEGIIEEY LÄPDHIDIEEGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY VPDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG MPLQPRNLSLMDKLLLDLDKLLMRPGSSTILSTRNWPNRAVEFS TSSLSYTVQSTRRRNPPPRTLHFISTSHSCAETPRSVEETLIRGA RVPVAPDSLSSPPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK PHGDSRRAQSAVVDEPNYQOPGERLLLPDFFPRPNTTQSFLLDT QYRRSCAVEYPHQARPGRGSAGFQLHGSTKSQSGGRPVSRTRQG P 6291 1732 602 LVAKMASSASATPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFAKYNRLGQLSCALCNTPVKSELLMQTHVLGKQHREKVAELKS AKEASQGSSASAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAMTTNFDKIGKEFIRATFSKPSGLSLLPDYEDEEBEEEEEEEGD GERKRGDASKPLSDAQGKEHSVSSSEVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEMDEFQKAMMQVNTISBAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKBEEN ADSDDGGELQDLLSQDMRVKGALL 6292 1835 1142 TCPGAMKMVAFWTRFYSNSCCLCCHVRTGTILLGVWYLTINAVV LLILLISLIADPDQ VNFSSSELGGDFFMDDANNCIAIAISLIMI LICAMATYGAYKQRAAMII FFCYQI FDFALMMLVAITVLIYPN SIGBYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISILLTFKGY LISCVMNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLCTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL				HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM				
RSEDPRSVINLLENVCSEAAQKRSLDR 1856 TLGRWLLGVYETVAPTLACLFRPRLRRRRRRRRRRRSYTKA VPQSLELKGITKHALMHHPPPBKLEEISPTSDSHEKDTSSQSKS DITRESSFTSADTGNSLSAFPSYTGAGISTEGSSDFSWGYGELD QNATEKVQTMFTALDELLYEQKLSVHTKSLQEECQQWTASFPHL RILGRQITTPSEGYRLIYPRSPSAVSASYETTLSQERDSTIFGIR GKKLHFSSSYAHKASSIAKSSSPCSMERDEEDSIIVSEGILEY LÄPDHIDIEEGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY VPDSWCKKVVSCMEQLITSHWEGFASDDESNAVATPSDESSCV LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG MPLQPRNLSLMDKLLDLDDKLLMFPGSSTILSTRNWFNRAVEFS TSSLSYTVQSTRRRNPPPTHFHISTSHSCAETPRSVEEILRGA RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGEQRQMK PHGDSSRAQSAVVDEPNYQQPQERLLIPDFFPRPNTTOSSILDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRGE PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTNFPKIGKEFIRATPSKPSGLSLLPDYEDEBEEEEEEEGD GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHGSIEKABIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMMKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDPGIECYRRVEKLRNRQDEINKLKEILITIKELQKKEEEN ADSDDEGELQDLLSQDMRVKGALL 6292 1835 1142 TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQVTNFSSSELGGDFFMDDANNCIAIAISLLMI LICAMATYGAKKQRAWIIPFFCYQIFDPALMVLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCVLVIIILLFISIILTFKGY LISCUMCYRYINGRNSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL	1			KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM				
1856 TLGRWLLGVYETVAPTLACLPRPRLRRRRRRRRNISRYTRKA			•					
VPQSLEKGITKHALNIHPPPEKLEISFTSDHEKUTSSQSKS DITRESFTSADTGNSLSAFPSYTGAGISTEGSDFSWGYGELD QNATEKVQTMFTAIDELLYEQKLSVHTKSLQEECQWTASFPHL RILGRQITTPSEGYRLYPRSPSAVSASYETTLSQERDSTIFGIR GKKLHFSSSYAHKASSIAKSSSFCSMERDEEDSIIVSEGIIEEY LÄFDHIDIEEGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY VPDSWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS TSSLSYTVQSTRRNNPPPRTLHPISTSHSCAETPRSVEEILRGA RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK PHGDSSRAQSAVVDEPNYQQPQERLLLEDFFPRPNTTGSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG PCMSRSCAVUDENNYQQPQERLLLEDFFRPNTTGSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG PFAKYNRLGQLSCALCNTPVKSEILWQTHVLGKQHREKVAELKG AKEASQSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTNFDKIGREFIRATPSKPSGLSLLPDVEDEEBEEBEEGGD GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTABALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIRELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL LILLISALADPDQYNFSSSELGGFFEYNDDANCTAIAISLLMI LICAMATTGAYKQRAAMIIPFFCVQIFPFALMMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCUWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL	6300							
DITRESSFTSADTONSLSAPPSYTGAGISTEGSSDFSWGYGELD QNATEKVQTMFTAIDELLYEQKLSYHTKSLQEECQUWTASFPHL RILGRQIITPSEGYRLYPRSPSAVSASYETTLSQERCSTIFGIR GKKLHFSSSYAHKASSIAKSSPCSMERDEEDSIIVSEGIIEEY LÄPDHIDIEEGFHCKKSEBAATEKQKLGYPPIAPFYCMKEDVLAY VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV LSELHPLVLPRVPQSKVLYITTSNPMSLCQASRHQPNVNDLLVHG MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTUSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG P 6291 1732 602 LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASSAPQSVKKRAPDADDQDVKRAKATLVPQVQPST SAWTTNFDKIGKEFIRATPSKPSGLLPDYEDEEEEEEEEGD GERKRGDASKPLSDAQCKEHSVSSSREVTSSVLENDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEEGRDRQ IGEIDEQIECYRRVEKLRNRQDEIKWKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL 6292 1835 1142 TCPGAMKNVAPWTRFYSNSCCLCCHWRTGTILLGVWYLINAVV LLILLSALADPDQYNFSSSELGGDFFMDDANCIAIAISLLMI LICAMATTGAYKQRAAWIIPFFCYQIFDFALMMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKLLVPPRTHAKFTDWKGYLMKRL	6290	3	1856 .					
QNATEKVQTMFTAIDELLYEQKLSVHTKSIQEECQQWTASFPHL RILGRQIITPSEGYRLYPRSPSAVSASYETTLSQERDSTIFGIR GKKLHFSSSYAHKASSIAKSSFCSMERDEEDSIIVSEGIIEEY LÄPPHIDIEBGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV LSELHPLVLPRVPQSKVLYITSNIPASLCQASRHQPNVRDLLVHG MPLQPRNLSIMBKLLDLDDKLLMRFGSSTILSTRNWPNRAVEFS TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGRPVSRTRQG P 6291 1732 602 LVAKMASSASATTPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEEGG GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKENDEFQKAMRQVNTISSAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL 6292 1835 1142 TCGGAMKVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLISALADPDQYNFSSSELGGDFFFMDDANMCIAIAISLIMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALMMLVAITVLTYPN SIQBYIRQLPPNFPYRDDWMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL	1.			VPQSLELKGITKHALNHHPPPBKLEEISPTSDSHEKDTSSQSKS				
RILGRQIITPSEGYRLYPRSPSAVSASYETTLSQERDSTIFGIR GKKLHFSSSYAHKASS IAKSSSFCSMERDEEDSIIVSEGIIEFY LÄPDHIDIEBGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVRDLLVHG MPPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS TSSLSYTVQSTRRNPPPRTLHPISTSHSCAETPRSVEEILRGA RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK PHGDSSRAQSAVVDEPNYQQPQERLLLIPDFFPRPNTTGSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG P 6291 1732 602 LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTINFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEEEGG GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APHIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL 6292 1835 1142 TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFFPALMMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVMNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTHAKFTDWKGYLMKRL				ONATE VIOLENT TO BE IN THE VIOLET OF LTRSHWEGFASDDESNVAVTRPDSESSCV LSELHPLVLPRVPQSKVLYITISNPMSLCQASRHQPNVNDLLVHG MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS TSSLSYTVQSTRRRNPPPTTLHPISTSHSCAETPRSVEEILRGA RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG P 6291 1732 602 LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFAKVNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEBEEEEEGD GERKRGDASKPLSDAQGKEHSVSSREVTTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKBEEN ADSDDEGELQDLLSQDWRVKGALL 6292 1835 1142 TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLISALADPDQYMFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQBYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL				PILOPOTITES FORD VERGE ON THE COMPONENT FORD
LAPDHIDIEEGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY VFDSVMCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCY LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG MPLQPRNLSLMDKLLDLDDKLIMRFGSSTILSTRNWPNRAVEFS TSSLSYTVQSTRRNPPPRTLHPISTSHSCAETPRSVEEILRGA RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG P 6291 1732 602 LVAKMASSASATTPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFAKVNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEGD GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTMPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL ADSDDEGELQDLLSQDWRVKGALL LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQSYIRQLPPNFPYRDDVMSVMPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL				GKKI.HESSSVAHKASSTAKSSSBAVSASIEIILSVEKUSIIFGIK				
VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV LSELHPLULPRYPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG MPLQPRNLSLMDKLLDLDKLLMRPGSSTILSTRNWPNRAVEFS TSSLSTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRGMK PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT QYRRSCAVEYPHQARPGGSAGPQLHGSTKSQSGGRPVSRTRQG P 6291 1732 602 LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEEGG GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECTRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL 6292 1835 1142 TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLIMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQRYIRQLPPNFPYRDDVMSVMPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL		produce a state of the co	والمخطوب السيادين	LAPOHIDIEEGEHGKKSEAATEKOKLGVDDIADEVCMKEDVI AV				
LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEIILKGA RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRNTTQSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG P LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASGGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEEGD GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL 6292 1835 1142 TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLTINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALMMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKLLVPPRTHAKFTDWKGYLMKRL		1		VPDSVWCKVVSCMEOLTRSHWEGFASDDESNVAVTRPDSESSCV				
MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS TSSLSTTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA RVFVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGEPQRQMK PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPPPNTTQSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGRPVSRTRQG P 6291 1732 602 LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTHFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEGD GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEALVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL 6292 1835 1142 TCPGAMKMVAPWTFFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFCCVGIFDFALMMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL	1	÷ . *	1	LSELHPLVLPRVPQSKVLYITSNPMSLCOASRHOPNVNDLLVHG				
TSSLSYTVQSTRRNPPPRTLHPISTSHSCAETPRSVEEILRGA RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG P LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTMFDKIGKEFIRATPSKPSGLSLLPPYEDEEEEEEEEEGD GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL 1142 TCPGAMKWAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL	1			MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS				
RVPVAPDSLSSPSTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG P LVAKMASSASARTPAGKRVINQEELRRIMKEKQRLSTSRKRIES PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEBEEEEEEGD GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL 6292 1835 1142 TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAPKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL			,	TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA				
QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG P 6291 1732 602 LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEEGD GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL TCSPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL				RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK				
P 6291 1732 602 LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEEGD GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL 6292 1835 1142 TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL		: 1	•	PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT				
6291 1732 602 LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEEGD GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEGIECYRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL		:						
PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEGD GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL 6292 1835 1142 TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL	6291	1722	- 603	_				
AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEEGD GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL	3231	1/34	. 6UZ	DEAKVARDI GOLEGAL ONTRUKCET THORING CHARLES				
SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEGD GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL								
GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL 1142 TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL			i					
APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL								
RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL								
IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN ADSDDEGELQDLLSQDWRVKGALL TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL			,					
ADSDDEGELQDLLSQDWRVKGALL 6292 1835 1142 TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL]	j	Ì					
6292 1835 1142 TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL	<u> </u>							
LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL	6292	1835	1142					
SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL	1			LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI				
LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL]							
AKEPPPPYVSA 6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL		1						
6293 2382 1035 FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL								
1 THELECTY DYNE TOWCAL MAKE I DWKG I LINKED	6202	2202						
	0233	2382	1035					
		i						
DTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIK				DIVIGGREREDYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIK				

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			MSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMK
			LEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCY
	`		HASSHAIFPATFCQKNDIBLTPPKGYEAQTFNWENYLEKTKSKA
			APSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRL
			LSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEP
			ATPLKAKEATKKKKKQFGKKRKRIPPTKTRPLRQGSKKPLLEDD
			PQGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSPELPVSVE
			NIKQETDD
6294	354	1814	AQLTTRGRTVAGGVRWIPSPFPDLELYSCCLGTDRGFPELSHHC
			KNVIATASDYDMAEITNIRPSFDVSPVVAGLIGASVLVVCVSVT
			VFVWSCCHQQAEKKHKNPPYKFIHMLKGISIYPETLSNKKKIIK
	!		VRRDKDGPGREGGRRNLLVDAAEAGLLSRDKDPRGPSSGSCIDQ
	,		LPIKMDYGEELRSPITSLTPGESKTTSPSSPEEDVMLGSLTFSV
	,		DYNFPKKALVVTIQEAHGLPVMDDQTQGSDPYIKMTILPDKRHR
1			VKTRVLRKTLDPVFDETFTFYGIPYSQLQDLVLHFLVLSFDRFS
			RDDVIGEVMVPLAGVDPSTGKVQLTRDIIKRNIQKCISRGELQV
			SLSYQPVAQRMTVVVLKARHLQKMDIAGLSGNPYVKVNVYYGRK
	,		RIAKKKTHVKKCTLNPIFNESFIYDIPTDLLPDISIEFLVIDFD
1			RTTKNEVVGRLILGAHSVTASGAEHWREVCESPRKPVAKWHSLS
6295	2795	617	
0295	2/95	617	VSSALLTGATSGSDAAKSEGASASPLSCTNAVAMDRPDEGPPAK TRRLSSSESPORDPPPPPPPPPLLRLPLPPPPQORPRLQEETEAA
			QVLADMRGVGLGPALPPPPPPPPLLRLPLPPPQQRPRLQEETEAA QVLADMRGVGLGPALPPPPPPYVILEEGGIRAYFTLGAECPGWDS
			TIESGYGEAPPPTESLEALPTPRASGGSLEIDFQVVQSSSFGGE
			GALETCSAVGWAPORLVDPKSKEEAIIIVEDEDEDERESMRSSR
			RRRRRRRKORKVKRESRERNAERMESILOALEDIOLDLEAVNI
			KAGKAFLRLKRKFIOMRRPFLERRDLIIOHIPGFWVKAFLNHPR
1.		,	ISILINRRDEDIFRYLTNLOVODLRHISMGYKMKLYFOTNPYFT
1			NMVIVKEFORNRSGRLVSHSTPIRWHRGOEPOARRHGNODASHS
	a a sayar da sa sa	همين ۾ ۾ يالي آ ۽ لهن	FFSWFSNHSLPEADRIAEIIKNDLWVNPLRYYLRERGSRIKRKK
	;	•:	OEMKKRKTRGRCEVVIMEDAPDYYAVEDIFSEISDIDETIHDIK
1.			ISDFMETTDYFETTDNEITDINENICDSENPDHNEVPNNETTDN
Ι,		:	NESADDHETTDNNESADDNNENPEDNNKNTDDNEENPNNNENTY
1.	1		GNNFFKGGFWGSHGNNQDSSDSDNBADEASDDEDNDGNEGDNEG
		•	SDDDGNEGDNEGSDDDDRDIEYYEKVIEDFDKDQADYEDVIEII
-		•	SDESVEEEGIEEGIQQDEDIYEEGNYEEEGSEDVWEEGEDSDDS
1			DLEDVLQVPNGWANPGKRGKTG
6296	727	1199	RHCGCDAQGACDSLPPTGTSSPVTARNAIPEARCCVWLLDGTTV
			EAVRPARERLARKELROKRMOOFSRDSAYSSNKDSTCLLTBRDT
			LGTSLQFPSPFSGTISFGSFSDSGIFPLGSQCCLGFQQFSISGK
			KWALIHKRVRLSVFGARWGRIYFGK
6297	1	922	QRAAAASPSSCGPRGAEYGALMAMEGYWRFLALLGSALLVGFLS
			VIFALVWVLHYREGLGWDGSALEFNWHPVLMVTGFVFIQGIAII
	,		VYRLPWTWKCSKLLMKSIHAGLNAVAAILAIISVVAVFENHNVN
			NIANMYSLHSWVGLIAVICYLLQLLSGFSVFLLPWAPLSLRAFL
			MPIHVYSGIVIFGTVIATALMGLTEKLIFSLRDPAYSTFPPEGV
			FVNTLGLLILVFGALIFWIVTRPQWKRPKEPNSTILHPNGGTEQ
	,		GARGSMPAYSGNNMDKSDSBLNNEVAARKRNLALDEAGQRSTM
6298	3	985	SVPLRRLSLSGTLQGAGTTTKMAVARLAAVAAWVPCRSWGWAAV
		· -	PFGPHRGLSVLLARIPQRAPRWLPACRQKTSLSFLNRPDLPNLA
1			YKKLKGKSPGIIFIPGYLSYMNGTKALAIEEFCKSLGHACIRFD
1		'	YSGVGSSDGNSEESTLGKWRKDVLSIIDDLADGPQILVGSSLGG
			WLMLHAAIARPEKVVALIGVATAADTLVTKFNQLPVBLKKEVEM
			KGVWSMPSKYSEEGVYNVQYSFIKEAEHHCLLHSPIPVNCPIRL
1	į	1	LHGMKDDIVPWHTSMQVADRVLSTDVDVILRKHSDHRMREKADI
1 :	İ	"	OLLVYTIDDLIDKLSTIVN

SEQ	Predicted	Predicted end	I had a second a seco
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO.	location	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
6299	512	814	RCDLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLDSAILTSS
	İ		SIDAMDDSAFSGPYKFPFTPPLESFNLCFYTSQVPVPPILGFYQ
L		,	MKEEEVQLRNNH
6300	121	692	AAPSCWSQRGVPAAGTPSSPRLLVSRAAAPSAGPWGAWRQGARA
			AQSPFSIPNSSSVPYGSQDSVHSSPEDGGGGRDRPVGGSPGGPR
1			LVIGSLPAHLSPHMFGGFKCPVCSKFVSSDEMDLHLVMCLTKPR
1			ITYNEDVLSKDAGECAICLEELQQGDTIARLPCLCIYHKGCIDE
1			WFEVNRSCPEHPSD
6301	616	284	GKFVPVNWEPPQPLPFPKYLRCYRCLLETKELGCLLGSDICLTP
			AGSSCITLHKKNSSGSDVMVSDCRSKEQMSDCSNTRTSPVSGFW
1			IFSQYCFLDFCNDPQNRGLYTP
6302	490	745	IFGFLHLFHMEHSFLLVCALFAHVFFSSSCGSSVALHSDPCLLS
1		· • • · · · · · · · · · · · · · · · ·	PVLLNCLPGDLRPLDELYAQKLKYKAISEELDHALNDMTSL
6303	2	1961	YWNEYGGGLLWQSWQEKHPGQALSSEPWNFPDTKEEWEOHYSOL
1	-		YWYYLEQFQYWEAQGWTFDASQSCDTDTYTSKTEADDKNDEKCM
1			KVDLVSFLSSPIMGDNDSSGTSDKDHSEILDGISNIKLNSEEVT
į			QSQLDSCTSHDGHQQLSEVSSKRECPASGQSBPRNGGTNEESNS
			SGNTNTDPPAEDSQKSSGANTSKDRPHASGTDGDESEEDPPEHK
-			PSKLKRSHELDIDENPASDFDDSGSLLGFKYGSGQKYGGIPNFS
ĺ			HRQVRYLEKNVKLKSKYLDMRRQIKMKNKHIFFTKESEKPFFKK
		- ,	SKILSKVEKFLTWVNKPMDEEASQESSSHDNGHDASTSCDSEEQ
			DMSVKKGDDLLETNNPEPEKCQSVSSAGELETENYERDSLLATV
			PDEQDCVTQEVPDSRQAETEAEVKKKKNKKKNKKVNGLPPEIAA
			VPELAKYWAQRYRLFSRFDDGIKLDREGWFSVTPEKIAEHIAGR
			VSQSFKCDVVVDAFCGVGGNTIQFALTGMRVIAIDIDPVKIALA
ł			RNNAEVYGIADKIEFICGDFLLLASFLKADVVFLSPPWGGPDYA
			TAETFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS
	<u> </u>	:	LAGPGGQVEIEQNFLNNKLKTITAYFGDLIRRPASET
6304	1	1438	HRARVDRSRESPGGDLRHPGRVRRDITLSGHPRLSTQHVVLLRE
	:	• 1	DEVGDPGTKDLGHPQHGSPIQETQSEVVTLVSPLPGSDMAALPA
	:		WRATSGLTLWPHTAEGRDLLGAENRALTGGQQAEDPTLASGAYQ
[1		WPGSVEKLQGSVWCDAETLLSSSRTGGQAPPWLTDHDVQMLRLL
		4 .	AQGEVVDKARVPAHGQVLQVGFSTEAALQDLSSPRLSQLCSQGL
1	i i	•	CGLIKRPGDLPEVLSFHVDRVLGLRRSLPAVARRFHSPLLPYRY
	·		TDGGARPVIWWAPDVQHLSDPDEDQNSLALGWLQYQALLAHSCN
			WPGQAPCPGIHHTEWARLALFDFLLQVHDRLDRYCCGFEPEPSD
; I			PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLQHP
			EDKLNFRLLEGIDGFPESAVKVLASGCLQNMLLKSLQMDPVFWE
_			SQGGAQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP
6305	99	420	NMIWRGRSTYRPRPRRSVPPPELIGPMLEPGDEEPQQEEPPTES
	1		RDPAPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD
	ļ		VQGKILTKSEQFKMPEGR
6306		1874	PTRPSKVKVPHTFLIHSYTRPTVCOACKKLLKGLFROGLOCKDC
	=	/ •	KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD
			ESEDSGVIPGSHSENALHASEEEEGEGGKAOSSLGYIPLMRVVO
1	l	1	SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFO
			NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA
	!		
			TYFVGEMPGGTPGGPSGQGAEAARGWETAIRQALMPVILQDAPS
	1		APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF
			GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR
1	İ		HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL
			TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC
			DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG
			VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID
			LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER
			YITHESDDARWEQFAAEHPLPGSGLPTDRDLGGACPPQDHDMQG

SEQ			
	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
	 		LAERISVL
6307	2136	589	CFLLPRGRDPEPPEAGAAAPCAPGAPDMSFRKVVROSKFRHVFG
			QPVKNDQCYEDIRVSRVTWDSTFCAVNPKFLAVIVEASGGGAFL
			VLPLSKTGRIDKAYPTVCGHTGPVLDIDWCPHNDEVIASGSEDC
			TVMVWQIPENGLTSPLTEPVVVLEGHTKRVGIIAWHPTARNVLL
			SAGCDNVVLIWNVGTAEELYRLDSLHPDLIYNVSWNHNGSLFCS
1			ACKDKSVRIIDPRRGTLVAEREKAHEGARPMRAIFLADGKVFTT
f			GFSRMSERQLALWDPENLEEPMALQELDSSNGALLPFYDPDTSV
			VYVCGKGDSSIRYFEITEEPPYIHFLNTFTSKEPQRGMGSMPKR
1			GLEVSKCEIARFYKLHERKCEPIVMTVPRKSDLFQDDLYPDTAG
			PEAALEAEEWVSGRDADPILISLREAYVPSKORDLKISRRNVLS
		1	DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGEAGKLEEVM
			QELRALRALVKEOGDRICRLEEQLGRMENGDA
6308	2	1118	GRPTRPEKMLLSLVLHTYSMRYLLPSVVLLGTAPTYVLAWGVWR
			LLSAFLPARFYOALDDRLYCVYOSMVLFFFENYTGVOILLYGDL
1 1			PKNKENIIYLANHOSTVDWIVADILAIRONALGHVRYVLKEGLK
			WLPLYGWYFAQHGGIYVKRSAKFNEKEMRNKLQSYVDAGTPMYL
j j			VIFPEGTRYNPEOTKVLSASQAFAAQRGLAVLKHVLTPRIKATH
1			VAFDCMKNYLDAIYDVTVVYEGKDDGGORRESPTMTEFLCKECP
			KIHIHIDRIDKKDVPEEQEHMRRWLHERFEIKDKMLIEFYESPD
			PERRKRFPGKSVNSKLSIKKTLPSMLILSGLTAGMLMTDAGRKL
		,	YVNTWIYGTLLGCLWVTIKA
6309	220	563	LVAEVKEPCSLPMLSVDMENKENGSVGVKNSMENGRPPDPADWA
			VMDVVNYFRTVGFEEQASAFQEQEIDGKSLLLMTRNDVLTGLQL
			KLGPALKIYEYHVKPLOTKHLKNNSS
6310	36	979	GPRCWKFLILSSVNCETLRIGKAWPQSSGQERYWTPRTHSSASE
			AQRGSLAELNVAAAGLWADCDQPLYDCPMCGLICTNYHILQEHV
			DLHLEENSFQQGMDRVQCSGDLQLAHQLQQEEDRKRRSEESRQE
1		:	IEEFQKLQRQYGLDNSGGYKQQQLRNMEIEVNRGRMPPSEFHRR
1			KADMMESLALGFDDGKTKTSGIIEALHRYYQNAATDVRRVWLSS
İ	· ±		VVDHFHSSLGDKGWGCGYRNFQMLLSSLLQNDAYNDCLKGMLIP
	;	.	CIPKIQSMIEDAWKEGFDPQGASQLIIRLQGTKAWIGACEVYIL
			LTSLRV
6311	1	675	PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL
			ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVAELEANL
	•		PCTCKVHFPDPNKLHCFQLTVTPDEGYYQGGKFQFETEVPDAYN
1			MVPPKVKCLTKIWHPNITETGEICLSLLREHSIDGTGWAPTRTL
1		,	KDVVWGLNSLFTDLLNFDDPLNIEAABHHLRDKEDFRNKVDDYI
1			KRYAR
		1400	GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW
6312	213	1400	dbbbvidthamandebevevi of occurrence in the man
6312	213	1400	GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT
6312	213	1400	
6312	213	1400	GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT
6312	213	1400	GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN
6312	213	1400	GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC
6312	213	1400	GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA
6312	213	1400	GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV
	213	1400	GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL
6312	213	2071	GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL
			GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL
			GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
			GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
			GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
			GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
			GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	(A=Aranine, C=Cysteine, D=Aspartic Acid, E=
NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid .	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
		,	SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC
1		•	QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH
1		1	LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK
1	1	}	PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVO
1			TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLODS
1	ł	į	QVHDSHMSBLPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ
1			MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAAREDHED
1	Į.		AEDLETKPTVDSEAEKAENEDRTALPVLE
6314	2	2071	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
	1 -	20.0	FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLOEFPEHHKMILD
ł	}		RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
1			TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE
1	1		FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIABTSNVI
			TESLPSAESEPVEIEVRIAEGTIEVEDEGIETLEEVASAKQSVK
			YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK
		:	QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE
-	1		SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC
į			QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH
1	ł		LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK
			PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ
		1	TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS
			QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ
			MPVEVQTELLEADLDHVTPEIMNQBERESSQADAAEAAREDHED
			AEDLETKPTVDSEAEKAENEDRTALPVLE
6315	1	1015	LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA
	· .		IDGKQARRINSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY
1			PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI
	·	.•	VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF
		•	HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
		And the second of the second	VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDTVFLGP
			GLLFLDQYFNNFIDEYVVLWMAMVISSFDMVIYFSALCLQISRH
1		,	LHLNIFKTACHOAPEOVOVLSSKSHONNMD
6316	1503	792	VSAGAGTGIMGGTTSTRRVTFEADENENITVVKGIRLSENVIDR
1			MKESSPSGSKSQRYSGAYGASVSDEELKRRVAEBLALEOAKKES
]		• •	EDQKRLKQAKELDRERAAANEQLTRAILRERICSEEERAKAKHL
1		•	ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA
	·		EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY
			MHCVNHAKOSMLEKGG
6317	102	839	PEAQTSAVLAREKGHLPTMRHEAPMOMASAODARYGOKDSSDON
		033	FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK
1			l l
			TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN FFGENAVODWGTOIVTYGWDNAOUTLUGWYCDMEDEBULGTEBC
{			EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG
)			QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD
J			PAITAAKQNTRLKETPPPPQPNCAC
6318	1765	733	PWHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRREAPPL
1 1			LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI
1			LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT
j i			VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM
			ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN
			DVASLEHTKOWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM
			EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFEANVLA
			ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP
6319	88	717	AATMRLNONTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELORLT
			ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES
!	}		CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML
]			SYGVTTLGLTKFEAKIGQGNBPSIRMFQKLHFEQVATSSVFQEV
	1		The state of the s

	•		•
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
			TLRLTVSESEHQWLLEQTSHVEEKPYRDGSAEPC
6320	90	1111	RPRTGREKVAMAAVDSFYLLYREIARSCNCYMEALALVGAWYTA
]		RKSITVICDFYSLIRLHFIPRLGSRADLIKQYGRWAVVSGATDG
1			IGKAYAEELASRGLNIILISRNEEKLQVVAKDIADTYKVETDII
1			VADFSSGREIYLPIREALKDKDVGILVNNVGVFYPYPQYFTQLS
			BDKLWDIINVNIAAASLMVHVVLPGMVERKKGAIVTISSGSCCK
İ			PTPQLAAFSASKAYLDHFSRALQYEYASKGIFVQSLIPFYVATS
1			MTAPSNFLHRCSWLVPSPKVYAHHAVSTLGISKRTTGYWSHSIQ
1			FLFAQYMPEWLWVWGANILNRSLRKEALSCTA
6321	1418	341	HRKAALGALMAGRLLGKALAAVSLSLALASVTIRSSRCRGIQAF
			RNSFSSSWFHLNTNVMSGSNGSKENSHNKARTSPYPGSKVERSQ
1			VPNEKVGWLVEWQDYKPVEYTAVSVLAGPRWADPQISESNFSPK
i			FNEKDGHVERKSKNGLYEIENGRPRNPAGRTGLVGRGLLGRWGP
1	}		NHAADPIITRWKRDSSGNKIMHPVSGKHILQFVAIKRKDCGEWA
			IPGGMVDPGEKISATLKREFGEBALNSLQKTSAEKREIEEKLHK
1			LFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGEIMDNLM
1		· ·	LEAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEKRDAHWSEDS
			EADCHAL
6322	2047	1083	NOEILKNVESSRTVQPHFLEFLLSLGWSVDVGRHPGWTGHVSTS
"""]	WSINCCDDGEGSQQEEVISSEDIGASIFNGQKKVLYYADALTEI
[AFVVPSPVESLTDSLESNISDQDSDSNMDLMPGILKQPSLTLEL
			FPNHTDNLNSSQRLSPSSRMRKLPQGRPVPPLGPETRVSVVWVE
1			RYDDIENFPLSELMTEISTGVETTANSSTSLRSTTLEKEVPVIF
			IHPLNTGLFRIKIQGATGKFNMVIPLVDGMIVSRRALGFLVRQT
	,		VINICRRKRLESDSYSPPHVRRKQKITDIVNKYRNKQLEPEFYT
			SLFQEVGLKNCSS
6323	1	656	PASTTDGAQEARVPLDGAFWIPRPPAGSPKGCFACVSKPPALQA
	•		PAAPAPEPSASPPMAPTLFPMESKSSKTDSVRAAGAPPACKHLA
			EKKTMTNPTTVIEVYPDTTEVNDYYLWSIFNFVYLNFCCLGFIA
	of the second of the second	the separate that a section of	LAYSLKVRDKKLLNDLNGAVEDAKTDRLINITRSGLAASCIMLW
	,		MALSVIATHRGLRSSASILVAEPHDWNTERPQVTFRERCPAL
6324	1	2061	EGAGMRRCPCRGSLNEAEAGALPAAARMGLEAPRGGRRRQPGQQ
7524	_		RPGPGAGAPAGRPEGGGPWARTEGSSLHSEPBRAGLGPAPGTES
			PQAEFWTDGQTEPAAAGLGVETERPKQKTEPDRSSLRTHLEWSW
	,	1	SELGTTCLWTETGTDGLWTDPHRSDLQFQPEBASPWTQPGVHGP
1		;	WTELETHGSQTQPERVKSWADNLWTHQNSSSLQTHPEGACPSKE
1		,	PSADGSWKELYTDGSRTQQDIEGPWTEPYTDGSQKKQDTEAARK
[i :	QPGTGGFQIQQDTDGSWTQPSTDGSQTAPGTDCLLGEPEDGPLE
		1	EPEPGELLTHLYSHLKCSPLCPVPRLIITPETPEPEAQPVGPPS
		1	RVEGGSGGFSSASSFDESEDDVVAGGGGASDPEDRSGSKPWKKL
		1	KTVLKYSPFVVSFRKHYPWVQLSGHAGNFQAGEDGRILKRFCQC
1	1		EQRSLEQLMKDPLRPFVPAYYGMVLQDGQTFNQMEDLLADFEGP
1			SIMDCKMGSRTYLEEELVKARERPRPRKDMYEKMVAVDPGAPTP
1	1	ľ	BEHAQGAVTKPRYMQWRETMSSTSTLGFRIEGIKKADGTCNTNF
1	1		KKTQALEQVTKVLEDFVDGDHVILQKYVACLEELREALEISPFF
1 .		1	KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHQTLSHRLP
			WAEGNREDGYLWGLDNMICLLQGLAQS
6325	165	944	GLRDPFRRKRRLKPQVKMSNYVNDMWPGSPQEKDSPSTSRSGGS
7323	1 205	1	SRLSSRSRSFSRSSRSHSRVSSRFSSRSRSKSRSRRRHQ
		1	RKYRRYSRSYSRSRSRSRSRSRYRERRYGFTRRYYRSPSRYRSRS
1			RSRSRSRGRSYCGRAYAIARGQRYYGFGRTVYPBEHSRWRDRSR
		-	TRSRSRTPFRLSEKDRMELLEIAKTNAAKALGTTNIDLPASLRT
			VPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQI
6326	238	680	GEPSPATQQKPSATGAGVLHQHFSSGHIYVLMGLLPPPWTISFT
6326	438	080	VOTTLQPPGGLPAAPVSGRMAFEPVGRDLARRMVPRAGKRTQTL
1	1		GARRVAAQGARPLPEDRRPKSGERLHVTVAPCWEFVLPSVSLTA
1.			GAKKVAAQGAKPDFEDKKPK5GEKDUVIVAFCWET VDF3V3DIA

- 070	1 5 - 3'		
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
į.	corresponding to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion, -possible nucleotide insertion)
	sequence	<u> </u>	\=\text{possible nucleotide insertion}
6327		1337	
0327	. 1	1337	SLARLAPAGGSVVMPTQQPAAPSTRAPKPSRSLSGSLCALFSDA
1	•		DSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQQKKKRKEEK
			GAEPETGSAVSAAQCQGPTRELPESGIQLGTPREKVPAGRSKAE
			LRAERRAKQEAERALKQARKGEQGGPPPKASPSTAGETPSGVKR
ł			LPEYPQVDDLLLRRLVKKPBRQQVPTRKDYGSKVSLFSHLPQYS
1			RQNSLTQFMSIPSSVIHPAMVRLGLQYSQGLVRGSNARCIALLR
			ALQQVIQDYTTPPNEELSRDLVNKLKPYMSFLTQCRPLSASMHN
,			AIKFLNKEITSVGSSKREEBAKSELRAAIDRYVQEKIVLAAQAI
į.			SRFAYQKISNGDVILVYGCSSLVSRILQEAWTEGRRFRVVVVDS RPWLEGRHTLRSLVHAGVPASYLLIPAASYVLPEVSTEEKDSKV
			GGEKV
6328	1030	276	HASAEVTTAAARGLGAMEEEMHTDAKIRAENGTGSSPRGPGCSL
7320	1030	2/0	RHFACEQNLLSRPDGSASFLOGDTSVLAGVYGPAEVKVSKEIFN
	}		KATLEVILRPKIGLPGVAEKSRERLIRNTCEAVVLGTLHPRTSI
			TVVLQVVSDAGSLLACCLNAACMALVDAGVPMRALFCGVACALD
l			SDGTLVLDPTSKQEKEARAVLTFALDSVERKLLMSSTKGLYSDT
Í			ELQQCLAAAQAASQHVFRFYRESLORRYSKS
6329	3	2016	SSEVAAGGGTRSAMAEGSGEVVTVSATGAANGLNNGAGGTSATT
""	}	2010	SNPLSRKLHKILETRLDNDKEMLEALKALSTFFVENSLRTRRNL
	,		RGDIERKSLAINEBFVSIFKEVKEELESISEDVQAMSNCCODMT
:	1 × 4		SRLQAAKEQTQDLIVKTTKLQSESQKLEIRAQVADAFLSKFQLT
} ·			SDEMSLLRGTREGPITEDFFKALGRVKQIHNDVKVLLRTNOOTA
Ī	!		GLEIMEQMALLQETAYERLYRWAQSECRTLTQESCDVSPVLTQA
			MEALQDRPVLYKYTLDEFGTARRSTVVRGFIDALTRGGPGGTPR
· ·		,	PIEMHSHDPLRYVGDMLAWLHQATASEKEHLEALLKHVTTOGVE
ł			ENIQEVVGHITEGVCRPLKVRIEQVIVAEPGAVLLYKISNLLKF
			YHHTISGIVGNSATALLTTIEEMHLLSKKIFFNSLSLHASKLMD
1 .			KVELPPPDLGPSSALNQTLMLLREVLASHDSSVVPLDARQADFV
*****	بعد ما منتشقه		QVLSCVLDPLLQMCTVSASNLGTADMATFMVNSLYMMKTTLALF
			EFTDRRLEMLQFQIEAHLDTLINEQASYVLTRVGLSYIYNTVQQ
1 '		•	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL
			LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR
	, ,		SPQQVQTLLS
6330	1151	333	FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL
•	* *		PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR
,			KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC
			EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN
			RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV
			NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP
		<u></u>	TYESCLLN
6331	3	495	QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL
			LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY
			RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA
	<u> </u>		IFGFMATFLCMASIWLSYKISCVTQSTDAAV
6332	1	878	VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI
] [į		NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS
			SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY
			SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD
})		ELRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD
			VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG
			KLSTMATHSQLVKTGTGLEPRQAVSSSH
6333	3	1467	TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG
			QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG
,			GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP
			MGQMPGMMSSVMPGMMMSHMSQASMQPALPPGVNSMDVAAGTAS

	<u></u>		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
<u> </u>	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
]	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		•	GAKSMWTEHKSPDGRTYYYNTETKQSTWEKPDDLKTPAEQLLSK
1			CPWKEYKSDSGKPYYYNSOTKESRWAKPKELEDLEGYONTIVAG
			SLITKSNLHAMIKAEESSKOEECTTTSTAPVPTTEIPTTMSTMA
			AAEAAAAVVAAAAAAAAAAAAAAAAANANASTSASNTVSGTVPVVPRP
<u> </u>		i ·	
1]		EVTSIVATVVDNENTVTISTEEQAQLTSTPAIQDQSVEVSSNTG
		i	BETSKQETVADFTPKKEEEESQPAKKTYTWNTKEEAKQAFKELL
		}	KEKRVPSNASWEQAMKMIINDPRYSALAKLSEKKQAFNAYKVQT
			EKK
6334	. 17	644	GGNPSGRAAGFAAAAMPSSPLRVAVVCSSNQNRSMEAHNILSKR
	i		GFSVRSFGTGTHVKLPGPAPDKPNVYDFKTTYDQMYNDLLRKDK
	1		ELYTQNGILHMLDRNKRIKPRPERFQNCKDLFDLILTCEERVYD
	1		QVVEDLNSREQETCQPVHVVNVDIQDNHEEATLGAFLICELCQC
1		Ì	IQHTEDMENBIDELLQEFEEKSGRTFLHTVCFY
6335	82	529	AARARPGVLCCRLLGAALGDQSRVEMSYIPGQPVTAVVQRVEIH
	1	,	KLRQGENLILGFSIGGGIDQDPSQNPFSEDKTDKGIYVTRVSEG
	1		GPAEIAGLQIGDKIMQVNGWDMTMVTHDQARKRLTKRSEEVVRL
			LVTRQSLQKAVQQSMLS
6336	1003	438	HEPASKGRAEVGNMRLSVAAAISHGRVFRRMGLGPESRIHLLRN
0330	1 2005	450	LLTGLVRHERIEAPWARVDEMRGYAEKLIDYGKLGDTNERAMRM
			ADFWLTEKDLIPKLFOVLAPRYKDOTGGYTRMLOIPNRSLDRAK
			MAVIEYKGNCLPPLPLPRRDSHLTLLNQLLQGLRQDLRQSQEAS
		4 4	
			NHSSHTAQTPGI
6337.	76	524	EGIQMLSVQPDTKPKGCAGCNRKIKDRYLLKALDKYWHEDCLKC
		,	ACCDCRLGEVGSTLYTKANLILCRRDYLRLFGVTGNCAACSKLI
			PAFEMVMRAKDNVYHLDCFACQLCNQRFCVGDKFFLKNNMILCQ
			TDYREGLMKEGYAPQVR
6338	66	1349	APNSESGTQGPLPTPANLFWTRRANPDPTTSMSATDRMGPKAVP
l .		· ·	GLRLALLLLGLGTPKSGVQGQEGLDFPEYDGVDRVINVNAKNY
			KNVFKKYEVLALLYHEPPEDDKASQRQFEMEELILELAAQVLED
1 2 2			KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVFKGDEVIEYDGEFS
1	,	70	ADTIVEFLLDVLEDPVELIEGERELQAFENIEDEIKLIGYFKSK
i			DSEHYKAFEDAAEEFHPYIPFFATFDSKGAKKLTLKLNEIDFYE
1	1	1 :	AFMEEPVTIPDKPNSEEEIVNFVEEHRRSTLRKLKPESMYETWE
1	1	I	DDMDGIHIVAFAEEADPDGFEFLETLKAVAQDNTENPDLSIIWI
1		I	DPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADRLWMEMDDEE
	•		DLPSAEELEDWLEDVLEGEINTEDDDDDDDD
6339	246	1813	NRCDRGGGGOAEROAGOGCRTOGAGPGFGFGHSFFSQGAMKAFH
		1	TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDS
}	I	1	VTESPORVIITEDDEDETTVELEGQDENQEGDFEDADTQEGDTE
		1	SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYY
1			
		1	LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL
		Ì	VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL
		1	KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL
		1	VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM
1		1	DTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQPLKLPDTKR
		1	TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE
		1	GKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRAEKERIM
L			NEEDPEKQRRLEEAALRREQKKLEKKQMKMKQIKVKAM
6340	2	583	EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSS
		1	SSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF
			PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA
		1	EKLAADGTVMNNFAHKCOLPEDVDPTSVTSALREDGSLTIRARR
			HPHTEHVQQTFRTEIKI
6341	2	645	KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ
0341		. 043	PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA
1		1	CCAVEMMHMAAPRYDMDRFGVVFRASPRQSDVMIVAGTLTNKMA
	i	i	I COUADIMINIMAL TOUNKERAAL WOOLKOODANT AUGITINIMA

	, , , , , , , , , , , , , , , , , , , 		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			PALRKVYDQMPEPRYVVSMGSCANGGGYYHYSYSVVRGCDRIVP
L			VDIYIPGCPPTAEALLYGILQLQRKIKRERRLQIWYRR
6342	2	1191	DPRVRAMLATLARVAALRKTCLFSGRGGGRGLWTGRPQSDMNNI
			KPLEGVKILDLTRVLAGPFATMNLGDLGAEVIKVERPGAGDDTR
İ			TWGPPFVGTESTYYLSVNRNKKSIAVNIKDPKGVKIIKELAAVC
1			DVFVENYVPGKLSAMGLGYEDIDEIAPHIIYCSITGYGQTGPIS
ł			QRAGYDAVASAVSGLMHITGPEVACLSHIAANYLIGQKEAKRWG
			TAHGSIVPYQAFKTKDGYIVVGAGNNQQFATVCKILDLPELIDN
			SKYKTNHLRVHNRKELIKILSERFEEELTSKWLYLFEGSGVPYG
			PINNMKNVFAEPQVLHNGLVMEMEHPTVGKISVPGPAVRYSKFK
	<u> </u>		MSEARPPPLLGQHTTHILKEVLRYDDRAIGELLSAGVVDQHETH
6343	2	936	GTAMVSDEDELNLLVIVVDANPIWWGKQALKESQFTLSKCIDAV
		1 1	MVLGNSHLFMNRSNKLAVIASHIQESRFLYPGKNGRLGDFFGDP
			GNPPEFNPSGSKDGKYELLTSANEVIVEEIKDLMTKSDIKGQHT
1			ETLLAGSLAKALCYIHRMNKEVKDNQEMKSRILVIKAAEDSALQ
			YMNFMNVIFAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKV
			POMPSLLQYLLWVFLPDQDQRSQLILPPPVHVDYRAACFCHRNL
ı	1		IBIGYVCSVCLSIFCNFSPICTTCETAFKISLPPVLKAKKKLK
6344	25.5		VSA
6344	2508	147	TMPTATLGNLRGYGMASPGLAAPSLTPPQLATPNLQQFFPQATR
		age of the second	QSLLGPPPVGVPMNPSQFNLSGRNPQKQARTSSSTTPNRKDSSS
1			QTMPVEDKSDPPEGSEEAAEPRMDTPEDQDLPPCPEDIAKEKRT
1			PAPEPEPCEASELPAKRLRSSEEPTEKEPPGQLQVKAQPQARMT
			VPKQTQTPDLLPEALEAQVLPRFQPRVLQVQAQVQSQTQPRIPS
İ	1	,	TDTQVQPKLQKQAQTQTSPEHLVLQQKQVQPQLQQEAEPQKQVQ
	•		PQVQPQAHSQGPRQVQLQQEAEPLKQVQPQVQPQAHSQPPRQVQ
1			LQLQKQVQTQTYPQVHTQAQPSVQPQEHPPAQVSVQPPEQTHEQ
	}	•	PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGGMEKTLPEP
المراجعة المواد	هُم بنيان بيا مجوراً وبيالا		VGTQVSMEEIQNESACGLDVGECENRAREMPGVWGAGGSLKYTI LQSSDSRAFSTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY
			ICKASCSSQQEFQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR
			DVLETEDEEPPPRRWCNTCQLYYMGDLIQHRRTQDHKIAKQSLR
		•	PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE
	4	and the second second	DHFITVDAVGCFEGDEEEEEDDEDEEEIEVEERLCKQVRSRDIS
	`		REEWKGSETYSPNTAYGVDFLVPVMGYICRICHKFYHSNSGAOL
1			
			L SHCKSLGHERNI OKYKAAKNOQOTTO DUQOOCATATAO TATAO TATAO
			SHCKSLGHFENLQKYKAAKNPSPTTRPVSRRCAINARNALTALF TSSGRPPSOPNTODKTPSKVTARPSOPPLDRRSTBLKT
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENEIELSLLQLR
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENEIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENEIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLABILKTQLRRKENBIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLABILKTQLRRKENBIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNBKLVQENREL
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENEIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNBKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENEIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNBKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENBIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNBKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENBIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNBKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENBIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRKTERDQNBKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENBIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNBKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENBIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNBKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENBIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNBKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL RVPMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENBIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNBKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL RVPMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA
6345	2	3483	TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENBIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNBKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL RVPMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l No:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	1	
		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			VILKWKFAYLPPSGSITTEDLGNFIRSEEPEVVQRLPPASSVST
			LVLAPRPKPRQRLTPVDKKVSFVDIMPHQSDVSQEGSVDEVKEN
			TEKMQQGKDDVSLLSEGQLAEQSLASSEDETEITEDLEPEVEED
			MSASDSDDCIIPGPISKNIKQPSEKIRIEIIALSLNDSQVTMDD
			TIQRLFVECRFYSLPAEETPVSLPKPKSGQWVYYNYSNVIYVDK
			ENNKAKRDILKAILQKQEMPNRSLRFTVVSDPPEDEQDLECEDI
			GVAHVDLADMFQEGRDLIEQNIDVFDARADGEGIGKLRVTVEAL
			HALQSVYKQYRDDLEA
6346	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
			AKYTQKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLLANSPLME
			DAPORLRWOAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
		l	QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
			QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
			TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
		1	DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
			FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
			IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
		1	KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
		ļ	PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
			RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
			ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
		· .	CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL
	•		ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC
		:	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW
	· ·	:	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEPYYDBFGFRVYKEEGDEPGSSLLANSPLME
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEPYYDBFGFRVYKEEGDEPGSSLLANSPLME
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG ODRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKBEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLIWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG ODRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKBEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLIWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLIWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLFRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFTTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEPYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITTLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLFRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFTTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEPYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITTLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEPYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRKHLAYL IADQGQLLGAGTITNLSQVVRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG ODRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLMWRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRKKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG ODRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLMWRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRKKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRRKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDPASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL
6347	2921	533	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLRIWDLFFYEGSRVLFQLTLGMLHLKEEBLIQSENSASI FNTLSDIPSQMEDAELLIGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENTVACSRSH RRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDPASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC
6347	2921	3679	ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMESNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEBLIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLFGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDPASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMESNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLRIWDLFFYEGSRVLFQLTLGMLHLKEEBLIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDPASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKBE
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEPYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITTLHWFTTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLFGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWFQEIL AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITTLHWFLTAFASVV DIKLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLFGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDPASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEPYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITTLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEPYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITTLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDPASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEPYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDPASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEPYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAKLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKBE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQBCLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPRBMQKAEEKEVPEDSLBECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEPYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAKLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKBE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVABKVQKSSSPRBMQKAEEKEVPEDSLBECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL AKYTQKEESAEQPEPYYDBFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAKLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLPASYFSTTLLGVQ TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKBE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQBCLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPRBMQKAEEKEVPEDSLBECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN

SEQ	Predicted	Predicted end	The second secon
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Sequence	\=possible nucleotide insertion)
<u> </u>	-		BCAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
			EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
į			YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
			CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDODPSCPRLSR
			ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
		i	QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD
			SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE
1	1		KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG
			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV
	[DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
			TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
		,	DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
			PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
			LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
			VGFSLDVGEIEKKGKGKKRRGRRSKKERRGRKEGEEDQNPPCP
			RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
1			SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6349	3	3679	AGAEKCFVTLLACFLAKQQNKYKYBECKDLIKSMLRNELQFKEE
			KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
			EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN:
		• •	DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
·			NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
Í			ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
			EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
			ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
		•	DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
			LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE
		•	ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
	, ½		EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG:
			YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
			COPYRSAFYVLEOORVGLAVNMDEIEKYQEVEEDODPSCPRLSR
	p		ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
			QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD
:	· · ·	•	SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE
			KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG
			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV
· ·			DMDEIEKYQEVEBDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
1	•		TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
			DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
			PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
			LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
			VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGBEDQNPPCP
			RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
			SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6350	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
	Ĭ	,	KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
			EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
			DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
			NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
	İ		ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
	[EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
		ľ	ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
			DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
	i		LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE
<u></u>		+	The state of the s

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
	sequence		CAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
1			f ·
			EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
	1		YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
ł			CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
ļ			ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
1	}		QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD
			SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE
			KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG
			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV
			DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
1			TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
1		,	DODPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
,			PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
			LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
			VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
			RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
			SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6351	1291	319	REARRRTERSQLGRMLVVEVANGRSLVWGAEAVQALRERLGVGG
	·		RTVGALPRGPRQNSRLGLPLLLMPEEARLLAEIGAVTLVSAPRP
			DSRHHSLALTSFKRQQEESFQEQSALAAEARETRRQELLEKITE
	, , , ,	•	GQAAKKQKLEQASGASSSQEAGSSQAAKEDETSDGQASGEQEEA
1			GPSSSQAGPSNGVAPLPRSALLVQLATARPRPVKARPLDWRVQS
			KDWPHAGRPAHELRYSIYRDLWERGFFLSAAGKFGGDFLVYPGD
	•		PLRFHAHYIAQCWAPEDTIPLQDLVAAGRLGTSVRKTLLLCSPQ
		;	PDGKVVYTSLQWASLQ
6352	235	923	WSEWLSPCHAAKCKGLSMLRITMKTRAISLAADATEFVQGRSAP
1			AMARSLVHDTVFYCLSVYQVKISPTPQLGAASSAEGHVGQGAPG
			LMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPPEE
			PAQAAMEGPQPENMQPRTRRTKFTLLQVEELESVFRHTQYPDVP
1			TRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANELRADP
			DDCVYIVVD
6353	65	672	RFAGAGATPEARARPPDVQAAEEEKEMDLPDSASRVFCGRILSM
			VNTDDVNAIILAQKNMLDRFEKTNEMLLNFNNLSSARLQQMSER
		<u>. </u>	FLHHTRTLVEMKRDLDSIFRRIRTLKGKLARQHPEAFSHIPEAS
	, i		FLEEEDEDPIPPSTTTTIATSEQSTGSCDTSPDTVSPSLSPGFE
			DLSHVQPGSPAINGRSQTDDEEMTGE
6354	965	510	PSLRPMEPTRDCPLFGGAFSAILPMGAIDVSDLRPVPDNQEVFC
] !			HPVTDQSLIVELLELQAHVRGEAAARYHFEDVGGVQGARAVHVE
]			SVQPLSLENLALRGRCQEAWVLSGKQQIAKENQQVAKDVTLHQA
			LLRLPQYQTDLLLTFNQPP
6355	158	1662	RGSSAAFRGSGLRGAMIRRVLPHGMGRGLLTRRPGTRRGGFSLD
			WDGKVSEIKKKIKSILPGRSCDLLQDTSHLPPBHSDVVIVGGGV
1 1	ľ		LGLSVAYWLKKLESRRGAIRVLVVERDHTYSQASTGLSVGGICQ
			QFSLPENIQLSLFSASFLRNINEYLAVVDAPPLDLRFNPSGYLL
ļ i			LASEKDAAAMESNVKVQRQEGAKVSLMSPDQLRNKFPWINTEGV
[ALASYGMEDEGWFDPWCLLQGLRRKVQSLGVLFCQGEVTRFVSS
]			SQRMLTTDDKAVVLKRIHEVHVKMDRSLEYQPVECAIVINAAGA
]			WSAQIAALAGVGEGPPGTLQGTKLPVEPRKRYVYVWHCPQGPGL
]			ETPLVADTSGAYFRREGLGSNYLGGRSPTEQEEPDPANLEVDHD
			FFQDKVWPHLALRVPAFETLKVQSAWAGYYDYNTFDQNGVVGPH
			PLVVNMYFATGFSGHGLQQAPGIGRAVAEMVLKGRFQTIDLSPF
			LFTRFYLGEKIQENNII
6356	354	633	TGLTSSCLPLQVMMTKRTKDMGKFSSVTVSTIDEEEEEIEAREV
			ADSYAQNAKVIEKQLERKGMSKRRLQELAELEAKKAKMKGTLID
			NQFK

L			TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR
			DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS
		İ	SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
<u> </u>			RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTBAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD
			DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI
6364	21	1201	RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG
	ļ		RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
	ļ		RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE
			DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR
.			SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
			NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD
			RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL
			DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI
6363	21	1201	RRTRLGSSFPRRRDSSAMESYDVIANOPVVIDNGSGVIKAGFAG
			TVQPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKR
			ALGCLIAFLGVFLITRNRKKPIPFBPYISMDAMPGMQNMHDKGM
	;		ASOMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF
			TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ
٠.		• •	PFLLYMLVEIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV
resident and the	and Bree to a committee and a silver the san is	enting and the carridge where is around histories within	ELGYFASYAFAPLSLIYPLSAVSVIASAIIGIIFIKEKWKPKDF LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW
	•		GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWWLGLFLMLLG
6362	350	1576	TTMDGSHSAALKLQQLPPTSSSSAVSEASFSYKENLIGALLAIF
			NSTGIWDIQETVRKTYVLIL
			APGRWRRQITSQEFCHFIQGRCTFTPDDGETLHIQAGDALMLPA
6361	615	158	RPGLGQLQHCALAPQAGNRRCRFHGRLHALTRSTHRGKPMSIMQ FKDTLNTPLPDSSPVAVPLGAPIAVASTLSVEHNDGVETGIWAC
6267	<u> </u>	150	PAQTAGNVFLKHGSELRIIPRDRVGSC
	,		RLPYKVLSVPESTPFTAVLKFAAEEFKVPAATSAIITNDGIGIN
6360	1	345	GTRGAVPSTLEEVVLPPRSCRVFWIHSGTTMSKVSFKITLTSDP
	·		MKFQALRLTMLQRLEQLVEAK
.:		•	LMEADLGVEVPHEVAQYIKFEMPVLDSFVEKLKEEEEREIIKLT
			EDGPSEFALYIVHESGERTKLKDCEYPLISRILHGPCEKIARIF
			GPLEEAEEAPQLMRTKSDASCMSQRRPKCRAPGEAQRIRRHRFS INGHFYNHKTSVFTPAYGSVTNVRVNSTMTTLQVLTLLLNKFRV
			PSTSWMPRRPSCPLKEPSPQNGNITAQGPSIQPVHKAESSTDSS
			GKSFQLRHREEEGTL11EGLLNIAWGLRRPIRLQMQDDREQVHL
6359	98	1086	VCRQEEEKMKEDCLPSSHVPISDSKSIQKSELLGLLKTYNCYHE
			GAFVLVLYDELKKVI
	* * * * * * * * * * * * * * * * * * * *		DTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM MQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMG
			REFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRAAYFGVY
-			QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKSGTE
}			EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHT
			AISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK
6358	2009	1040	ASDALHSLSAPVLRLSSRSAARPATMTEQAISFAKDFLAGGIAA
			DSMNGEDLLLTGEVSWRPLVEKNPQSILKPHSPTYNDEGL
		1	CRIIVHFMWEDVQQRGRVMGVNPYILKKNMILMTNHFYAAILGY DEGILSDDHGLAAALWRTFFNRKCEDPRHLELLVEYVRKOIOYL
		}	TDFEEFFLRCQMPDTFNSWFLITLLHVWMCLVRMKQEGRSGKYM
			QPVEEKVGAFTKIIBAMGFTGPLKYSKWKIKIAALRMYTSCVEK
			RTSQWPQMSQSQACGGSEQIPGIDIQLNRKYHTTRKLSTTKDSP
6357	2	915	GLLRNMALLVRVLRNQTSISQWVPVCSRLIPVSPTQGQGDRALS
	sequence		\=possible nucleotide insertion)
	amino acid	amino acid sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
NO:	nucleotide ·	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
ID	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	Amino acid segment containing signal montide

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
!	amino acid	sequence	Codon, /=possible nucleotide deletion,
!	sequence	•	\=possible nucleotide insertion)
			RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE
	·		RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
6365	234	1989	KHKSRASCAARAQAFGPSREREVHSRFRSGLRRLGESNSGCCTM
1			ASMGTLAFDEYGRPFLIIKDQDRKSRLMGLBALKSHIMAAKAVA
1	<u> </u>		NTMRTSLGPNGLDKMMVDKDGDVTVTNDGATILSMMDVDHQIAK
			LMVELSKSQDDEIGDGTTGVVVLAGALLEEAEQLLDRGIHPIRI
			ADGYEQAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGSKV
1			VNSCHROMAEIAVNAVLTVADMERRDVDFELIKVEGKVGGRLED
			TKLIKGVIVDKDFSHPQMPKKVEDAKIAILTCPFEPPKPKTKHK
			LDVTSVEDYKALQKYEKEKFEEMIQQIKETGANLAICQWGFDDE
			ANHLLLQNNLPAVRWVGGPEIELIAIATGGRIVPRFSELTAEKL
			GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGGNKMIIEE
	and the second	and the second	AKRSLHDALCVIRNLIRDNRVVYGGGAAEISCALAVSQEADKCP
ľ			TLEQYAMRAFADALEVIPMALSENSGMNPIQTMTEVRARQVKEM
ļ			NPALGIDCLHKGTNDMKQQHVIETLIGKKQQISLATQMVRMILK
			IDDIRKPGESEE GNKEGAHSSTFWVLLSIFLGAVAMLCKEQGITVLGLNAVFDILV
6366	257	1898	IGKFNVLEIVOKVLHKDKSLENLGMLRNGGLLFRMTLLTSGGAG
1			MLYVRWRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYYSLNA
1			WLLLCPWWLCFDWSMGCIPLIKSISDWRVIALAALWFCLIGLIC
1			OALCSEDGHKRRILTLGLGFLVIPFLPASNLFFRVGFVVAERVL
1	, ,;		YLPSVGYCVLLTFGFGALSKHTKKKKLIAAVVLGILFINTLRCV
1			LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAAI
ì		1	RYYREAVRLNPKYVHAMNNLGNILKERNELQEAEELLSLAVQIQ
			PDFAAAWMNLGIVQNSLKRFEAAEQSYRTAIKHRRKYPDCYYNL
	•	·	GRLYADLNRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTGNL
1	,		AOAEAVGREALELIPNDHSLMFSLANVLGKSQKYKESEALFLKA
1 .			IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT
		1	KENYGLLRRKLELMQKKAV
6367	287	1934	SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS
			QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKNPRRNLSLMRE
			KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT
	and an all its mathematics are the first the property amount have	Control to the second of the s	GHSSLNTHIRADTGHKSSEYQEYGENPYRNKECKKAFSYLDSFQ.
			SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF
			CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER
		1	THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV
	,		FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG
			EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH
	1		ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR
	1		YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC
			GKAFIRASSCREHERTHTINR
6368	1	327	RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE
1 3300	_	1	DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK
1			DQFVCGETVPAPSANKELVKC
6369	1	1745	AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT
	_	1	PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET
1			FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG
1			ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD
ļ			TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY
			DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL
[IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE
1			CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM
			THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA
			FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG
			EKPHECKECGKVFKYFSSLRIHERTHTGEKPHECKQCGKAFRYF
		<u> </u>	

	1 Barrier 12 and 12	T = 47 :	· · · · · · · · · · · · · · · · · · ·
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
·	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			SSLHIHERTHTGDKPYECKVCGKAFTCSSSIRYHERTHTGEKPY
			ECKHCGKAFISNYIRYHERTHTGEKPYQCKQCGKAFIRASSCRE
			HERTHTINR
6370	1711	329	FVLSEQRLRTERTWPRSPGLGRGAAAAGARTAGAGLLRLLLGCG
1			ALVGGLRPVTMTTPANAQNASKTWELSLYELHRTPQEAIMDGTE
]			IAVSPRSLHSELMCPICLDMLKNTMTTKECLHRFCSDCIVTALR
Ĭ		ĺ	SGNKECPTCRKKLVSKRSLRPDPNFDALISKIYPSREEYEAHQD
			RVLIRLSRLHNQQALSSSIEEGLRMQAMHRAQRVRRPIPGSDQT
			TTMSGGEGEPGEGEGDGEDVSSDSAPDSAPGPAPKRPRGGGAGG SSVGTGGGGTGGVGGGAGSEDSGDRGGTLGGGTLGPPSPPGAPS
1			PPEPGGEIELVFRPHPLLVEKGEYCQTRYVKTTGNATVDHLSKY
1			LALRIALERRQQQEAGEPGGPGGGASDTGGPDGCGGEGGGAGGG
			DGPEEPALPSLEGVSEKQYTIYIAPGGGAFTTLNGSLTLELVNE
1			KFWKVSRPLELCYAPTKDPK
6371	3	288	GVANMSTAMNFGTKSFQPRPPDKGSFPLDHLGECKSFKEKFMKC
į			LHNNNFENALCRKESKEYLECRMERKLMLQEPLEKLGFGDLTSG
			KSEAKK
6372	2141	625	RVSAIASEGKAEERYKKLEDLLEKSFSLVKMPSLQPVVMCVMKH
1			LPKVPEKKLKLVMADKELYRACAVEVRRQIWQDNQALFGDEVSP
İ	•		LLKQYILEKESALFSTELSVLHNFFSPSPKTRRQGEVVQRLTRM
			VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRAELLMSLHDLDVG
}			EICTVDPCHKFTWCLDACIRERFVDSKRARELQGFLDGVKKGQE
		`	QVLGDLSMILCDPFAINTLALSTVRHLQELVGQETLPRDSPDLL LLLRLLALGQGAWDMIDSQVFKEPKMEVELITRFLPMLMSFLVD
			DYTFNVDQKLPAEEKAPVSYPNTLPESFTKFLQEQRMACEVGLY
			YVLHITKQRNKNALLRLLPGLVETFGDLAFGDIFLHLLTGNLAL
			LADEFALEDFCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV
			APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEQLDHRKPSPA
			QAAETPALELPLPSVPAPAPL
6373	67	711	PSRAARASPARLPAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK
	· ·		DIKEYVKWMMYWIIFALFTTAETFTDIFLCWFPFYYELKIAFVA
			WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL
e e can annue	programma in a september of the programma and the second section in the section in the second section in the section in the second section in the second section in the section in	i, tra i megaturu — i kiliji qili. Ilili, i kili meji usu, i kili me dalah dalah dalah dalah dalah dalah dalah Kilimpata i Kamada tersaman mengelarah dalah dalah dalah dalah dalah dalah dalah dalah dalah dalah dalah dalah	VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD
6374		2105	GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSSGTA
05/4	535	2105	HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS
]			CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC
			CPABLQTEGSNGKKEVLSGFOVVLEDTVLFPEGGGOPDDRGTIN
· 1			DISVLRVTRRGEOADHFTOTPLDPGSOVLVRVDWERRFDHMOOH
			SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA
			IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR
		·	VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL
	ļ		SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL
			QKWNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII
	l		ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL
<u></u>			EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE
6375	1	1535	AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT
		}	CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK
		.	PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY
'		.	FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY
			SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER
			HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP
			FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA
			SLLGSSLYRIATSKRYHLOPMHLLSLAVLIVVFSLFMLTFSTSP
	İ		GQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPETEQAGVLN
<u> </u>			OFFICE - TOT THE DETERMINED IN LOUDE THE WAY A TELEVISION OF THE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	1 1 1		WFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAV
ľ]		VGLFTVVRHDAELRVPSPTEEPYAPEL
6376	380	1437	ISSTDIDHYRFSFLVNSKMPSKESWSGRKTNRAAVHKSKOEGRO
0370]	2457	QDLLIAALGMKLGSPKSSVTIWQPLKLFAYSQLTSLVRRATLKE
	1		NEOIPKYEKIHNFKVHTFRGPHWCEYCANFMWGLIAOGVKCADC
l	1		GLNVHKQCSKMVPNDCKPDLKHVKKVYSCDLTTLVKAHTTKRPM
1			VVDMCIREIESRGLNSEGLYRVSGFSDLIEDVKMAFDRDGEKAD
1			ISVNMYEDINIITGALKLYFRDLPIPLITYDAYPKFIESAKIMD
į	į.		
			PDEQLETLHEALKLLPPAHCETLRYLMAHLKRVTLHEKENLMNA
		1045	ENLGIVFGPTLMRSPELDAMAALNDIRYQRLVVELLIKNEDILF
6377	2311	1845	SRIRRRSSRRPREPPGPSRRRRRRRPDPRTMPSEKTFKQRRTFE
		-	QRVEDVRLIREQHPTKIPVIIERYKGEKQLPVLDKTKFLVPDHV
1		}	NMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPISEVYESE
, , , , , , , , , , , , , , , , , , , ,			KDEDGFLYMVYASQETFGMKLSV
6378	686	191	GAGPWEAFPDGIGRRSRRARLPQYKRPPGRVGGGDSGRRNMAVA
	1		DLALIPDVDIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYK
]		i	WAEYHADIYDKVSGDMQKQGCDCECLGGGRISHQSQDKKIHVYG
L			YSMAYGPAQHAISTEKIKAKYPDYEVTWANDGY
6379	35	378	BRAGSPSPSRAALRRCAPQRSQAPRWPDRAACRRSFQGSQGRAY
1		}	LFNSVVNVGCGPABERVLLTGLHAVADIYCENCKTTLGWKYEHA
			FESSQKYKEGKYIIELAHMIKDNGWD
6380	1414	462	PAVQGQRGAGPPTGRGSGNMARFALTVVRHGETRFNKEKIIQGQ
			GVDEPLSETGFKQAAAAGIFLNNVKFTHAFSSDLMRTKQTMHGI
			LERSKFCKDMTVKYDSRLRERKYGVVEGKALSELRAMAKAAREE
1			CPVFTPPGGETLDQVKMRGIDFFEFLCQLILKEADQKEQFSQGS
İ .	, ,	1	PSNCLETSLAEIFPLGKNHSSKVNSDSGIPGLAASVLVVSHGAY
		1	MRSLFDYFLTDLKCSLPATLSRSELMSVTPNTGMSLFIINFEEG
•			REVKPTVQCICMNLQDHLNGLTENSLGLNLPSKSNHFEPLKGVP
			LALFTSLLC
6381	1668	218	AVVRAQGSRGFSGAGWRPRQAAAMNFSEVFKLSSLLCKFSPDGK
		1	YLASCVQYRLVVRDVNTLQILQLYTCLDQIQHIEWSADSLFILC
}	•		AMYKRGLVQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT
		and the second s	TEFHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER
CONTRACTOR MANAGEMENT (SE	and the property of the state o	To the common the common of th	RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIEWAPNGCVLAVWD
			TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG
] .			SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG
1		1	LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP
i		1	KIGIGMLAFSPDSYFLATRNDNIPNAVWVWDIQKLRLFAVLEQL
1			SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA
			VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT
6382	1 2	1062	FEEDEDRNLCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK
	_		KHHVLETEKTPKDWVROHRKEEKMKSHKLEEEFEWLKKSEVLYY
		1	TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL
1		l	LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS
	1	1	AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF
			HNGRYLRRELIGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG
1		į	KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM
1			IDFAHTTCRLYGEDTVVHEGODAGYIFGLOSLIDIVTEISEESG
1		<u> </u>	<u> </u>
(303	1 2250		E CDA DCD DCD VCCO DA ADARA DA ADARA DA ADARA VODO COVOCUCA A CDEEV
6383	3159	1061	SPAPGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK
1			GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP
1		1	AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK
1			PPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGKS
[SSSSSASAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS
1		1	GWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVEQKVQSLQA
1	1	I	TFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNEI

	•		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	Cacarine M. Thronding, Kanginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
·	1	sequence	Codon, /=possible nucleotide deletion,
	sequence	· .	\=possible nucleotide insertion)
			LKDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIAIF
1			TEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVKEIQTS
1	1		AKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAFKEAAD
			TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGP
			KEDGGFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMQVASARQT
			ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLASTVRSL
1	1		GETQLVLYGDVEBLKRSVGBLPSTVESLQKVQEQVHTLLSQDQA
1	ł	i	QAARLPPQDFLDRLSSLDNLKASVSQVEADLKMLRTAVDSLVAY
ł			SVKIETNENNLESAKGLLDDLRNDLDRLFVKVEKIHEKV
6384	738	1904	IWEVPVCLTHLLHLQQANQPLPPPSSSINEEDADEANRAIGEKR
			AAPDSGKKPKTPKTKQQKDPNEPQKPVSAYALFFRDTQAAIKGQ
			NPNATFGEVSQIVASMWDSLGEEQKQVYKRKTEAAKKEYLKALA
İ		<u>}</u>	AYRASLVSKAAAESAEAQTIRSVQQTLASTNLTSSLLLNTPLSQ
			HGTVSASPQTLQQSLPRSIAPKPLTMRLPMNQIVTSVTIAANMP
			SNIGAPLISSMGTTMVGSAPSTQVSPSVQTQQHQMQLQQQQQQ
			OCOMOCMOCOCI CONOMINO TO COMOCCITE TO THE CONOCCITE OF TH
			QQQMQQMQQQQLQQHQMHQQIQQQMQQQHFQHHMQQHLQQQQQH
1			LQQQINQQQLQQQLQQQQLQLQLQHMQHQSQPSPRQHSPVASQI
6385	2	1504	TSPIPAIGSPQPASQQHQSQIQSQTQTQVLSQVSIF
0303	2	1584	PRVRAADVAAGAQAVVSAGMAKSNGENGPRAPAAGESLSGTRES
1 1			LAQGPDAATTDELSSLGSDSEANGFAERRIDKFGFIVGSQGAEG
1			ALEEVPLEVLRQRESKWLDMLNNWDKWMAKKHKKIRLRCQKGIP
1		•	PSLRGRAWQYLSGGKVKLQQNPGKFDELDMSPGDPKWLDVIERD
1		5	LHRQFPFHEMFVSRGGHGQQDLFRVLKAYTLYRPEEGYCQAQAP
1			IAAVLLMHMPAEQAFWCLVQICEKYLPGYYSEKLEAIQLDGEIL
			FSLLQKVSPVAHKHLSRQKIDPLLYMTEWFMCAFSRTLPWSSVL
1	•		RVWDMFFCEGVKIIFRVGLVLLKHALGSPEKVKACQGQYETIER
			LRSLSPKIMQEAFLVQEVVELPVTERQIEREHLIQLRRWQETRG
i i	;	,	ELQCRSPPRLHGAKAILDAEPGPRPALQPSPSIRLPLDAPLPGS
1 1			KAKPKPPKQAQKEQRKQMKGRGQLEKPPAPNQAMVVAAAGDACP
1			POHVPPKDSAPKDSAPQDLAPQVSAHHRSQESLTSQESEDTYL
6386	819	195	TVCGSFYLGIMQRASRLKRELHMLATEPPPGITCWQDKDQMDDL
		• •	RAQILGGANTPYEKGVFKLEVIIPERYPFEPPQIRFLTPIYHPN
		· · · · · · · · · · · · · · · · · · ·	IDSAGRICLDVLKLPPKGAWRPSINTATVITSIQLIMSEPNEDD
a electron printer men	THE WAR IN THE WATER TO SEE STATE OF THE PARTY	the attributed may published the far her a	PLMADISSEFKYNKPAFLKNARQWTEKHARQKQKADEEEMLDNL
1 1			PEAGDSRVHNSTQKRKASQLVGIEKKFHPDV
6387	<u> </u>	662	
""	-	60 <i>2</i>	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
	}		KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNQK
1			NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
1 1			REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
 			STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
6388	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
1			KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNQK
j l			NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
1			REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
<u> </u>			STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
6389	1074	497	AEPGDRMAGHRLVLVLGDLHIPHRCNSLPAKFKKLLVPGKIQHI
1		İ	LCTGNLCTKESYDYLKTLAGDVHIVRGDFDENLNYPEQKVVTVG
1	·		QFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHKFEAF
1 1	1		EHENKFYINPGSATGAYNALETNIIPSFVLMDIQASTVVTYVYQ
	i		LIGDDVKVERIEYKKP
6390	158		
5550	720	535	GEERKEGRAPGKAFAPERNPAKMEKEETTRELLLPNWQGSGSHG
1 1			LTIAQRDDGVFVQEVTQNSPAARTGVVKEGDQIVGATIYFDNLQ
1-630-1			SGEVTQLLNTMGHHTVGLKLHRKGDRFFPSLGQTWDP
6391	5386	2897	VRWNSKTECYLSIQTQENFPANLNELVNCIVISSLVTTQRKLKA
			MSLLGSRNQLARAVLNPNPMDFCTKDLLTTTSERIIAYLRDFNE
			DQKKAIETAYAMVKHSPSVAKICLIHGPPGTGKSKTIVGLLYRL

	·		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			LTENQRKGHSDENSNAKIKQNRVLVCAPSNAAVDELMKKIILEF
İ			KEKCKDKKNPLGNCGDINLVRLGPEKSINSEVLKFSLDSQVNHR
			MKKELPSHVQAMHKRKEFLDYQLDELSRQRALCRGGREIQRQEL
	·		DENISKVSKERQELASKIKEVQGRPQKTQSIIILESHIICCTLS
1			TSGGLLLESAFRGQGGVPFSCVIVDEAGQSCEIETLTPLIHRCN
			KLILVGDPKQLPPTVISMKAQEYGYDQSMMARFCRLLEENVEHN
Ì			MISRLPILQLTVQYRMHPDICLFPSNYVYNRNLKTNRQTEAIRC
			SSDWPFQPYLVFDVGDGSERRDNDSYINVQEIKLVMEIIKLIKD
			KRKDVSFRNIGIITHYKAQKTMIQKDLDKEFDRKGPAEVDTVDA
			FQGRQKDCVIVTCVRANSIQGSIGFLASLQRLNVTITRAKYSLF
			ILGHLRTLMENQHWNQLIQDAQKRGAIIKTCDKNYRHDAVKILK
1			LKPVLQRSLTHPPTIAPEGSRPQGGLPSSKLDSGFAKTSVAASL
1 ,			YHTPSDSKEITLTVTSKDPERPPVHDQLQDPRLLKRMGIEVKGG
	1 '		IFLWDPQPSSPQHPGATPPTGEPGFPVVHQDLSHVQQPAAVVAA
			LSSHKPPVRGEPPAASPEASTCQSKCDDPEEELCHRREARAFSE
6392			GEQEKCGSETHHTRRNSRWDKRTLEQEDSSSKKRKLL
6392	972	186	GRTGVDLASSMAHRLQIRLLTWDVKDTLLRLRHPLGEAYATKAR
			AHGLEVEPSALEQGFRQAYRAQSHSFPNYGLSHGLTSRQWWLDV
			VLQTFHLAGVQDAQAVAPIAEQLYKDFSHPCTWQVLDGAEDTLR
	1	1	ECRTRGLRLAVISNFDRRLEGILGGLGLREHFDFVLTSEAAGWP
		٠.	KPDPRIFQEALRLAHMEPVVAAHVGDNYLCDYQGPRAVGMHSFL
6393	2017	730	VVGPQALDPVVRDSVPKEHILPSLAHLLPALDCLEGSTPGL
0333	2017	730	TGGSKMAAVATCGSVAASTGSAVATASKSNVTSFQRRGPRASVT
			NDSGPRLVSIAGTRPSVRNGQLLVSTGLPALDQLLGGGLAVGTV
ł	1		LLIEEDKYNIYSPLLFKYFLAEGIVNGHTLLVASAKEDPANILQ
			ELPAPILIDDKCKKEFDEDVYNHKTPESNIKMKIAWRYQLLPKME IGPVSSSRFGHYYDASKRMPQELIEASNWHGFFLPEKISSTLKV
			EPCSLTPGYTKLLQFIQNIIYEEGFDGSNPQKKQRNILRIGIQN
	,		LGSPLWGDDICCAENGGNSHSLTKFLYVLRGLLRTSLSACIITM
			PTHLIQNKAIIARVTTLSDVVVGLESFIGSERETNPLYKDYHGL
· ·	1.		IHIRQIPRLNNLICDESDVKDLAFKLKRKLFTIERLHLPPDLSD
1	1 1 1	. I	TVSRSSKMDLAESAKRLGPGCGMMAGGKKHLDF
6394,	1418	511	GAAAGGEGARRPAAMATVMAATAAERAVLEBEFRWLLHDEVHA
to experient and committee.	m is magnetic commencer of the property of the second	AND THE PERSON OF THE PERSON O	VLKQLQDILKEASLRFTLPGSGTEGPAKOENFILGSCGTDOVKG
	1		VLTLQGDALSQADVNLKMPRNNQLLHFAFREDKQWKLQQIQDAR
			NHVSQAIYLLTSRDQSYQFKTGAEVLKLMDAVMLOLTRARNRLT
	,	:	TPATLTLPEIAASGLTRMFAPALPSDLLVNVYINLNKLCLTVYQ
			LHALQPNSTKNFRPAGGAVLHSPGAMFEWGSQRLEVSHVHKVEC
			VIPWLNDALVYFTVSLQLCQQLKDKISVFSSYWSYRPF
6395	13	658	PSGRPTRPLCCAARRGAARHGGSVSGWPAGRTPTETSNPGSSVM
			ESVTFEDVAVEFIQEWALLDSARRSLCKYRMLDQCRTLASRGTP
			PCKPSCVSQLGQRAEPKATERGILRATGVAWESQLKPEELPSMQ
1			DLLEEASSRDMQMGPGLFLRMQLVPSIEERETPLTREDRPALQE
<u></u>			PPWSLGCTGLKAAMQIQRVVIPVPTLGHRNPWVARDSGE
6396	1	1221	ANILSSPSKRGQKGTLIGYSPEGTPLYNFMGDAFQHSSQSIPRF
		ľ	IKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTNSLGLI
İ			SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF
			INGLFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL
			IGICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHGHSH
İ			GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD
			PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK
1			IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV
1			TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES
			MKYCKDGTYIM
6397	391	122	GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK
	<u> </u>		KLIAAQTGTRWNKIVLKKWYTIFKDHVSLGDYEIHDGMNLELYY

	SEQ	Predicted	Predicted end	
	ID	beginning	nucleotide	Amino acid segment containing signal peptide
	NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	1.0.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W-Trembonhan V Character V 17.
		amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		sequence	Sequence	\=possible nucleotide insertion)
		- Degacines		Q Q
	6398	353	1306	WARD HKQMGPLINRCKKILLPTTVPPATMRIWLLGGLLPFLLLLSGLQ
	0350	, 333	1300	
	1			RPTEGSEVAIKIDFDFAPGSFDDQYQGCSKQVMEKLTQGDYFTK
	İ	,		DIEAQKNYFRMWQKAHLAWLNQGKVLPQNMTTTHAVAILFYTLN SNVHSDFTRAMASVARTPQQYERSFHFKYLHYYLTSAIQLLRKD
	1			SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQFLSTSLLKEEA
	1			QEFGNQTLFTIFTCLGAPVQYFSLKKEVLIPPYELFKVINMSYH
	1			PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPIAIASLSFLTS
				VIIFSKSRV
	6399	75	1245	PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKRGVAVSGPTK
	1	,,	1213	RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQKKMAECEAEN
				EDLLKKLELYKEACEGQHKLECDLQQREEEIAELQKALSDMQVC
	1.			LFQEREHVLRLYSENDRLRIRELEDKKKIQNLLALVGTDAGEVT
	1.	4	•	YFCKEPPHKVTILQKTIQAVGECEQSESSAFKADPKISKRRPSR
	ì			ERKESSEHYQRDIQTLILQVEALQAQLGEQTKLSREQIEGLIED
-				RRIHLEEIQVQHQRNQNKIKELTKNLHHTQELLYESTKDFLQLR
	1	• ,		SENQNKEKSWMLEKDNLMSKIKQYRVQCKKKEDKIGKVLPVMHE
	ļ	•	•	SHHAQSEYIKVMSLCRNEVVYFSGRVEGIPKNLQFVM
	6400	2520	1053	KTMKCDEVVYEVQSAILRHNCGYAMKTGKFFHNLMERKDFETWL
			2000	DNISVTFLSLTDLQKNETLDHLISLSGAVQLRHLSNNLETLLKR
				DFLKLLPLELSFYLLKWLDPQTLLTCCLVSKQWNKVISACTEVW
			,	QTACKNLGWQIDDSVQDALHWKKVYLKAILRMKQLEDHEAFETS
		'		SLIGHSARVYALYYKDGLLCTGSDDLSAKLWDVSTGQCVYGIQT
	ł		•	HTCAAVKFDEQKLVTGSFDNTVACWEWSSGARTQHFRGHTGAVF
_]			SVDYNDELDILVSGSADFTVKVWALSAGTCLNTLTGHTEWVTKV
	ĺ			VLQKCKVKSLLHSPGDYILLSADKYEIKIWPIGREINCKCLKTL
				SVSEDRSICLOPRLHFDGKYIVCSSALGLYQWDFASYDILRVIK
•			•	TPEIANLALLGFGDIFALLFDNRYLYIMDLRTESLISRWPLPEY
•				RKSKRGSSFLAGEASWLNGLDGHNDTGLVFATSMPDHSIHLVLW
	÷	· ·	• • •	KEHG
	6401	109	766	PGAAWSRPDLRGCCTGPQPALRMLVLPSPCPQPLAFSSVETMEG
· 60 /			•	PPRRTCRSPEPGPSSSIGSPQASSPPRPNHYLLIDTQGVPYTVL
a salama salama	1	La de Caración de	an the second reserve as a second	VDEESOREPGASGAPGOKKCYSCPVCSRVFEYMSYLORHSITHS
CONTRACTOR SPECIAL CONTRACTORS	HE BY THE THREE SALE	ารที่เด็ก กลุ กระกับวิทยาลเก็บพระเกราะ	gaggigg and gibragines and only to overse season washing	EVKPFECDICGKAFKRASHLARHHSIHLAGGGRPHGCPLCPRRF
				RDAGELAQHSRVHSGERPFQCPHCPRRFMEONTLOKHTRWKHP
	6402	1196	279	TTSQCGGIRQSSAIPVASMEFAAICLRNALLLLPEEQQDPKQEN
•				GAKNSNQLGGNTESSESSETCSSKSHDGDKFIPAPPSSPLRKOE
				LENLKCSILACSAYVALALGDNLMALNHADKLLQQPKLSGSLKF
		,		LGHLYAAEALISLDRISDAITHLNPENVTDVSLGISSNEQDQGS
				DKGENEAMESSGKRAPQCYPSSVNSARTVMLFNLGSAYCLRSEY
				DKARKCLHQAASMIHPKEVPPEAILLAVYLELQNGNTQLALQII
				KRNQLLPAVKTHSEVRKKPVFQPVHPIQPIQMPAFTTVQRK
	6403	2	1690	RGIHTSVLQGNLQNQMYSHNVVIMNLNNLNLTQVQQRNLITNLQ
				RSVDDTSQAIQRIKNDFQNLQQVFLQAKKDTDWLKEKVQSLQTL
]	AANNSALAKANNDTLEDMNSQLNSFTGQMENITTISQANEQNLK
				DLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHH
				LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLR
			}	MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGP
		'		PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGPIG
				PAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPP
ĺ		[GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGP
				KGPPGPPGPSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY
İ			}	FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH
			l	WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC
				AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL
	6404	1012	222	AAALAMAAPAPGLISVFSSSQELGAALAQLVAQRAACCLAGARA
<u> </u>				

Γ	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	, i	\=possible nucleotide insertion)
				RFALGLSGGSLVSMLARELPAAVAPAGPASLARWTLGFCDERLV
				PFDHAESTYGLYRTHLLSRLPIPESQVITINPELPVEEAAEDYA
				KKLRQAFQGDSIPVFDLLILGVGPDGHTCSLFPDHPLLQERBKI
				VAPISDSPKPPPQRVTLTLPVLNAARTVIFVATGEGKAAVLKRI .
	,			LEDQERNPLPAALVQPHTGKLCWFLDEAAARLLTVPFEKHSPL
İ	6405	1	1456	AALPRPTPRAPLGREGTGSDSEMAASMFYGRLVAVATLRNHRPR
ł	1			TAQRAAAQVLGSSGLFNNHGLQVQQQQQRNLSLHEYMSMELLQE
				AGVSVPKGYVAKSPDEAYAIAKKLGSKDVVIKAQVLAGGRGKGT
ļ				FESGLKGGVKIVFSPEEAKAVSSQMIGKKLFTKQTGEKGRICNQ
Ì				VLVCERKYPRREYYFAITMERSFQGPVLIGSSHGGVNIEDVAAE
l				TPEAIIKEPIDIEEGIKKEQALQLAQKMGFPPNIVESAAENMVK
Ì				LYSLFLKYDATMIBINPMVEDSDGAVLCMDAKINFDSNSAYRQK
ļ				KIFDLQDWTQEDERDKDAAKANLNYIGLDGNIGCLVNGAGLAMA
		,		TMDIIKLHGGTPANFLDVGGGATVHQVTEAFKLITSDKKVLAIL
				VNIFGGIMRCDVIAQGIVMAVKDLEIKIPVVVRLQGTRVDDAKA
l				LIADSGLKILACDDLDEAARMVVKLSEIVTLAKQAHVDVKFQLP
i		· · ·		I
	6406	1036	167	HPRQMRGEDTPEAPPYSSGRYDSIXTEVSGCPEDLTVGRAPTAD
				DDDDDDDDDDDDKMNDSEGMDPERLKAFNMFVRLFVDENLDRM
				VPISKQPKEKIQAIIESCSRQFPEFQERARKRIRTYLKSCRRMK
				KNGMEMTRPTPPHLTSAMAENILAAACESETRKAAKRMRLEIYO
•			·	SSQDEPIALDKQHSRDSAAITHSTYSLPASSYSQDPVYANGGLN
				YSYRGYGALSSNLQPPASLQTGNHSNGESGEARALASRPAPSWV
				CRAALGSGMGRGKQRPVMERGCLTA
	6407	492	150	VGLCLAVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGV
			:	SWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNAC
		1		VLTISPVQPEDDADYYCSVGYGFSP
	6408	1458	903	RGCITSSQAWRLFGGVTRGFNMRIEKCYFCSGPIYPGHGMMFVR
			,	NDCKVFRFCKSKCHKNFKKKRNPRKVRWTKAFRKAAGKELTVDN
•				SFEFEKRRNEPIKYORELWNKTIDAMKRVEBIKOKRQAKFIMNR
				LKKNKELQKVQDIKEVKQNIHLIRAPLAGKGKQLEEKMVQQLQE
·9·				DVDMEDAP
many a Color of the Color of th	6409	150	446	NTALANLLRCFTCDRLCGGCTAPAPPAHQGIVLQPVMPSCDPGP.
which is the second to be the second	4-WENNER STANKE			GPACLPTKTFRSYLPRCHRTYSCVHCRAHLAKHDELISKSFQGS
			•	HGRAYLFNSV
•	6410	85	607	RGGTAGCVACLGCWGQSSSPKAAFPAGSACLPADSCPCLLFQAC
			1	AISGLFNCITIHPLNIAAGVWMIMNAFILLLCEAPFCCQFIEFA
				NTVAEKVDRLRSWQKAVFYCGMAVVPIVISLTLTTLLGNAIAFA
		1		TGVLYGLSALGKKGDAISYARIQQQRQQADEEKLAETLEGEL
	6411	302	772	RLSIMASSLNEDPEGSRITYVKGDLFACPKTDSLAHCISEDCRM
		-		GAGIAVLFKKKFGGVQELLNQQKKSGEVAVLKRDGRYIYYLITK
		1		KRASHKPTYENLQKSLEAMKSHCLKNGVTDLSMPRIGCGLDRLQ
		1		WENVSAMIEEVFEATDIKITVYTL
	6412	61	1709	RPVTSFSPLPGSCGGRLGTRTMLGRSLREVSAALKQGQITPTEL
ļ			ľ	CQKCLSLIKKTKFLNAYITVSEEVALKQAEESEKRYKNGQSLGD
j		1	1	LDGIPIAVKDNFSTSGIETTCASNMLKGYIPPYNATVVQKLLDQ
		1		GALLMGKTNLDEFAMGSGSTDGVFGPVKNPWSYSKQYREKRKQN
			1	PHSENEDSDWLITGGSSGGSAAAVSAFTCYAALGSDTGGSTRNP
:			· .	AAHCGLVGFKPSYGLVSRHGLIPLVNSMDVPGILTRCVDDAAIV
				LGALAGPDPRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEYLV
		I		PELSSEVQSLWSKAADLFESEGAKVIEVSLPHTSYSIVCYHVLC
		[1	TSEVASNMARFDGLQYGHRCDIDVSTEAMYAATRREGFNDVVRG
		1		RILSGNFFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLL
,				TPTTLSEAVPYLEFIKEDNRTRSAQDDIFTQAVNMAGLPAVSIP
				VALSNQGLPIGLQFIGRAFCDQQLLTVAKWFEKQVQFPVIQLQE
				LMDDCSAVLENEKLASVSLKQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
6413	2	885	HEPRCAGMAASLWMGDLEPYMDENFISRAFATMGETVMSVKIIR
	İ		NRLTGIPAGYCFVEFADLATAEKCLHKINGKPLPGATPAKRFKL
-	1		NYATYGKQPDNSPEYSLFVGDLTPDVDDGMLYEFFVKVYPSCRG
}			GKVVLDQTGVSKGYGFVKFTDELEQKRALTECQGAVGLGSKPVR
1	1		LSVAIPKASRVKPVEYSQMYSYSYNQYYQQYQNYYAQWGYDQNT
			GSYSYSYPQYGYTQSTMQTYEEVGDDALEDPMPQLDVTEANKEF
			MEQSEBLYDALMDCHWQPLDTVSSEIPAMM
6414	1	538	RGGRAALLPWRRFPCCRPRPQPARPSSRATPGPRSPGMATSIGV
			SFSVGDGVPEAEKNAGEPENTYILRPVFQQRFRPSVVKDCIHAV
	i		LKEELANAEYSPEEMPQLTKHLSENIKDKLKEMGFDRYKMVVQV
1			VIGEQRGEGVFMASRCFWDADTDNYTHDVFMNDSLFCVVAAFGC
			FYY
6415	2	1168	FVRQWQSSHRRACGLGCEARAGGGEEPRGRASSVAGWVGAFRAP
1			FIEAAVAGLGAGSGKRRRGWKMPVHSRGDKKETNHHDEMEVDYA
}			ENEGSSSEDEDTESSSVSEDGDSSEMDDEDCERRRMECLDEMSN
ļ	1		LEKQFTDLKDQLYKERLSQVDAKLQEVIAGKAPEYLEPLATLQE
	·		NMQIRTKVAGIYRELCLESVKNKYECEIQASRQHCESEKLLLYD
ļ			TVQSELEEKIRRLEEDRHSIDITSELWNDELQSRKKRKDPFWPD
			KKKPGVVSGPYIVYMLQDLDILEDWTTIRKAMATLGPHRVKTEP
			PVKLEKHLHSARSEEGRLYYDGEWYIRGQTICIDKKDECPTSAV
6416	410	1519	ITTINHDEVWFKRPDGSKSKLYISQLQKGKYSIKHS EIAPADLEIPACAPVLLSRATSSTMSVTGGKMAPSLTQEILSHL
0410	410	1319	GLASKTAAWGTLGTLRTFLNFSVDKDAQRLLRAITGQGVDRSAI
i	1		VDVLTNRSREQRQLISRNFQERTQQDLMKSLQAALSGNLERIVM
j	•		ALLQPTAQFDAQELRTALKASDSAVDVAIEILATRTPPOLQECL
	,		AVYKHNFQVEAVDGITSETSGILQDLLLALAKGGRDSYSGIIDY
			NLAEQDVQALQRAEGPSREETWVPVFTQRNPEHLIRVFDQYQRS
			TGQELEEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ
	1		ETEPNYQVLIRILISRCETDLLSIRAEFRKKFGKSLYSSLQDAV
			KGDCQSALLALCRAEDM
6417	1	845	RGESRVLWSELEGEAGGAGGWASSLNARMDNRFATAFVIACVLS
l			LISTIYMAASIGTDFWYEYRSPVQENSSDLNKSIWDEFISDEAD
	granista de tijas apat	o tratament in a communication	EKTYNDALFRYNGTVGLWRRCITIPKNMHWYSPPERTESFDVVT
	Balance and the second and are	Comment Comments	KCVSFTLTEQFMEKFVDPGNHNSGIDLLRTYLWRCQFLLPFVSL
]		GLMCFGALIGLCACICRSLYPTIATGILHLLAGLCTLGSVSCYV
] :		AGIELLHQKLELPDNVSGEFGWSFCLACVSAPLQFMASALFIWA
	'		AHTNRKEYTLMKAYRVA
6418	2	662	TRTRPRRPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH
	 		TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIFTTQQEAELVQ
			YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRRGRQ
	ļ ļ		TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTERQVKIWFQ
			NRRMKWKKENNKDKFPVSRQEVKDGETKKEAQELEEDRAEGLTN
6419	1	973	PGRPRVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP
			MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL
			PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV
			FWNLVWYFRRLDLPSNLPGLILSSEHCNKYSKIPRHCMSEDSKY
		,	VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF
	ļ.		NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYREI
			LFLSLVALGRENIDIDAFDKEYKMAYDRLTPSQVKSTHNCDRPP
]		STGVMECRKTFGEPYL
6420	207	1187	RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN
			YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH
			NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEDGPALIIFYH
		ļ	GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC
		.	ALHGPREKCVEILRSGHLLAISPGGVREALISDETYNIVWGHRR
			GFAQVAIDAKVPIIPMFTQNIREGFRSLGGTRLFRWLYEKFRYP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			FAPMYGGFPVKLRTYLGDPIPYDPQITAEELAEKTKNAVQALID
6155	1044		KHORIPGNIMSALLERFH
6421	· 1844	362	WALSLRROPERMSNKLLSPHPHSVVLRSEFKMASSPAVLRASRL
1			YQWSLKSSAQFLGSPQLRQVGQIIRVPARMAATLILEPAGRCCW
			DEPVRIAVRGLAPEQPVTLRASLRDEKGALFQAHARYRADTLGE LDLERAPALGGSFAGLEPMGLLWALEPEKPLVRLVKRDVRTPLA
1	· ·		
1	1		VELEVLDGHDPDPGRLLCQTRHERYFLPPGVRREPVRVGRVRGT
			LFLPPEPGPFPGIVDMFGTGGGLLEYRASLLAGKGFAVMALAYY
			NYEDLPKTMETLHLEYFEEAMNYLLSHPEVKGPGVGLLGISKGG
Í			ELCLSMASFLKGITAAVVINGSVANVGGTLRYKGETLPPVGVNR NRIKVTKDGYADIVDVLNSPLEGPDQKSFIPVERAESTFLFLVG
	1		QDDHNWKSEFYANBACKRLQAHGRRKPQIICYPETGHYIEPPYF
1	1 .		PLCRASLHALVGSPIIWGGEPRAHAMAQVDAWKQLQTFFHKHLG
		1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	PLCRASHALVGSPIIWGGEPRAHAMAQVDAWKQLQIFFHKHLG GREGTIPSKV
6422	181	2133	EGENLSWFQEFWGDIAKEFYWKTPCPGPFLRYNFDVTKGKIFIE
0422	1	2133	WMKGATTNICYNVLDRNVHEKKLGDKVAFYWEGNEPGETTQITY
1	1	· ·	HOLLVQVCQFSNVLRKQGIHKGDRVAIYMPMIPELVVAMLACAR
	1		IGALHSIVFAGFSSESLCERILDSSCSLLITTDAFYRGEKLVNL
		İ	KELADEALOKCOEKGFPVRCCIVVKHLGRAELGMGDSTSQSPPI
	1		KRSCPDVQISWNQGIDLWWHELMQEAGDECEPEWCDAEDPLFIL
			YTSGSTGKPKGVVHTVGGYMLYVATTFKYVFDFHAEDVFWCTAD
	1		iGWITGHSYVTYGPLANGATSVLFEGIPTYPDVNRLWSIVDKYK
	,	1	VTKFYTAPTAIRLLMKFGDEPVTKHSRASLOVLGTVGEPINPEA
			WLWYHRVVGAQRCPIVDTFWQTETGGHMLTPLPGATPMKPGSAT
			FPFFGVAPAILNESGEELEGEAEGYLVFKQPWPGIMRTVYGNHE
		,	RFETTYFKKFPGYYVTGDGCQRDQDGYYWITGRIDDMLNVSGHL
		1	LSTAEVESALVEHEAVAEAAVVGHPHPVKGECLYCFVTLCDGHT
			FSPKLTEELKKQIREKIGPIATPDYIQNAPGLPKTRSGKIMRRV
		1	LRKIAQNDHDLGDMSTVADPSVISHLFSHRCLTIQ
6423	614	1237	ANLKEIPROLPPETVLLYLDSNQITSIPNEIFKOLHQLRVLNLS
1			KNGIEFIDEHAFKGVAETLQTLDLSDNRIQSVHKNAFNNLKARA
1	1	,	RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRP
	وعادها أرامه والمسابقة بأريبي ويوالم	Lineagent ment with the second	FLNAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQN
gradicia, de solo	er grego i garoperanji konstantin nitopinačji i naditi kini	A transfers build a second of the course of the workings of	QEDARRHLEYLKSLPSRQKKADEPDDISTVV
6424	1	1188	KKVSWPVAAMVHCSCVLFRKYGNFIDKLRLFTRGGSGGMGYPRL
		,	GGEGGKGGDVWVVAHNRMTLKQLKDRYPRKRFVAGVGANSKISA
1			LKGSKGKDWEIPVPVGISVTDENGKIIGELNKENDRILVAQGGL
			GGKLLTNFLPLKGQKRIIHLDLKLIADVGLVGFPNAGKSSLLSC
		1	VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH
1	,		MNKGMGHKFLKHIERTRQLLFVVDISGFQLSSHTQYRTAFETII
		[LLTKELELYKEELQTKPALLAVNKMDLPDAQDKFHELMSQLQNP
			KDFLHLFEKNMIPERTVEFQHIIPISAVTGEGIEELKNCIRKSL
	<u></u>	<u></u>	DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII
6425	1850	1144	LAMEGGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG
			LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR
		,	CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA
			WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE
		1	RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE
		<u> </u>	KRPCTSMHFQLPIQA
6426	30	565	SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR
			LHAEFAAERDWEQFHQPRNLLLALVGEVGELABLFQWKTDGEPG
		1	PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI
			NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT
L		<u> </u>	ST
6427	145	959	AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK
1			NIREYVRWMMYWIYFALFMAAEIVTDIFISWFPFYYEIKMAFVL

SEQ	Predicted	Predicted end	I have a sid gogment a sub-little in the
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location		H=Histidine, I=Isoleucine, K=Lysine,
· ·	corresponding	corresponding to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 : .	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid		Codon, /=possible nucleotide deletion,
	sequence	sequence	Codon, /=possible nucleotide deletion,
ļ	sedueuce		\-possible nucleotide insertion)
			WLLSPYTKGASLLYRKFVHPSLSRHEKEIDAYIVQAKERSYETV
			LSFGKRGLNIAASAAVQAATKSQGALAGRLRSFSMQDLRSISDA
			PAPAYHDPLYLEDQVSHRRPPIGYRAGGLQDSDTEDECWSDTEA
			VPRAPARPREKPLIRSQSLRVVKRKPPVREGTSRSLKVRTRKKT
			VPSDVDS
6428	1982	444	SGSGGKMEDHQHVPIDIQTSKLLDWLVDRRHCSLKWQSLVLTIR
			EKINAAIQDMPESEEIAQLLSGSYIHYFHCLRILDLLKGTEAST
			KNIFGRYSSQRMKDWQEIIALYBKDNTYLVELSSLLVRNVNYEI
1			PSLKKQIAKCQQLQQBYSRKEEECQAGAAEMREQFYHSCKQYGI
1			TGENVRGELLALVKDLPSQLAEIGAAAQQSLGEAIDVYQASVGF
[VCESPTEQVLPMLRFVQKRGNSTVYEWRTGTEPSVVERPHLEEL
			PEQVAEDAIDWGDFGVEAVSEGTDSGISAEAAGIDWGIFPESDS
[•	KDPGGDGIDWGDDAVALQITVLEAGTQAPEGVARGPDALTLLEY
J			TETRNQFLDELMELEIFLAQRAVELSEEADVLSVSQFQLAPAIL
	·		QGQTKEKMVTMVSVLEDLIGKLTSLQLQHLFMILASPRYVDRVT
	·		EFLQQKLKQSQLLALKKELMVQKQQEALEEQAALEPKLDLLLEK
			TKELQKLIEADISKRYSGRPVNLMGTSL
6429	3413	3442	EPSSWTAAPRGPLAAHPLEAAVQEDDRRALSFDSRIKVFANGTL
			VVKSVTDKDAGDYLCVARNKVGDDYVVLKVDVVMKPAKIEHKEE
			NDHKVFYGGDLKVDCVATGLPNPEISWSLPDGSLVNSFMQSDDS
			GGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAENQVGKDEMRVR
	:		VKVVTAPATIRNKTCLAVQVPYGDVVTVACEAKGEPMPKVTWLS
			PTNKVIPTSSBKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGE
·			DRKTVWIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAEG
) ;			IPTPRVLWAFPEGVVLPAPYYGNRITVHGNGSLDIRSLRKSDSV
			QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH
!	,		TISLNCSAAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLH
			ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL
			VSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEGPQTLGRVSL
.		•	LDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPR
:			ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG
			VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT
	15.00	<u> </u>	TYTHVF
6430	1946	602	RTRVSTGLRRTLLWSEAVGASSTRGDTG1PGSGEGGAGPGGGEG
	, •		AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDFNKFCSFVLA
:	•		YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI
			QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM
			KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS
•			HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTPGDGEKRSRIKKSK
			KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEEEEEEEEEEMA
Ì			TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE
			TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR
			PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG
1			GPPKSGEP
6431	3	605	WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR
1		-	LEEEALRRKERLKALREKTGRKDKEDGBPKTKHLREEEEEGEKH
			RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV
			IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER
	ļ		LKGQEDSLASAVDAATEQKTCDSD
6432	56	1692	GGLGTMGSRIKONPETTFEVYVEVAYPRTGGTLSDPEVOROFPE
		2022	DYSDQEVLQTLTKFCFPFYVDSLTVSQVGONFTFVLTDIDSKQR
ĺ			FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ
			WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN
			LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA
			AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN MALDDVVILNVDTNTLETPFDDLQSLPNDVISSLKNRLKKVSTT

SEQ	Description 1	73	
, , ,	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
ID		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
, ,	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j ;	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TGDGVARAFLKAQAAFFGSYRNALKIEPEEPITFCEEAFVSHYR
į l			SGAMRQFLQNATQLQLFKQFIDGRLDLLNSGEGFSDVFEEEINM
, .			GEYAGSDKLYHQWLSTVRKGSGAILNTVKTKANPAMKTVYKFDI
l l			AENGCAPTPEEQLPKTAPSPLVEAKDPKLREDRRPITVHFGQVR
			PPRPHVVKRPKSNIAVEGRRTSVPSPEQNTIATPATLHILQKSI
			THFAAKFPTRGWTSSSH
6433	1524	484	APVTKRKEVFAKDSKGSALDAGRDPKRPALPETLCESGWASNTA
		}	PTTPPQPGWCLCGKDFKSSCQTPGREKERRLATMHGSCSFLMLL
1	i		LPLLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDML
i i			HMRWDEELAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDV
			PLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCG
			SHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP
		,	SGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMG
			AEGPDKPSVVSGLNSGPGHVWGPLLGLLLLPPLVLAGIF
6434	40	2002	MPQLNFGMADPTQMGGLSMLLLAGEHALGTPEVFSGTCRPDVSE
			SPELRQKSPLFQFAEISSSTSHSDASTKQCQTSALFQFAEISSN
			TSQLGGAEPVKRCGKSALFQLAEMCLASEGMKMEESKLIKAKES
			DGGRIKELEKGKEEKEIKMEKTDETRLQKEABFEKSAKBNLRDS
			KELRNFEALQIDDIMAIKMEDPKEIRKEELEEDHKCSHFPDFSY
	i		SASSKIIISDVPSRKDHMCHPHGIMIIEDPAALNKPEKLKKKKK
			KSKMDRHGNDKSTPKKTCKKRQSSESDIESVIYTIEAVAKGDWG
·)			IEKLGDTPRKKVRTSSSGKGSILDAKPPKKKVKSREKKMSKEKS
	Ì		SDTTKESRPPDFISISASKNISGETPEGIKAEPLTPMEDALPPS
			LSGQAKPEDSDCHRKIETCGSRKSERSCKGALYKTLVSEGMLTS
		i i	LRANVDRGKRSSGKGNSSDHEGCWNEESWTFSQSGTSGSKKFKK
,		 	TKPKEDCLLGSAKLDEEFEKKFNSLPQYSPVTFDRKCVPVPRKK
			TKPKEDCLLGSAKLDEEFEKKFNSLPQYSPVTFDRKCVPVPRKK KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT
			· ·
			KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT
6435	2227	657	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ
6435	2227	657	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA
6435	2227	657	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE
6435	2227	657	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE
6435	2227	657	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA
6435	2227	657	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD
6435	2227	657	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMEAM
6435	2227	657	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMBAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI
6435	2227	657	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMBAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY
6435	2227	657	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMEAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR
6435	2227	657	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEERDDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMBAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA
6435	2227	657	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMEAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR
6435	e in a second in the second		KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMEAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY
ar a se an	1295	657 341	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMEAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY GACRPPVRQDPDSGPDYEALPAGATVTTHWVAGAVAGILEHCVM
	e in a second in the second		KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDOLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMEAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDLRNVI GRCKDTLSTITGPTTQNTYGRNEGAMMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMHHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL
	e in a second in the second		KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQSHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQPAAPAPPAVSPREALMBAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVBFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQBVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGTLEHCVM YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL NVTATGAGPAHALYPACYEKLKKTLSDVIHPGGNSHIANGAAGC
	e in a second in the second		KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQSHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQPAAPAPPAVSPREALMEAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVBFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQBVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG
	e in a second in the second		KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQSHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQPAAPAPPAVSPREALMBAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVBFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQBVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGTLEHCVM YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG AFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL
	e in a second in the second		KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEERDIEE QQDEFFSGDNGVDLLIEDQLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMEAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG AFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS
	e in a second in the second		KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASOPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMEAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRQGHSDVDFA VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY GACRPPVRQDPDSGPDYEALPAGATVTTHWVAGAVAGILEHCVM YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG AFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT
6436	1295	341	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEERDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMEAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGTLEHCVM YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG AFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS AFRTVYQVGGVTAYPRGVQARVIYQIPSTAIAWSVYEFFKYLIT KRQEEWRAGK
ar a se an	e in a second in the second		KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASOPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMBAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERITVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGVAGTLEHCVM YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC VATLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG AFYRSYTTQLIMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT KRQEEWRAGK
6436	1295	341	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASOPT.VIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMBAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGTLEHCVM YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL NVTATGAGPAHALYFACYEKLKTLSDVIHPGGNSHIANGAAGC VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG AFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL SGACAGAVAAAATTPLDVCKTTLLNTQESLALNSHITGHITGMAS AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT KRQEEWRAGK PPAPAPPASPARHVTRTARGHLEGGSRAPPLLQAVFLQIKMMVK LIHTLADHGDDVNCCAFSFSLLATCSLDKTIRLYSLRDFTELPH
6436	1295	341	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTJVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMEAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG AFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS AFRTVYQVGGVTAYPRGVQARVIYQIPSTAIAWSVYEFFKYLIT KRQEEWRAGK PPAPAPPASPARHVTRTARGHLEGGSRAPPLLQAVFLQIKMMVK LIHTLADHGDDVNCCAFSFSLLATCSLDKTIRLYSLRDFTELPH SPLKFHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGQMLAV
6436	1295	341	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMEAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC VATLLHDAAMNPAEVKQRMQMYNSPYHRVTDCVRAVWQNEGAG AFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT KRQEEWRAGK PPAPAPPASPARHVTRTARGHLEGGSRAPPLLQAVFLQIKMMVK LIHTLADHGDDVNCCAFSFSLLATCSLDKTIRLYSLRDFTELPH SPLKFHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGQMLAV MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAQSYKLYRCG
6436	1295	341	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMEAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG AFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT KRQEEWRAGK PPAPAPPASPARHVTRTARGHLEGGSRAPPLLQAVFLQIKNMVK LIHTLADHGDDVNCCAFSFSLLATCSLDKTIRLYSLRDFTELPH SPLKFHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGQMLAV MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAQSYKLYRCG SVKDGSLAACAFSPNGSFFVTGSSCGDLTVWDDKMRCLHSEKAH
6436	1295	341	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD PTRESVLQPSPQVPATTVAHTATQQFAAPAPPAVSPREALMEAM HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC VATLLHDAAMNPAEVKQRMQMYNSPYHRVTDCVRAVWQNEGAG AFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT KRQEEWRAGK PPAPAPPASPARHVTRTARGHLEGGSRAPPLLQAVFLQIKMMVK LIHTLADHGDDVNCCAFSFSLLATCSLDKTIRLYSLRDFTELPH SPLKFHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGQMLAV MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAQSYKLYRCG

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
·	sequence		\=possible nucleotide insertion)
			TNTENILHTLTQHTRYVTTCAFAPNTLLLATGSMDKTVNIWQFD
			LETLCQARSTEHQLKQFTEDWSEEDVSTWLCAQDLKDLVGIFKM
			NNIDGKELLNLTKESLADDLKIESLGLRSKVLRKIEELRTKVKS
			LSSGIPDEFICPITRELMKDPVIASDGYSYEKEAMENWDPAKRN RTSPP
6438	109	901	
0430	103	301	EVQILRAKMFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNV NPALPLSPTGLAGSLTNALSNGLLSGGLLGILENLPLLDILKPG
			GGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPOLLELGLVOSP
			DGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRD
1	:		KQERIHLVLGDCTHSPGSLQISLLDGLGPLPIQGLLDSLTGILN
			KVLPELVQGNVCPLVNEVLRGLDITLVHDIVNMLIHGLQFVIKV
6439	23	412	SIQTASAITTEMASQSQGIQQLLQAEKRAAEKVADARKRKARRL
			KQAKEEAQMEVEQYRREREHEFQSKQQAAMGSQGNLSAEVEQAT
			RRQVQGMQSSQQRNRERVLAQLLGMVCDVRPQVHPNYRISA
6440	3 .	517	RARWNSDMGDLPGLVRLSIALRIQPNDGPVFYKVDGQRFGQNRT
		•	IKLLTGSSYKVEVKIKPSTLQVENISIGGVLVPLELKSKEPDGD
			RVVYTGTYDTEGVTPTKSGERQPIQITMPFTDIGTFETVWQVKF
6441		13.53	YNYHKRDHCQWGSPFSVIEYECKPNETRSLMWVNKESFL
544I	234	1373	KSGGLRRRQRPGRSAAVGEEELPPGMEKFKAAMLLGSVGDALGY
	'		RNVCKENSTVGMKIQEELQRSGGLDHLVLSPGEWPVSDNTIMHI
ì			ATAKALTTDYWCLDDLYREMVRCYVEIVEKLPERRPDPATIEGC AQLKPNNYLLAWHTPFNEKGSGFGAATKAMCIGLRYWKPERLET
	· ·		LIEVSVECGRMTHNHPTGFLGSLCTALFVSFAAQGKPLVQWGRD
ľ			MLRAVPLAEEYCRKTIRHTAEYQEHWFYFEAKWQFYLEERKISK
			DSENKAIFPDNYDAEEREKTYRKWSSEGRGGRRGHDAPMIAYDA
	'	*	LLAAGNSWTELCHRAMFHGGESAATGTIAGCLFGLLYGLDLVPK
1			GLYQDLEDKEKLEDLGAALYRLSTEEK
6442	34	796	AEDPAGGLAGQDTMFARGLKRKCVGHEEDVEGALAGLKTVSSYS
		·	LQRQSLLDMSLVKLQLCHMLVEPNLCRSVLIANTVRQIQEEMTQ
1			DGTWRTVAPQAAERAPLDRLVSTEILCRAAWGQEGAHPASGLGD
. [• '			GHTQGPVSDLCPVTSAQAPRHLQSSAWEMDGPRENRGSFHKSLD
3			QIFETLETKNPSCMEELFSDVDSPYYDLDTVLTGMMGGARPGPC
6443	2	555	EGLEGLAPATPGPSSSCKSDLGELDHVVEILVET
9443	·	555	MASPAASSVRPPRPKKEPQTLVIPKNAAEEQKLKLERLMKNPDK AVPIPEKMSEWAPRPPPEFVRDVMGSSAGAGSGEFHVYRHLRRR
-	<u> </u> :		EYORODYMDAMAEKOKLDAEFOKRLEKNKIAAEEOTAKRRKKRO
	<u> </u> '		KLKEKKLLAKKMKLEQKKQEGPGQPKEQGSSSSAEASGTEEEEE
	.		VPSFTMGR
6444	390	899	GSTPRGKMRAPIPEPKPGDLIEIFRPFYRHWAIYVGDGYVVHLA
			PPSEVAGAGAASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD
		•	DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA
			RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ
6445	2	753	AGAAGAAGAARSPRPQAHTKGVRGLPSRRRSPDCGRMELAAGSF
1	ļ		SEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLY
			EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGE
			TVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM
			PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIP
6446		1651	SWLINWAAKNGVPNFLKDMARACQNYLKKT
0440	1	1651	RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS
			DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAERTFSHCKS
j		•	EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS
1			VVEKLKHMEARALSAEAALARAREDLOKMKQFAQDFVMHTDVRT
	ļ		CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD
			FIYQNPHIFKDKVVLDVGCGTGILSMFAAKAGAKKVLGVDQSEI
——— —			

			•
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 .	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
			LYOAMDIIRLNKLEDTITLIKGKIEBVHLPVEKVDVIISEWMGY
	,		FLLFESMLDSVLYAKNKYLAKGGSVYPDICTISLVAVSDVNKHA
			DRIAFWDDVYGFKMSCMKKAVIPEAVVEVLDPKTLISEPCGIKH
İ		·	IDCHTTSISDLEFSSDFTLKITRTSMCTAIAGYFDIYFEKNCHN
			RVVFSTGPQSTKTHWKQTVFLLEKPFSVKAGEALKGKVTVHKNK
1			KDPRSLTVTLTLNNSTQTYGLQ
6447	1554	1068	RLGPAEWHLSGPCHATLGAANRGRALGVRAAWRGAPLCQRVMMP
044/	1334	1000	SRTNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIA
ı			LATVLFLIGAFLIIIGSLLLSGYISKGGADRAVPVLIIGILVFL
ļ			PGFYHLRIAYYASKGYRGYSYDDIPDFDD
6448	74	559	GOVLSHCYHYRSSRWRRGGLSRGRGAGVMALVPYEETTEFGLOK
0440	'*	557	FHKPLATFSFANHTIQIRQDWRHLGVAAVVWDAAIVLSTYLEMG
			AVELRGRSAVELGAGTGLVGIVAALLACRIRYERDNNFLAMLER
		and a second	
(140	F03	1676	QFIVRKVHYDPEKDVHIYEAQKRNQKEDL EYGVCENLRKLEITGVSCRDVYAKLLHRYRHILGLWOPDIGPYG
6449	597	1876	GLLNVVVDGLFIIGWMYLPPHDPHVDDPMRFKPLFRIHLMERKA
1			
			ATVECMYGHKGPHHGHIQIVKKDEFSTKCNQTDHHRMSGGRQEE
İ		ļ	FRTWLREEWGRTLEDIFHEHMQELILMKFIYTSQYDNCLTYRRI
1			YLPPSRPDDLIKPGLFKGTYGSHGLEIVMLSFHGRRARGTKITG
Ì			DPNIPAGQQTVEIDLRHRIQLPDLENQRNFNELSRIVLEVRERV
		1 :	RQEQQEGGHEAGEGRGRQGPRESQPSPAQPRAEAPSKGPDGTPG
}			EDGGEPGDAVAAAEQPAQCGQGQPFVLPVGVSSRNEDYPRTCRM
1		÷ .	CFYGTGLIAGHGFTSPERTPGVFILFDEDRFGFVWLELKSFSLY
<u></u>			SRVQATFRNADAPSPQAFDEMLKNIQSLTS
6450	848 .	269	FVPAPRTVSGKRSLPGEWEERGEGEQRTGREFSGNGGRAVEAAR
			MRLLCGLWLWLSLLKVLQAQTPTPLPLPPPMQSFQGNQFQGEWF
			VLGLAGNSFRPEHRALLNAFTATFELSDDGRFEVWNAMTRGQHC
		2	DTWSYVLIPAAQPGQFTVDHRVWTHEQAGRPQDQPAGQELVAAS
			RDAGPVHLPGQSSGPLG
6451	232	939	HSPTPPTSPRASTMEDVKLEFPSLPQCKEDAEEWTYPMRREMQE
	1		ILPGLFLGPYSSAMKSKLPVLQKHGITHIICIRQNIEANFIKPN
1		l	FQQLFRYLVLDIADNPVENIIRFFPMTKEFIDGSLQMGGKVLVH
1/2 / 2/2 E	The second of the	Para disease of the second	GNAGISRSAAFVIAYIMETFGMKYRDAFAYVQERRFCINPNAGF
1		1 :	VHQLQEYEAIYLAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHE
	<u> </u>		EEDDFGTMQVATAQNG
6452	1	652	RTRGESSNMEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQ
1	:		LKFLKPKINSFYAFEVKDAKGRTVSLEKYKGKVSLVVNVASDCQ
1			LTDRNYLGLKELHKEFGPSHFSVLAFPCNQFGESEPRPSKEVES
4	,		FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWK
			YLVNPEGQVVKFWRPEEPIEVIRPDIAALVRQVIIKKKEDL
6453	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC
			RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK
		1	DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
			FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT
L			PADSSGTAEGGSGVASPAQADKAEL
6454	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC
			RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK
			DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
1			FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT
1			PADSSGTAEGGSGVASPAQADKAEL
6455	1042	173	RVHLATVSASAAWDALGLPVRSHMQGSTRRMGVMTDVHRRFLQL
		1	LMTHGVLEEWDVKRLQTHCYKVHDRNATVDKLEDFINNINSVLE
			SLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAENELDLF
· ·			RKALELIIDSETGFASSTNILNLVDQLKGKKMRKKEAEQVLQKF
1			VQNKWLIEKEGEFTLHGRAILEMEQYIRETYPDAVKICNICHSL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine.
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequence	\=possible nucleotide insertion)
			LIOGOSCETCGIRMHLPCVAKYFOSNAEPRCPHCNDYWPHEIPK
			VFDPEKERESGVLKSNKKSLRSROH
6456	2	555	RPQSRSISMWRNSLLQVSSGLRWLRVCAMVDILGERHLVTCKGA
1		·	TVEAEAALQNKVVALYFAAARCAPSRDFTPLLCDFYTALVAEAR
1			RPAPFEVVFVSADGSSQEMLDFMRELHGAWLALPFHDPYRHELR
1	,		KRYNVTAIPKLVIVKQNGEVITNKGRKQIRERGLACFQDWVEAA
			DIFQNFSV
6457	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
ļ., , ļ		y * +	TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
6458	23	892	SFLTLSSQLKPKPVGEENICLDLKS
0420	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSQLKPKPVGEENICLDLKS
6459	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
1 . 1			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
·			SFLTLSSQLKPKPVGEENICLDLKS
6460	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
:			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
		a	IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
1 .1			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
:	,	. •	DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
		•	SFLTLSSQLKPKPVGEENICLDLKS
6461	1653	360	LQQRTLRITAVGQTHPIAWMAWEPSLGAFYGPASFITFVNCMYF
		550	LSIFIQLKRHPERKYELKEPTEEQORLAANENGEINHODSMSLS
			LISTSALENEHTFHSQLLGASLTLLLYVALWMFGALAVSLYYPL
]			DLVFSFVFGATSLSFSAFFVVHHCVNREDVRLAWIMTCCPGRSS
	ſ		YSVQVNVQPPNSNGTNGBAPKCPNSSAESSCTNKSASSFKNSSQ
			GCKLTNLQAAAAQCHANSLPLNSTPQLDNSLTEHSMDNDIKMHV
			APLEVQFRTNVHSSRHHKNRSKGHRASRLTVLREYAYDVPTSVE
			GSVQNGLPKSRLGNNEGHSRSRRAYLAYRERQYNPPQQDSSDAC
			STLPKSSRNFEKPVSTTSKKDALRKPAVVELENQQKSYGLNLAI
		· · · · · · · · · · · · · · · · · · ·	QNGPIKSNGQEGPLLGTDSTGNVRTGLWKHETTV
6462	3	773	SEELDREKKLKEDSPRKTPNKESGVPSLPVSLTSIKEEPKEAKH
	1		PDSQSMEESKLKNDDRKTPVNWKDSRGTRVAVSSPMSQHQSYIQ
]].			YLHAYPYPQMYDPSHPAYRAVSPVLMHSYPGAYLSPGFHYPVYG
		•	KMSGREETEKVNTSPSVNTKTTTESKALDLLQQHANQYRSKSPA
	1		PVEKATAEREREAERERDRHSPFGQRHLHTHHHTHVGMGYPLIP
6463	2	350	GQYDPFQGLTSAALVASQQVAAQASASGMFPGQRRE VILCILGGWIFKNADRSMEKKKGEPRTRAEARPWVDEDLKDSSD
0303	-	350	LHQAEEDADEWOESEENVEHIPFSHNHYPEKEMVKRSQEFYELL
,	į		httpacedadewgeseenveripfshamipekemvkrsgefiell nkrrsvrfisnegvpmevidnvirtagl
6464	12	1154	GILRQKEREERNRIHKKEILFLEHLLVVPSEMSSLSGKVQTVLG
			OTATOWN STANDARD TOTAL T

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
			LVEPSKLGRTLTHEHLAMTFDCCYCPPPPCQEAISKEPIVMKNL
			YWIQKNAYSHKENLQLNQETBAIKEELLYFKANGGGALVENTTT
			GISRDTQTLKRLABETGVHIISGAGFYVDATHSSETRAMSVEQL
			TDVLMNEILHGADGTSIKCGIIGEIGCSWPLTESERKVLQATAH
i			AOAOLGCPVIIHPGRSSRAPFOIIRILQRAGADISKTVMSHLDR
			TILDKKELLEFAQLGCYLEYDLFGTELLHYQLGPDIDMPDDNKR
			IRRVRLLVEEGCEDRILVAHDIHTKTRLMKYGGHGYSHILTNVV
			PKMLLRGITENVLDKILIENPKQWLTFK
6465	126	1396	KMTVFFKTLRNHWKKTTAGLCLLTWGGHWLYGKHCDNLLRRAAC
5±05	120	1370	OEAQVFGNOLIPPNAQVKKATVFLNPAACKGKARTLFEKNAAPI
1	,		LHLSGMDVTIVKTDYEGOAKKLLELMENTDVIIVAGGDGTLOEV
1			VTGVLRRTDEATFSKIPIGFIPLGETSSLSHTLFAESGNKVOHI
			TDATLAIVKGETVPLDVLQIKGEKEQPVFAMTGLRWGSFRDAGV
		, = 1	KVSKYWYLEPLKIKAAHFFSTLKEWPQTHQASISYTGPTERPPN
			EPEETPVORPSLYRRILRRLASYWAQPQDALSQEVSPEVWKDVQ
			LSTIELSITTRNNOLDPTSKEDFLNICIEPDTISKGDFITIGSR
		:	KVRNPKLHVEGTECLQASQCTLLIPEGAGGSFSIDSEBYEAMPV
ļ			EVKLLPRKLOFFCDPRKREOMLTSPTQ
	1134		VARGTELSOLEKAHPPADMGRRKSKRKPPPKKKMTGTLETQFTC
6466	1134	828	<u> </u>
	·		PFCNHEKSCDVKMDRARNTGVISCTVCLEEFQTPITYLSEPVDV
-	365		YSDWIDACEAANQ
6467	301	2571	GELRVLALAHGELACHAVLTASLLSLRSRLMDSDMDYERPNVET
1			IKCVVVGDNAVGKTRLICARACNATLTQYQLLATHVPTVWAIDQ
			YRVCQEVLERSRDVVDDVSVSLRLWDTFGDHHKDRRFAYGRSDV
	:	, .	VVLCFSIANPNSLHHVKTMWYPEIKHFCPRAPVILVGCQLDLRY
1	.		ADLEAVNRARRPLARPIKPNEILPPEKGREVAKELGIPYYETSV
			VAQFGIKDVFDNAIRAALISRRHLQFWKSHLRNVQRPLLQAPFL
	,		PPKPPPPIIVVPDPPSSSEECPAHLLEDPLCADVILVLQERVRI
	•	:	FAHKIYLSTSSSKFYDLFLMDLSEGELGGPSEPGGTHPEDHQGH
			SDQHHHHHHHHGRDFLLRAASFDVCESVDEAGGSGPAGLRAST
			SDGILRGNGTGYLPGRGRVLSSWSRAFVSIQEEMAEDPLTYKSR
1 .			LMVVVKMDSSIQPGPFRAVLKYLYTGELDENERDLMHIAHIAEL
1			LEVFDLRMMVANILNNEAFMNQEITKAFHVRRTNRVKECLAKGT
			FSDVTFILDDGTISAHKPLLISSCDWMAAMFGGPFVESSTREVV
].		FPYTSKSCMRAVLEYLYTGMFTSSPDLDDMKLIILANRLCLPHL
1 .	ŀ		VALTEQYTVTGLMEATQMMVDIDGDVLVFLELAQFHCAYQLADW
	``	·	CLHHICTNYNNVCRKFPRDMKAMSPENQEYFEKHRWPPVWYLKE
	[.		EDHYQRARKEREKEDYLHLKRQPKRRWLFWNSPSSPSSSAASSS
			SPSSSSAVV
6468	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
			LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
			KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
	<u> </u>		SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN
J.	ľ		QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
1			TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
			GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL
1			PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLF
			ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES
1	ļ		TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
ļ	1		GKGKFSRAHFVLLSLL
6469	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
			LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
1			KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
1			SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN
1	1		QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
1			TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
L			

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1.	sequence	Doquemoc	\=possible nucleotide insertion)
———			GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL
			PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLF
			ITIALIGTGWAPIKHILSDKDKKIFMIVIPRRVLANVAYIIIBS
1			TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
ļ			GKGKFSRAHFVLLSLL
6470	2726	1437	AAASGVSSRADAPVLAQSPASAGNGRPSTPRVPGSRRHPSAPRS
			GPLPREDGCRTPGPQLLPLPGALLRPRTLLSSAAETGRSRHPDT
			QHPSSGGRCRGGTESPSSAAGRPASMAEAEEDCHSDTVRADDDE
1			ENESPAETDLQAQLQMFRAQWMFELAPGVSSSNLENRPCRAARG
1			SLQKTSADTKGKQEQAKEEKARELFLKAVEEEQNGALYEAIKFY
			RRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDDSKMADLLS
1]		YFQQQLTFQESVLKLCQPELESSQIHISVLPMEVLMYIFRWVVS
-	· .		SDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVWGRSCIKLV
		e di kanalawan kata	PYTSWREMFLERPRVRFDGVYISKTTYIRQGEQSLDGFYRAWHQ
			VEYYRYIRFFPDGHVMMLTTPEEPQSIVPRLRTR
6471	1750	299	FFFDKMAAGGSGVGGKRSSKSDADSGFLGLRPTSVDPALRRRRR
			GPRNKKRGWRRLAGEPLGLEVDOFLEDVRLOERTSGGLLSEAPN
			EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLILENTSK
1			VPAPKDVLAHQVPNAKKLRRKEQLWEKLAKQGELPREVRRAOAR
1		•	LLNPSATRAKPGPODTVERPFYDLWASDNPLDRPLVGODEFFLE
1			QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHOTLLS
4		\$	AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCEGLLE
1			ESDGEGEPGQGEGPEAGDAEVCPTPARLATTEKKTEQQRRREKA
1			VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRR
,			ROARREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLKPEG
			NILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFREIQL
6472	3	897	SCGSDRAQWAMEFPFDVDALFPERITVLDQHLRPPARRPGTTTP
			ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRHVVY
			ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPLCIL
			DFYIHESVQRHGHGRELFQYMLQKERVEPHQLAIDRPSQKLLKF
			LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHSRAA
1			AVDPTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPWPLN
		·	RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP
6473	, 22	912	SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVPTNKACFDCGAK
		·	NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNWFQ
			LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ
] ; [•		LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAW
'			DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL
			KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE
6474	. 3	460	KLREQQAADAKKQAEESMVASMRLAYQELQIDR
03/4	· 3	462	LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS
			KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA
			KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP
6475	3	463	PSTLSVKGQIETVRVKGTEN
07/5	3	462	LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS
			KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA
	ļ		KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP
6476	106	1000	PSTLSVKGQIETVRVKGTEN
0 3 / 0	709	1090	ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL
			KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE
			RQLAKRQHLEEQRLQQERQREQEQRRERKRKISCLSFALDDLDD
			QADAAEARRAGNLGKNPDVDTSFLPDRDREEEENRLREELRQBW
			EAQREKVKDEEMEVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL
]	QGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK
.			SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF
Ll			PASRWEAYDPEKKWDKYTIR

SEQ Predicted Predicted end Amino acid segment containing ID beginning nucleotide (A=Alanine, C=Cysteine, D=Aspa	
)	artic Acid V- '
NO: nucleotide location Glutamic Acid, F=Phenylalanine	
1	
corresponding to first L=Leucine, M=Methionine, N=Asg	
amino acid residue of S=Serine, T=Threonine, V=Valin	
1 1	nknown *-Ston
, 02	·
SEPVLFLKPSTAYAPEGSPILMPAYTRNLF	
AVPEAAAMDYVGGYALCIDMTARDVQDECI	
SCPVSAFVPKEKIPDPHKLKLWLKVNGELI	
IISYVSKIITLEEGDIILTGTPKGVGPVKI	PINDETENGTIONSM
TFKVEKPEY	OC CATEFORMAL DE PUBLICA
6478 2 1495 FVSSRILPESLASSEASTLEAMGRKEEDDO	
IFMEVLGSGAFSEVFLVKQRLTGKLFALKO	
EIAVLKKIKHENIVTLEDIYESTTHYYLVI	
RGVYTEKDASLVIQQVLSAVKYLHENGIVI	
ENSKIMITDFGLSKMEQNGIMSTACGTPG'	
VDCWSIGVITYILLCGYPPFYEETESKLFI	
DDISESAKDFICHLLEKDPNERYTCEKAL	
YPSVSLQIQKNFAKSKWRQAFNAAAVVHHI	
EVENRPPETQASETSRPSSPEITITEAPVI	
QHGRRPTAPGGRSLNCLVNGSLHISSSLVI SSCLNIGSKGKSSYCSBPTLLKKANKKONI	
	FKSEVMVPVKASGSS
HCRAGQTGVCLIM	r ananyny povent a
6479 3 949 SCRGPGWHPAGGQAGAMELLSALSLGELAN	
YFIVSILYLKYEPGAVELSRRHPIASWLC	
LGEPLIDYFSNNSSILLASAVWYLIFFCP	
IFVAMKEVVRVRKIAVGIHHAHHHYHHGW	
LMSNFEQLLRGVWKPETNEILHMSFPTKA	
LPVSKASLIFIFTLFMVSCKVFLTATHSH	
FGSACGGDHHHDNHGGSHSGGGPGAQHSA	MPARSAEEDSEGSKK
KKAKKAD	MEETOL OPPUDGT CV
6480 192 514 DFMSIYFPIHCPDYLRSAKMTEVMMNTQP	
QIFPDPSDFDRCCKLKDRLPSIVVEPTEG	PAESCEDKMEKEERP
VQEDEQDICEETAKENKEQ	DITUDDAL TOTUUM
6481 110 1131 KSRMDLDVVNMFVIAGGTLAIPILAFVAS	
WRRTLGMQVRYVHHEDYQFCYSFRGRPGH	
MWLSVVKFLPKNLHLVCVDMPGHEGTTRS	
QFVECLKLNKKPFHLVGTSMGGQVAGVYA	
AGLQYSTDNQFVQRLKELQGSAAVEKIPL	
SYVRFKVPQQILQGLVDVRIPHNNFYRKL	
NMDKIKVPTQIIWGKQDQVLDVSGADMLA	
HSVVMERPRKTAKLIIDFLASVHNTDNNK	
6482 2517 568 EPVSKVSQSRRKAGVPTANIEESQAVEAA	
ALALSRVELHKNPBKEPYKSKYSARALLE	
RPEAEDGPGAGDHALGLPAEVVEPEGPVA	
NHIDTEELSAGEEHLVKCLRLLRRYRLSH	
LWSEREEIETAQAYLESSEALYNQYMKEV	
EKLTEQERSKRPEKVYTHNLYYLAQVYQH	
KRQLEHNAYHPIEWAINAATLSQFYINKL	
FGQTGKISATEDTPEAEGEVPELYHQRKG	
NAQLSMQDNIGELDLDKQSELRALRKKEL	
GELCDAISAVEEKVSYLRPLDFEEARELF	
IDGYVTDHIEVVQDHSALFKGLAFFETDM	
PLTVDLNPQYYLLVNRQIQFEIAHAYYDM	MULKVAIADRLRDPD
SHIVKKINNLNKSALKYYQLFLDSLRDPN	
MLAKFRVARLYGKIITADPKKELENLATS	
RAAQEIEVELELSKEMVSLLPTKMERFRT	
6483 3 623 NSHLLCGLRARAPLSANGREARAMEQRLA	
PAASQGAQTPGEKAEAAATLKAAPGWLKR	PLVWKPRPASARAQP
GLVQEAAQPQGSTSETPWNTAIPLPSCWD	QSFLTNITFLKVLLW
LVLLGLFVELEFGLAYFVLSLFYWMYVGT	

Sed Predicted Predicted Predicted Not Incleotide Incleot				
Inclection Cortesponding to first Section Helistidine, Italeucuine, Kelyysine, Lebeucine, Kelysine, Lebeucine, Membethionine, NaAsparagine, Perodine, Gollutamine, Razyainine, Sestine, T-Threonine, Vevaline, amino acid residue of amino acid sequence Sectine, T-Threonine, Vevaline, Sestine, T-Threonine, Vevaline, Veraline, Sequence Sequence Sectine, T-Threonine, Vevaline, Veraline, Veraline, Sequence Sectine, T-Threonine, Vevaline, Veraline, Veraline, Veraline, Sequence Sectine, T-Threonine, Vevaline, Ver	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cortesponding Corresponding Corresponding Corresponding Cofirst amino acid amino acid cesidue of amino acid cesidue of amino acid cesidue of amino acid cesidue of amino acid cesidue of amino acid cesidue of amino acid cesidue of amino acid cesidue of amino acid cesidue of amino acid cesidue of	1 -		ł	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first mino acid residue of irest mino acid residue of amino acid residue of amino acid sequence sequenc	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence sequence sequence sequence sequence (No. +possible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide insertion) VPNPGCRAIOGILARGEMERICALPRIAGR 6484 201 965 GLAVKTKMSGLEFGTOVDPEISLFVKASGBOSSIGNCEPCGLE PILLARGEMERICALPRIAGRAM SECRETARIO AMINIMARY AND A				H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence shall be sequences sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seque				L=Leucine, M=Methionine, N=Asparagine,
maino acid sequence sequence sequence sequence sequence sequence sequence codon, /=possible nuclectide deletide deletion, /=possible nuclectide delet				P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence Vepossible nuclectide insertion Vepossible nuclection Vepossible nuclectide insertion Vepossible nuclectide insertion Vepossible nuclectide verification Vepossible nuclection Vepossible nuclectide verification Vepossible nuclectide verification Vepossible nuclectide verification Vepossible nuclection Vepossible nuclectide verification Vepossible nuclectide verification Vepossible nuclectide verification Vepossible nuclection Vepossible nuclectide verification Vepossible nuclectide verification Vepossible nuclectide verification Vepossible nuclection Vepossible nuclectide verification Vepossible nuclectide verification Vepossible nuclection Vepossible nuclection Vepossible n			I	S=Serine, T=Threonine, V=Valine,
Sequence Sepossible nuclectide insertion	:	1	Į.	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
VPNPGCERIGGTLTARGUERELGGRPLAGR	1 .	1	sequence	Codon, /=possible nucleotide deletion,
6484 201 965 QLAWKTKNSGLRETGTÖYDER ILLEVKAGSDGSSIGNEFFECKER MILLIKGVENDYTVÖMTEKERE LEKOLAFOTHEP LYVIKELER DPIKEBELGOTLAPPRYPHLSPKYKESEPOVGCNLPAKESAPYIK KNEKKEANNEVESKLKEFFKELDYTINTELLÖBELTDEDABESPYIK REFLIGGOLTLADCSLLEKINTI KVAAKKYRDFDIPAFFSGVW RYLHINAVAREETHTCERKE IRLYTAVAKAKKS 6485 6 1091 PVOLVERVEFILPEDESCKLEKECGSSESSKSINSMESILLEDDER DEEPPPULLVHERBESPEVGMUNHEKKYPTPOLYSVORDEK KASVIVISGIMMPRIKKEPTVSLKSLKHPDCKEKQTLINQAREDE NODIGGCVSLITUTVEVLECKSSPESVAGNERSILLEDDER ANGKLVEYIGGIMPRIKKEPTVSLKSLKHPDCKEKQTLINQAREDE NODIGGCVSLITUTVEVLLCCSSPESSKSINSMESILLEDDER ANGKLVEYIGGIMPRIKKEPTVSLKSLKHPDCKEKQTLINQAREDE NODIGGCVSLITUTVEVLLCCSSPESSKSINSMESILLEDDER ANGKLVEYIGGAKABSHLRAILKSRYGPRIKLGTIESSSGYVIT CVATVLEDDEGOLDLVKYLQGVIGGOPCKNULDTRISSSGYVIT CVATVLEDDEGOLDLVKYLQGVIGGOPCKNULDTRISSSGYVIT CVATVLEDDEGOLDLVKYLQGVIGGOPCKNULDTRISSSGYVIT CVATVLEDDEGOLDLVKYLQGVIGGOPCKNULDTRISSSGYVIT CVATVLEDDEGOLDLVKYLQGVIGGOPCKNULDTRISSSGYVIT CVATVLEDDEGOLDLVKYLQGVIGGOPCKNULDTRISSSGYVIT CVATVLEDDEGOLDLVKYLQGVIGGOPCKNULDTRISSSGILL LEERRIKRR 10 581 10 581 110 LONGARGHESSENTYGTIYMLAFSEMPKPDYSELSSGALTENDIT CVATVLEDDEGOLDLVKYLQGVIGGOPCKNULDTRISSSGILL LEERRIKRR 110 LONGARGANISSSRVTGTIYMLAFSEMPKPDYSELSSGALTENDIT CVATVLAMELTSTANDIT CVATVLAMELT CVATVLAMELTSTANDIT CVATVLAMELTSTANDIT CVATVLAMELTSTANDIT CVATVLA		sequence		\=possible nucleotide insertion)
### ### ##############################				VFNPGCBAIQGTLTAEQLERELQLRPLAGR
DFIKIEBPLECTLAPPRYPHLESKYKESPOVGCHLARKSSYTIK NTOKRANINTSKELLKEPRKLUDTINTPLLIBDISABEPPYS RRIFLIGDOLTLADCSLLIPKLHI I KVAAKKYRD DI PASFSGWR RYLHNAYARBEPHTYCPDEKE HENTYANNAKJE 6485 6 1091 FYDLVERVEFLPCPDSOKIEKGOGSSESKGINSMRSILEEDEE DEEPPRVLLYHEPRS FEVGMLUWKHKKYPWPAVVSKYRKK KASVIYIEGHMAPKHKSFTVSLKSLKHFDCKEKKYLLKNAREDP NQDIOMCVSLITDTRVELGCSSFAGSFLEYVAADISFYPKRSIQ ODMICTKLPQLSKOSSPEEDVOKTADISSKAKTADISSKYTT CVSTYLEEDEGOLDLVYKYLGGVGEVAGUAUGRROBERRARD RANGKUVSIGTDTRVELGCSSFAGSFLEYVAADISFYPKRSIQ ODMICTKLPQLSKOSSPEEDVOYCOVGVAKULQRROBERRARD RANGKUVSYIGKAKGASSHLRAILKSRKSKMLGTILSSSTYT CVSTYLEEDEGOLDLVYKYLGGVGVAKULQRROBERRFILD VLLPBAII CAISAGDEVYKYTAEKKYIKGPSLSYREKSIFPHOL LERNIRRR 6486 10 581 LVUQAGGAHLSPSRVTQTYVMLAFSEMPKPPDYSSELSDSLTLA GGGRESSPLIRRAMMNERPGRWGIVCULLASAAPYTYVE ISKTYNRIALEHIOQHDEBELSGTTWIHSLKAQLLSLPRWWTV ISKTYNRIALEHIOQHDEBELSGTTWIHSLKAQLLSLPRWWTV KASNQISELQLIDT SFEKPERGENSVTLHTDVGDIKISVFCERTPRTCEMFLALCASN YNNGCIFHRI KGFWQTUDDIKTISVFCERTPRTCEMFLALCASN YNNGCIFHRI KGFWQTUDDIKTISVFCERTPRTCEMFLALCASN YNNGCIFHRI KGFWQTUDDIKTISVFCERTPRTCEMFLALCASN YNNGCIFHRI KGFWQTUDDIKTISVFCERTPRTCEMFLALCASN YNNGCIFHRI KGFWQTUDDIKTISVFCERTPRTCEMFLALCASN YNNGCIFHRI KGFWQTUDDIKTISVFCERTPRTCEMFLALCASN YNNGCIFHRI KGFWQTUDDIKTISVFCERTPRTCEMFLALCASN YNNGCIFHRI KGFWQTUDDIKTISVFCERTPRTCEMFLALCASN YNNGCIFHRI KGFWQTUDDIKTISVFCERTPRTCEMFLALCASN YNNGCIFHRI KGFWQTUDDIKTISVFCERTPRTCEMFLALCASN YNNGCIFHRI KGFWQTUDDIKTISVFCERTPRTCEMFLACHSNIT SVVH KDEFFFGGGI SSCPFGGTILGPPDSVDVDVSTTVERSI FLEVL SSLGSSLFROARNINFHKNITHSNWAPATITANPPAQ 6488 878 241 TALQEFGTSOPFFTINFHRYSISVFCERSEGURISTSVMI KDEFFFGGGI SSCPFGGTILGPPDSVDVDVSTTVERSI FLEVL SSLGSSLFROARNINFHKNITHSNWAPATITANPPAQ WEBPPLYPVLIVYVDLSKGLARRISP SIMMGRUMISTSVMIT KDEFFFGGGI SSCPFGGTILLGPPDSVDVDVSTTVERSI FLEVL SSLGSSLFROARNINFHKNITHSNWAPATITANPPAQ GERMYKTTVOTALDRICETTINKH SQS ISAPL TARDTALLSSSI STANDANGGSSI PALARRYTSAKWELEFGGG DHCTASNWT HBGGWWATHAPPEGQULAS CSTSDRTAAWERSPHAVGS DSSPNAMAKYOTIPSTAMPEGQULAS CSTSDRTAAWERSPHAVGS DSSPNAMAKYOTIPSTAMPEGQULAS CSTSDRTAAWERSPHAVGS DSSPNAMAKYOTIPSTRYKARATATHTVTDFVDHDLAR	6484	201	965	QLAVKTKMSGLRPGTQVDPEIELFVKAGSDGESIGNCPFCQRLF
### ATOKEANNINPEKSLIKEPKELDDYLINTPLIDEIDPDSAEEPPV REFLIGOQUITALDCSLIPEIALIN IXVAAKKYDDIPARFSGWW RYHHNAYAREEPTHYC PROKETENTYANVAKOKS 6485 6 1091 FVOLVERWEIGPPSDKIEKEKGOSSESMISMESTLEEDEE DESPPRYLLYHEDRS FEVGMLVWHKHKYP PWPAVVKSVRGRK KASVLYIEGHMPRAKGFTVSLKSLKHFDCKEKGTLLNGAREDP NQDIGWCVSLITTPRVELGGSSFASSFLEYARGARDP NQDIGWCVSLITTPRVELGGSSFASSFLEYARGARDP RANGKLWSTIGKAKGASSHLARLIKSKRESSHLEYPURSIG ODVLGTKLPGLSKOSPESPVVGCPLGGROPCKRULDRSRARDD RANGKLUSTIGKAKGASSHLARLIKSKRESSHLGTFLSSSCYVT CVSTYLEDEGQLDLVVXYLGGVYOGEVGARVLQRTNGGRTRETILD VLLPBEATICALSAGEDVTKATALKSKRESSHLGTFLSSSCYVT CVSTYLEDEGQLDLVVXYLGGVYOGEVGARVLQRTNGGRTRETILD VLLPBEATICALSAGEDVTKATALKSKRESSHLGTFLSSSCYVT CVSTYLEDEGQLDLVVXYLGGVYOGEVGARVLQRTNGGRTRETILD VLLPBEATICALSAGEDVTKATALKSKRESSHLGTFLSSSCYVT CVSTYLEDEGGLDLVVXYLGGVYOGEVGARVLQRTNGGRTRETILD VLLPBEATICALSAGEDVTKATALKSKRESSHLGTFLUGTNOGTHAR EARDEN FRENCH FILE CGTGRPSGPLHRANSMONFRQGGVYMLAPSEMKEPDVSELSSCTLA GGTGRPSGPLHRANSMONFRQGGPTTWICHALCASN YNGCIFHRNIKGFNVCTGPPTGRGGGSLWGKREGEVSEVL KANNGISRLQLIDT STEVNRLLLEHLOQHPSELFOTWHIKKAQLLSFFWUTV IFLVPYLQMPLPLYSCTRADPKTVGYCITPLCLAVICKRHGAFV VANGUSHANNIGPNTNGSGPFTTVKCQPLIALCASN YNGCIFHRNIKGFNVCTGDPTGTGRGGSLWGKREGEVSEVL KHNYRGVVSHANNIGPNTNGSGPFTTVKCQPLIALCASN YNGCIFHRNIKGFNVCTGDPTGTGRGGSLWGKREGEVSEVL KHNYRGVVSHANNIGPNTNGSGPFTTVKCQPLIALCASN YNGCIFHRNIKGFNVCTGDPTGTGRGGSLWGKREGEVSEVL KHNYRGVVSHANNIGPNTNGSGPFTTVKCQPLIALCASN YNGCIFHRNIKGFNVCTGDPTGTGRGGSLWGKREGEVSEVL KHNYRGVVSHANNIGPNTNGSGPFTTVKCCHPLALCASN MEPPHLYVLLYVYDLAKGLAGRASSPFTTWFGRGFSWPPSSFVP MEPPHLYVLLYVYDLAKGLAGRASSPFTTWFGRGFSWPPSSFVP MEPPHLYVLLYVYDLAKGLAGRASSPFTTWFGRGFSWPPSSFVP MEPPHLYVLLYVYDLAKGLAGRASSPFTTWFGRAFSBFWPSSFVP MEPPHLYVLLYVYDLAKGLAGRASSPFTTWFGRAFSBFWGRGFSBFRQF GERBENGEVERRETTPARTERSFRTLQGRESSELKATARRICCML YHDDHRBCSSCFTTMANWERSELFGGGTTAGNKT THABACSGARTTSTAWTSAAVKLREACSGGGSGGSHQLLLLTPR TMDACSGARTTSTAWTSAAVKLREACSGGGMCHEFTMFVARSTAADH NGLKWTYNTAARPEGGVLASSCSTWRASSRSGENFGTAFNIT HSGSVWRVTMATTSDTVKFARKMAGMATACSADGIVRTYE APDVWNLSGNSGLGHEISCKLSGSTSTAAWERSHANDNACGTOL GSBWAKRTTLVDSRTSTVTVFARKMAGMATATCSADGIVRTYE APDVMN	1			MILWLKGVKFNVTTVDMTRKPEELKDLAPGTNPPFLVYNKELKT
6485 6 1091 FVDLVRAVEFIETHTCPRICE ENTYNNAVAGE ENTYNNAV	1		}	DFIKIEEFLEQTLAPPRYPHLSPKYKESFDVGCNLFAKFSAYIK
6485 6 1091 FYDLWANDEFFITCPBOKEIRNTYANVAKOKS 6485 6 1091 FYDLWANDEFFICPCDBOKLERCCSSESSESSASSANSMESTLEEDEE DEEPPRVLLYHERESSEVUMLVHERKIKKYPPWDAVVKSVRQRDK KASVLYIEGHMDRWANGFYDLKSLKHPDCKEKQTLINQAREDF NQDIGWCVSLITDYRVLGCGSPAGSFIRYVAADISYPVRKSIQ OVLGTKIPQISKSSESPRVUGCHLQRQPCRKMDPDRSRAARD RARQKIVSYIGKAKGASEHKRAILKSRKPSRWLQTFILSSSYVT CVETYLEDEGQLDLVVKTLQGVYQEVGAKVLQATNOGRIRFILD VLLPBRIICAL SAGDEVYVATABEKYIIGSSLSYREKSIPNOL LEERNRRRR 6486 10 581 LVVQAGGAHLSPSRVTQGIYYMLAFSEMPKPPDYSELSDSLTLA GGGRFSGPLHRAWRMNFRQRNGMIGVGLYLLASAAPYYVER ISKTYNKLALHHOQHPBEPLGTTVTMISLALJSLPFWWTV IFLVPYLQMPLFLYSCTRADPKTVGYCIJPICLAVICRHQAFV KASNQISRLQLIDT 6487 352 863 SFIKFLRGRSNSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN YYNGCIFHRNIKGFWQTGDPTGTTGGGNSIMGKKFEBYSELL KHNYRGVVSHANNBOPNTGSFPITTGGGPLLDSLYTLANPAQ 6488 878 241 TALOEPGTSGPFSLRYPAPEDGTGFFRKENGEVSELL KHNYRGVVSHANNBOPNTGSFFITTGGFPLDWKTYTFCKVLD GLETTLDELEKLPVNERTTRPLNDVHIKDITHANPFAQ 6488 878 241 TALOEPGTSGPFSLRYPAPEGTGFFRKFURSTETEBILEVL SSLGSSLFRGBATNLFBINCNTFSNEVAQHLTCRKIPSYTTDLP MEPPILYPVKLYVYLJSKGLARRLSP INLKQLOEGIWHTSIVVH KDEFFFFGSGGISSCPPGGTLAGPDSVOVGETUTEBILEVL SSLGSSLFRGBATNLFBINCNTFSNEVAQHLTCRKIPSYTTDLP SEVLSTPPGGALAPLLBOLIQPPGGSSVETTEBIELEVL SSLGSSLFRGBATNLFBINCNTFSNEVAQHLTCRKIPSYTTDLP SEVLSTPPGGALAPLLBOLIQPPGGSSVETTEBIELEVL SSLGSSLFRGBATNLFBINCNTFSNEVAQHLTCRKIPSYTTDLP SEVLSTPGGGARPFDEFTRPLINDTYTYTGKG GLEMBGMBVVGVRRRTPARISEFFELQEREBRRLQQRTTPKGT ISWOVDATDLFDRYDEEVEDVSGSSFFQISHMENTHYTYTYTYTGKG GLEMBGMBVVGVRRRTPARISEFFELQEREBRRLQQRTTPKGT ISWOVDATDLFDRYDEEVEDVSGSSFFQISHNHAMTASKT HGSGVWKVFNAHPERGGVLASCSFDRTAAWEEIVGESNDKLRG QSHWVKRTTLVDRSTSVTDVKFARKMGLMLATCSADGTURT YE APDVMNLSQSGLJCHISICSKLSCSCISNNFSSRABSPMIAVGSD DSSPNAMAKVQIFETNENTKKVAKABTLMTVTDPVHORFABADH KDLIHDVSFDFRGRMATCSSDQSVKVWDKSESGDMKTASKT HGSGWWKVTAHPERGGVLASCSFDRTAAWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFARKMGLMLATCSADGTVRTYE APDVMNLSQSGLQBHISCKLGSCISNNFSSRABSPMIAVGSD DSSPNAMAKVQIFETNENTKKVAKABTLMTVTDPVHDIAFABNL GRSPHILLAITHVORFTURNKTKVAKABTLMTVTDPVHDIAFABNL GRSPHILLAITHVORFTURNKTKVAKABTLMTVTDPVHDI	1			NTOKEANKNFEKSLLKEFKRLDDYLNTPLLDEIDPDSAEEPPVS
6485 6 1091 FVDLVRAVEFLECDSGKLEKECUSSEESMGSNSMESTLEEDEE DEEPPPKLIVHERDES FEWUMUVHEKKIYEPWAVVKSVRONDK KASULVIEGHANDRAMGPTVSLKSLCHHPDCKEKQTLLINQAREDF NQDIGWCVSLITDYRVRLIGCOSPAGSFLERYPAADISTVRKSIQ QDVLGTKLPQUSKGSPEBPVUGCPLGQRQPCRRMLPDESRRARD RANGKLVBYIGKAKGAESHLRAILKSRKPSRMLQTFLSSSGYVT CVSTYLEDEGGGLDLVVKLYLGVVGVGVGKGYNENDRIRFILD VLLPEAITCAISAGDEVDYKTABEKYIKGPSLSYREKBIFONGL LEERNRRRR 6486 10 581 LVLQAGGAHLSPSRVTOGTYYMLAFSEMPKPDPDYSELDSLTLA GGGGRFSGPLHRAMRMNSFRQRWGHIGGVIYLLASAAAPYYVFB ISETYNRLALEHIQQHPEEPLEGTTWHSLKAQLISLEFWWTV IFLVFYLQMFLFLYSGTRADPKTVGGTIPICLAVICRRIQAFV KASNGISRLGLIDT 6487 352 863 SFLKFLRGKMSVTLHTDVGGIKIEVFCERTPKTCERPLALCASN YNGGIFFRIN KGFWUGGDFTGTGGGGSIWGKKFEDEYSEYL KHVKRGVVSMANNGNTMGSGFFITTGKQPHLDMKYTVFGKVID GLETLDELEKLFVNEKTTRPLNDVHIKDITHANPAQ 6488 878 241 TALGEFGTSGPPLSLRFALDSGTGRFKELPGARGPSWFPSFVFW MEPPNLYPVKLYVVDLSKGLARRLSP IMLGKQLBGIHMTSIVVH KDEFFFGSGGISSCPFGGTLLGPPDSVVDGSTEVTEBIFLEVL SSLGSSLFRGEAYNLFEHNCNTFSNEVAQFILTGRKIPSYTTDLP SCHLSTPFGGGALFLIDSIGIPPGGSSVGFRNGGS 6489 1457 375 KVAKMATALSEEELDNEDYYSLLNVRRASSEELKAARPRICKL VRPDKRRDFELKSQAERLFFLUNGAYERGSSEEKAARPRICKL SUGVDATDLEPRDESPEPPLIVPGARGSSEEKAARPRICKL TATDTAILSGSLSTQNGGGSINPALRRASSEELKAARPRICKL GLEMGWSVVERRATPABIREFEELQARERERRIQGTTPKFT ISWOUADTLEPRDFEVEPPUSGSSFPOLTAALUPTYGKR GLEMGWSVVERRATPABIREFEELQARERERRIQGTTPKFT TATDTAILSGSLSTQNGGGGSINPALRASKEELFAGG DLQGFFGLKJRFRLSTGRATVTRALQFSSRGIRPGITTVLAR NILDKTVSVLJQHICSSFLLJVORPERNATRASKTBILGNITTVLAR NILDKTVSVLJQHECSSFLLJVORPERSFRAPSSFPHLUP TWDBACCGGARTPSTAMTSAAVKLRBACLSGPGSGSHOLLLLTTR SKRRTGGG GSMVKRTTALVDSRTSVTDVKPAPKHMGLMLATCSADGIVRIFG APDWNNISQWSLYMRTTVUDSRTSVTDVKPAPKHMGLMLATCSADGIVRIFG APDWNNISQWSLYMRNTTVUDSRTSVTDVKPAPKHMGLMLATCSADGIVRIFG APDWNNISQWSGGGTSSPSTGNSTSLONGKGGGFTKFEHTHVAQFD NINSQWRVYMANPEFGQULASCSFORTAAVWSEIGGSHHCTASWT HGGSWWRVTMAHPEFGQULASCSFORTAAVWSEIGGSHHCTASWT HGGSWWRVTMAHPEFGQULASCSFORTAAVWSEIGGSHHCTASWT HGGGWFFFILATHTVDDVHITTVLASGGDGCVTLMKANTMONKCTGIL KONGSPHULASIGGSINFSLGSGSSTSFTASSMANKUGSD DSSPNAMAKVQIFEINNTKAYARETMVTDVPUHDLFADNI GRSPHILAILHTVORPTVDIAFANN				RRLFLDGDQLTLADCSLLPKLNIIKVAAKKYRDFDIPAEFSGVW
DEEPPRVLLYHEPRSPEVGMLVWHKHKKYPFWPAVVKSVRQRIK KASVLYIGHMIPKHKGTTVSLKSIKHFDCKEKGTILLQAREEP NQDIGMCVSLITDYRVRIGGSTAGSFLKHFDCKEKGTILLQAREEP NQDIGMCVSLITDYRVRIGGSTAGSFLKHFDCKEKGTILLQAREEP RAMQKLVSVIGKAKGASEHRAILKSRKPSYAADISYPVRKSIQ ODVLGTKLPQLSKGSPEBPVVGCPLGQRQPCRKMLPDRSRAARD RAMQKLVSVIGKAKGASEHRAILKSRKPSLOTILSSQVT CVSTYLEDBGQLDLVVKYLQGVYQEVGAKVLQATNODBIRFILD VLIPPAIL CAISAGDBVDYKTAREKYIKGPSLSYREKEIPDNQL LERRNRRRR 6486 10 581 LVLQAGGAHLSPSRVTQGIYYMLAFSEMPKPPDYSELSDSLTLA GGTGRFSGPLHRAWRNWHFRQRRGWIGVGLYLLASAAPYTVPE ISSTYNRLALEHTQQHPEPELEGTTWTHISLKAQLLSLPFWWTV IFLYPYLQMFLPLYSCTRADPKTVQGCITLAVICKHQAFV KASNQISRLQLIDT 6487 352 863 STKPLRGKRWSVILHTDUGDIKIEVPCEPTPKTCENPLALCASN YYNGCIFHRNIKGFWQTGDPTGTGRGNSIWGKKFEDEYSEYL KHNVRGVVSNANNGENTNGSOFFITYGKQHLDMKYTYPGKVID GETUDELEKLFVPNKKTYTPLNOVHIKDITHANPFAQ 6488 878 241 TALQEFGTSGPFLSEFFALPSGTGRFKFLFQARGPSWPSSFRV MBPPNLYSVKLYVYLDSKALARRLSPINLOGLGGIWHTSTVVH KDEFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTEBIFLZVL SSLGSLSFGGANTLFBINCHTSNEWAGLGGIWHTSTVVH KDEFFFGSGGISSCPGGTLLGPPDSVVDVGSTEVTEBIFLZVL SSLGSLSFGGANTLFBINCHTSSENEVAGLGGIWHTSTVVH KDEFFFGSGGISSCPGGTLLGPPDSVVDVGSTEVTEBIFLZVL SSLGSLSFGGANTLFBINCHTSSENEVAGTREN, PSTYTDLP SSLLSTPPGQALPPLLDSIQIQPPGGSSVGRPNQGS 6489 1457 375 KVAKMATALSEEELDNEDYYSILNVRRASSEELKAAPKRICML YHDDKHRDPBLKSQAELKHVHQAYEVLDEPQTTATVDIYGKR GLEMBGWEVVERRRTPABIEEFEELQREBERRLQGRTFMFKTVLAR NLDKNTVGYLQWKCSSPLLQVGPRHATRACAPEPSFRPFLHVP TWDABCCSGARTPSTATMSAAVKURRECSGGRFGENFGCTMFWKT ISVGVDATDLFDVFDSEFSPVTVTNCALQPSGRFGRHGCMTLASWKT HGGSWWRVTAHPEFGQVLASCSFDRTAAWWEEIVGESDNKLRG QSHWKRTTLVDSRTSVTVDKRAPKHGMATCSADGIVRTYE APDVMNLSQNSLQHBISCKLSCSCISMNPSSSRAHSPMLAVGSD DSSPNAMAKVQIFEYNENTRKYAKABTLMTVTDPVHIDTAPNNL GRSFHILAIATKDVRIFTILKPVRKELTSSGGFKFEHITVAGFD NINSQVWRVSMNITGTVLASSGDDCVLWKANSTEADHURGFRH GGSWWRVTHAHPEFGQULASCSFDRTAAWWEEIVGESNDKLRG QSHWKRTTLVDSRTSVTDVKRAPFKHGLMLATCSADGIVRTYE APDVMNLSQNSLQHBISCKLGSCISMNPSSRGWHCTASWKT HGGSWWRVTHAHPEFGQULASCSFDRTAAWWEEIVGESNDKLRG QSHWKRTTLVDSRTSVTDVKRAPGGRGFTETMFVARSIAWHT HGGSWWRVTHAHPEFGQULASCSFDRHLATASWFT HGGSWWRVTHAHPEFGQULASCSFDRHCTASWKT HGGSWRVT				
KASULYIEGHMNYKMGFTVSLKSLKHFDCKEKQTLLKQAREDP NQDIGGVUSLTDYKPRIGGOSPAGSERYADISYPVRSIG ODVLGTKLPOLSKGSPESPVGCPLGQRQPCRKMLPDRSRAND RANGKLVSFYIGKAKGAESHLRAILKSRKPSRWLQTFLSSSQTVT CVETYLEDEGQLDLVVKTLGGVYQEVGAKVLQRTNCDRIRFILD VLLPEAITCAISAGDEVDYKTAEKYIKGPSLSYRKKSIPONGL VLLPEAITCAISAGDEVDYKTAEKYIKGPSLSYRKKSIPONGL ERRNRRR 6486 10 581 LVLQAGGAHLSPSRVTQGIYYMLAFSEMPKPPDYSELSDSLTLA GGTGFFSGPLHRAWRNNFRGRWGHIGGVIYLLASAAPYVVER ISKTYNRLALEHTQGHPEPLEGTTWTHSLKAGLLSLDFWWTV IPLVPYLQMPLFLYSCTRADPKTVGYCIPICLAVICNRQAFV KASNQISRLQLIDT 6487 352 863 SFIRFERGKMSVTLHTDVGDIKIEVFCERTPKTCENPLALCASN YYMGCIFFRNIKIKGPWQTGDPTGTGRGGNSIWGKKFEDEYSEYL KHVNGOVSMANNGDYNTGSQFFITTGKQPHLDMKYTVFGKVID GLETTLDELEKLPVNEKTYRPLNDVHIKDTHANPPAQ 6488 878 241 TALGDFGTSGPFLSLRPALPSGTGRFKELPGARGPSMPSPERVE MEPPNLYPVLKLYVDLSKGLARRLSP HLAGLGLGHHTSTVVH KDEFFFGSGGISSCPPGGTLLGPDDVVDVGSTEVTEEIFLEYL SSLGESLFRGEAYNLFEHNCNTFSWEWAQFLTGRKIPSYTTDLP SEVLSTPFGQARPHLDSIGJGPPGGSGGGGG WYMARTALSEEELDNEDYYSLLNVRREASSEELKAAPRILCML VARDMHRDPELKSQAERLFHLUNGAYEVLSDPGTRAIVDIYGGR GLEMGWEVVERRRTPASIREFERLQRERSERLQCRTHYKGT ISVGUADADLFDRYBESEFURLVHQAYEVLSDPGTRAIVDIYGGR GLEMGWEVVERRRTPASIREFERLQRERSERLQCRTHYKAT ISVGUADADLFDRYBESEFURLDVRGFRFRAINHISCSIEAPL TATDTAILSGSLSTONGNGGGSINTALRRVTSAKGMGELFFGG DLQGPLFGLKLFRNLTPRCFYTTMCALOFSSGSHQLLLLTTP TWBACCSGARTPSTAMTSAAVKLRRACLSGPGSGSHQLLLTTP TWBACCSGARTPSTAMTSAAVKLRRACLSGPGSGSHQLLLTTP TWBACCSGARTPSTAMTSAAVKLRRACLSGPGSGSHQLLLLTTP TWBACCSGARTPSTAMTSAAVKLRRACLSGPGSGSHQLLLLTTP TWBACCSGARTPSTAMTSAAVKLRRACLSGPGSGSHQLLLLTTP TWBACCSGARTPSTAMTSAAVKLRRACLSGPGSGSHQLLLLTTP TWBACCSGARTPSTAMTSAAVKLRRACLSGPGSGSHQLLLLTTP TWBACCSGARTPSTAMTSAAVKLRRACLSGPGSGSHQLTTSWKT HGSGWWRYTHANPEGGOULASCSFORTAAWREI IVGSSDDKLRG QSHWKRTTLVDSRTSTVDVKRAPKHMGLMTCSADGTWRIF HGSGWWRYTMAHPEFGQVLASCSFORTAAWREI IVGSSDDKLRG QSHWKRTTLVDSRTSTVDVKRAPKHMGLMATCSADGTWRIF HGSGWWRYTWAHPEFGQULASCSFORTAAWREI IVGSSDNKLRG QSHWKRTTLVDSRTSTVDVKRAPKHGMLATCSADGTWRIF HGSGWWRYTWAHPEFGQULASCSFORTAAWREI IVGSSDNKLRG QSHWKRTTLVDSRTSVTDVKRAPKHGMLATCSADGTWRIF HGSGWWRYTWAHPEFGQULASCSFORTAAWREI IVGSSDNKLG QSHWKRTT	6485	6	1091	
NODIGRCUSLITDYRVRLGCGSPAGSFLRYYADDISYPVRKSIQ ODVLGTKLPOLSKGSPEBPUVGCPLQGPVQCRUMLDPRSRADD RANGKLVBYIGKARGASSHLRAILKSRKPSRNLQTFLSSSQYVT CVETYLEDEGQLDLVVKYLQGVYQEVGAKVLQTNTGGRIRFILD VLLPBAIICAISAGDEVDYKTABEKYLKGSLSYBEKBIEDNGL LERRNRRR 10 581 LVLQAGAGAHLSPSRVTGGIYYMLAFSEMPKPPDYSELSDSLTLA GGTGRFSGPLHRAMRNNTRQRMGWIGVGLYLLASAAPYYVEB ISRTYNRLALHHIQQHEBPLLEGTTWHLKAQLLSLPFWWTV IFLVPYLQMFLFLYSCTRADPKTVGYCIIPICLAVICNRHQAFV KASNQISRLQLIDT 6487 352 863 SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN YYNGCIFHRNIKGFMVQTGDPJGTGRGGSINGKKFEDEYSEYL KHNVRGVVSMANNGFBTNNSGSPFITVGAPLDMLMKYTVFCKVLD GLETLDELEKLPVWEKTYRPLNDVHIKDTTHANPFAQ 6488 878 241 TALGEFSTGSPTLSLRFALFSGTGFFKELPGARGPSWFPSFRVF MEPPNLYPVKLYYVDLSKGLARRLSPIMLGKQLEGIWHTSIVVH KDSFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTERIFLEYL SSLGSLSTPFGGALRFRLDSTGNFKVLFGARGPTSWFFSFRVF MEPPNLYPVKLYYVJLSKGLARRLSPIMLGKQLEGIWHTSIVVH KDSFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTERIFLEYL SSLGSLSTRGGANTLERNCNTFSNEVAFLTGRKIFSTYTTDLP SEVLSTPFGQALRPLLDSIOLOPPGSSVGRPNGGS 6489 1457 375 KVAKMATALSEELDBEVFYSLLAVRESSEELKAAYRFLCML YHDDKRKOBPELKSQASRLPNLVHQAYEVLSDPQTRAIYDIYGKR GLEMBEVVERRTTDABITERFFERLQRTRFRKHIQRTNPKGT ISVGVDATDLIPDRYDEEYSDVSGSSFFOTEINKHHISGSLEPL TATDTAILSGSLSTQNGNGGSINFALRRVTSAKGMGELEFGAG DLQGFLFGLKLFRNLTRFKFYTITTCLPSSGTGRFGLITVLJAR NLDKNTVGYLQMKCSSPLGVORPHRNTRACAPEDSFRPFLHVP TWDBECSGARTPSTAMTSAAVKLREACLSGPGSGGGHQLLLLTPR SKRPTGGG 6490 3 1183 HEAGCEVWLGYGFRAAAAAATVLFGGAGPTETMFVARSIAADH KOLIHDVSFDFHGRRANTCSDGSVKVWKSESGDMCTASKKT HGGSVWRVTWAHPEFGQVLASCSFDRTAAVWEE TVGESNDKLRG GSHWVRATTLVDSRTSVTDVXFAPKHMALATCSADGIVRIYE APDVWNLSGNSLQHEISCKLSCSCISWNPSSSRAHSPMLAVGSD DSSPNAMAKVQIFFVENSGSGGFDGTAAVWEE TVGESNDKLRG GSHWVRATTLVDSRTSVTDVXFAPKHMISMINSSAGARKIS HGGGEWRVTTHVDSFFORRMATCSSDGSVKVMDKSESGDMCTASKKT HGGSWRVTWAHPEFGQVLASCSFDRTAAVWEE TVGESNDKLRG QSHWVKTTLVDSRTSVTDVKFAPKHMISMINSSAGARKIS HCGSFPHLAIATKVDSFTDFFLGSNDTSLGSHGTHAVWEE GSSPAPHARAKVQIFEVENTSPLGSNDFSLGSHTAAVWEE TVGESNDKLRG QSHWVKTTLVDSRTSVTDVKFAPKHMISMINSSAGARKIS HGGSWRVTHAPBEFGQUTASCSFDRTAAVWEE TVGESNDKLRG QSHWVKTTLVDSFTSVTDVKFAPKHMISMINGSSGADMCTASKYT HGGSWR	1		İ	DEEPPRVLLYHEPRSFEVGMLVWHKHKKYPFWPAVVKSVRQRDK
ODVLGTKLPOLSKGSPEBPVUGCPLGGRQCKRULDENSRARAD RANGKLVEYIGKAGGASHLRAILKSPRILOTHLSSGYTY CVETYLEDBGQLDLVVKYLQGVYQEVGAKVLQRTNGGRIRFILD VLLPRAITCAISAGDEVDYKTABEKYIKGPSLSYREKSIFDNQL LERRNRRRR 6486 10 581 LVLQAGGAHLSPSRVTQGIYYMLAFSEMPKPDYSELSDSLTLR GGTGRFSGPLIRAARMANFRQRMMGINGVGLYLLASAAPYTVBE ISBTYNRLALEHIQOHPEEPLEGTTWTHSLKAQLLSLPFWWTV IFLVPYLQMFLFLYSCTRADRYTGYCITPICLAVICKRQAFV KASNQISKLQLIDT 6487 352 863 SFLKPLRGKMSVTLHTDVODIKIEVFCERTPKTCENFLALCASN YNGGIFRENIKGFMGVTGDPTGTGRGGNSINGKKFEBEYSEYL KHNVRGVVSMANNGPNTNGSGPFTTYGKQPHLDMKYTVFGKVID GLETLDELEKLPVNEKTYRPLNDVHIKDITHANPFAQ 6488 878 241 TALQEFGTSGPFLSHPALPSGTGRFKPLPLGARGFSWPSPFRVF MEPPNLYEVKLYVYDLSKGLARRLSPTMLGQLEGIHTTSIVH KOEFFFGSGGISSCPPGGTLLSPPDSVORTSTWEETSILVL SSLGESLFRGANNLFENNCNTFSNEVAGFLIGRKIFSYITDLP SEVLSTPFGOALRPLLDSIOTQPFGSCRPNGQS 6489 1457 375 KVAKMATALSEEELDNEDYYSLLNVRREASSEELKARYRRLCML YHEDKHROPELKSQASRLFNLVHQAYEVLSDPQTTAAYDIYGKR GLEMBGMSVVERRTRAETSIREFFRLQRERERRLQQTTMPKGT ISWQDATDLFDRYDEEVEDVSGSFFQIENKHHISQSIEAPL TATDTAILSGSLSTONGGGSINPHCATCAKCHEELFFGA DLQGPLFGLKLFNNLTFRCFVTTNCALQFSSRGIRPGLITVILAR NLDKNTVGYLQMKCSSPLQVQRPHRNTAACAPEPSRFPFPLHVP SKRRTGGG 6490 3 1183 HERGCEVVLGYGFRAAAAAATVLFGGAGPTETMFVARS TAADH KOLIHDVSFDFHGRRMATCSSDGVKVWDKSESGDWHCTASWKT HSGSVRRVTWAHPEFGQVLASCSFDRTAAVWESTVESNDKLIRG GRSFHILAIATKDVRIFTLRSVRRELTSSGGFTKPEHTYVAGFD NHNSQVRVSWNITGTVLASSGDDGCVRLWKANYMDWKCTGIL KONGSPVNGSSQGTENPSLOSHIPSLGNSINGSSAGRKHS 183 HERGCEVVLGYGFRAAAAAAATVLFGGAGPTETMFVARS TAADH KOLIHDVSFDFHGRRMATCSSDGSVKVWMKSESGDWHCTASWKT HSGSVRRVTWAHPEFGQVLASCSFDRTAAVWEETVGESNDKLIRG GRSFHILAIATKDVRIFTLKSVRKELTSSGGFTKFBHTVVAGFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDWKCTGIL KONGSPVNGSSSQGTENPSLOSHIPSLGNSINGSSAGRKHS 1840 HERGCEVVLGYGFRAAAAAAATVLFGGAGPTETMFVARSITAAHT HGLIHDVSFDFHGRRMATCSSDGSVKVWMKSESGDWHCTASWKT HGGSWRVTWAHPEFGQVLASSGDFTAAVWEETVGESNDKLIRG QSHWVRTTLVDSRTSVTDVKFAPKHMGLATCAADGTVRIYE APDVMNLSQNSLQHBISCKLSCSCISWPSSSRAHSPMLAVGSD DSSPNAMAKVQIFEVENTETSKYKASETLTMTVTDVYURSFARMITVAGFD SGSPMAMAKVQIFEVENTRYKYKASTATMTVTDVYBLIFAPANL GRSFHILAIATKDVRIFTLARVKASTATMTVTDVYBLTAAGFO	1			KASVLYIEGHMNPKMKGFTVSLKSLKHFDCKEKQTLLNQAREDF
RANGKLVEYIGKARGAESHLRAILKSRKPSRNLOFTSLSSQYYT CVETYLEDEGOLDLVVKYLOGYVQEVGAKVLQRTNGGRISHFILD VLLPERIICAISAGDEVDYKTAEEKYIKGPSLSYREKEIFDNQL LEERNRRRR 10 581 LVLQAGGAHLSPSRVTQGIYYMLAFSEMPKPPDYSELSDSLTIA GGTGRESGPLHRAWRMMNFRQRMGUGVGLYLLASAAAPYYVEB ISSTYNRLALHIQQHEPPLEGTTWHSLKAQLLSUPFWWTV IFLVPYLQMFLPLYSCTRADPKTVGYCIIPICLAVICNRQAFV KASNQISRIQLIDT 6487 352 863 SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN YNNGCIFHRNIKGFMVQTGDPTGTGRGGSISUGKKFEDEYSEYL KHNVRGVVSMANNGPTNNSOSPTITVGDRJDMKYTGVFTCKVLD GLETLDELEKLPVWEKTYRPLNDVHIKDTTHANPFAQ 6488 878 241 TALGERGTGPSLSTRAPLFSGTGFFLDGARGFSWPSPFRVP MEPPNLYPVLLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH KDFFFFGSGISSCPPGGTLIGPFDSVVDVGSTSTETIFLEYL SSIGESLFRGEANNLERHNCNTFSNEVAGFLTGRKIPSYITDLP SEVLSTPFGGALRPLLDSIQTQPFGGSSVGRNGGS 6489 1457 375 KVAKMATALSEELDBEDYTSLLNVRREAGSEELKAAYRRLCML YHPDKHRDDELKSOAERLFNLVHQAYSVLSDPGTTAIYDIYGR GLEMGGWSVVBRRTDABIREFFGLORERERRLQORTNYKGT ISVOVDATDLFDRYDELYEDVSSSSFPQIEINKHHISQSIEAPL TATDTAILSGSLSTONGNGGSINFALRRVTSAKWEELPFGAG DLQGFLFGLKLFRNLTFRFFTTTICALGREBERRLQORTNYKGT ISVOVDATDLFDRYDEEYEDVSGSSFPQIEINKHHISQSIEAPL TATDTAILSGSLSTONGNGGSINFALRRVTSAKWEELPFGAG DLQGFLFGLKLFRNLTFRFFTTTTCALGSREGRFRLQUTTVLAR NLDKNTVGYLQWICCSSPLLQVQRPHRNTRACAPEPSFRPPLHVP TMDARCSGARTPSTAAVKLERACLSGPSGSGSHQLLLLTPR SKRRTGGG GSHWIKTTLVDSRTSVTDVKFAPKHMGLMATCSADGTVRIYE APDVWNLSGWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFFYEMTRYAKAETHVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPYRKETISGDFTKFFHIVAGFD NINSQVWRVSWNITTTVLASSGDDGCVRLMKANYMDWKCTGIL GRSFHILAIATKDVRIFTLKPYRKETISGSFTRFTARSWT HGSGWWRYTHAHPEFGQVLASCSFDRTAAVWEE LYGSNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMATCSADGTVRIYE APDVWNLSGSQQGTINFSLGSSGGTRHSINGSSAGRRHS HGGGEWWLSYGFRAAAAAAATVLFGGAGPTETMFVARSIAADH KOLLHDVSFPFHGRRMATCSSDGSVKVMBKESGDMHCTASWKT HGSGWWRYTHAPEFGQVLASCSFDRTAAVWEE LYGSNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMATCSADGTVRIYE APDVWNLSGSQQGTSNFSLGSSGGTRHSINGSSAGRRHS HGGGSWRVTWAHPEFGQVLASCSFDRTAAVWEE LYGSNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMALTCSADGTVRIYE APDVMILSGNSLGHEISCKLSCSCISWPSSSRAHSPMLAVGSD DSSPNAMAKVQIFEVNETTRYAKAGETHTTTTUTQFPU				NQDIGWCVSLITDYRVRLGCGSFAGSFLBYYAADISYPVRKSIQ
CVSTYLEDEGGLDLVVKYLGGVQEVGAKUQRTNGGRIRFILD VLDEGALICAISAGDEVDYKTAEEKYIKGPSLSYREKEIFDNOL LEERNRRRR 6486 10 581 LVLQAGGAHLSPSRVTQGIYYMLAFSEMPKPPDYSELSDSLTLA GGTGRSGPLHRAWRMINFRQRWGWIGVGLVLLASAAFYYVEE ISSTYMRLALEHIQQHPEFPLEGTTWTHISLKAQLLSLPFWWWTV IFLVPYLGMPFLEVSGYTRADPKTVGYGLIPICLAVICNRQAFV KASNQISRLQLIDT 6487 352 863 SFIKPLRRKMSVTLHTDVGDIKIEVFCERTFKTCENFLALCASN YYNGCIFHRNIKGFWQTGDPTGTGRGGNSIWGKKFEDEYSEVL KHNYRGVVSMANNGPNTNGSGFITTGKQPHLDMKYTVFGKVDL GLETLDELEKLPVEKTYPELDNULDITHANPFAQ 6488 878 241 TALQEFGTSGPPLSIRPALPSGTGRFKPLFGARGPSWFPSPRVF MBPPNLYFVKLYVYDLSKGLARRLSPINLGKGLEGIWHTSIVVH KDEFFFGSGGISSCPFGGTLLGFPDSVVDVUSTTSVTEETIFLEVL SSLGESLFRGBAYNLFBHNCNTFSNEVAGPITGKIFSYITDLP SSLLSTPFGGALRILDSIQLOPGGSSVGRPNGGS 6489 1457 375 KVAKMATALSEELDNEDYYSLLNVEREASSEELKAAYRRLCML YHPDKHRDPELKSQAERLFNLHVQAYELVSBDGTRATYDIYGKR GLEMBGWEVVERRRTFABIRBEFERLQERRERRLQQRTNPKGT ISVGVDATDLFDRYDESYBDVSGSSFPQIERNMHISQSIEAPL TANDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTFVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TVDBACSGCARTPSTAWTSAAVKLERBCLSGGGGSGGGCHENFGT TANDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTFVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TVDBACSGCARTPSTAWTSAAVKLERBCLSGGGGSGSGCLLLLITPR SKRRTGGG GHWVRRTTLUDSRTSVTDVKPRFRHMALMATCSADGIVRIYE APDVWNLSQWSLQHEISCKLSCSCISWPSSSRAHSPMIAVGSD DSSPNAMAKQIFFYNENTRYAKARETLMTVTDPVHDLRAPANL GRSFHILLAIATKDVRIFTILKPVRKELTSSGGPYKFEHILVAQFD NINSQVWRVSNNITGTVLASSGDDGCVAHKANYMDNWKCTGI L KCNGSPVNGSSQQGTSNPSLGSNITSSLQNSLRSSGMHCTASWKT HSGSWWRVTWAHPFFGQVLASCSFDRTAAWBEBIVGESNDKLRG QSHWVLSFTHLVDSFFFGRWATCSSDGSWKSSESGMHCTASWKT HSGSWWRVTWAHPFFGQVLASCSFDRTAAWBEBIVGESNDKLRG QSHWVLSFTTLVDSRTSVTDVKPARKMSSSGDMCTASWKT HSGSWWRVTWAHPFFGQVLASCSFDRTAAWBEBIVGESNDKLRG QSHWVLSFFFTHRATTSATAGRAFSPRTAWSSDALGRCTASWKT HSGSWWRVTWAHPFFGQVLASCSFDRTAAWBEBIVGESNDKLRG QSHWVLSFFTHRATTSATGSGFTKFFTHFVARSIAADH KDLIHDVSFFFTHRATTSATGSGFTKFFTHFVARSIAADH KDLIHDVSFFFTHRATTSATGSGFTKFFTHFVARSIAADH KDLIHDVSFFFTHRATTSATGSGFTKFFTHFVARSIABHL GRSWRTWAHPFF		1		QDVLGTKLPQLSKGSPEEPVVGCPLGQRQPCRKMLPDRSRAARD
VLLPEAIICAISAGDEUDYKTAEEKYIKGPSLSYREKBIPDNQL LERRNRRR 6486 10 581 LVLQAGGAHLSPSRVTQGIYYMLAFSEMPKPPDYSELSDSLTLA GGTGRFSGPLHRAWRMNFRQRWGHIGVGLYLLASAAAPYYVPE ISKTYMRLALEHIQOHPEPELEGTTYHTISLKAQLLSLPFWWTV IFLVPYLQMPpLYSCTRADPKTVGYCIIPICLAVICNRQAFV KASNQISRLQLIDT 6487 352 863 SFLKPLRGKMSVTLHTDVGDIKIEVFCCERTPKTCENFLALCASN YYMGCIFHRNIKGFWVQTGDPTGTGRGRSIXWGKKFEPEVSEVL KNHVRGVVSMANNGPNINGSOPFITYGKQPHLDMKTYVFGKVID GLETLDELEKLPVREKTYRPLNDVHIKDITHAMPPAQ 6488 878 241 TALQEFGTSGPPLSLRFALPSGTGRFKPLFGARGPSWPPSPRVP MBEPBLYPVKLYVVDLSKGLARRLSPIMLGKQLEGTWHTSIVVH KDEFFFGSGGISSCPPGGTLLGPPDSVVDVOSTBVTEBIFLEVL SSLGSELFGRAYNLFHNCNTTS NEVAQPITGKKIP SYITDLP SEVLSTPPGQALRPLLDSIQIPPGGSSVGRPNQGS 4489 1457 375 KVAKMATALSEELDNEDYYSLLNVRREASSEELKAAYRRLCML YHDKHRDPELKSQAELFNLHVAYLSDPQTRATVDIYGKK GLEMEGWBVVBRRTTPABIREFFELLQRERSERSLQQNTNPRGT ISGVUDATDLFDRVBDESPBVGSSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINPALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTFRCFVTINCALQFSSGIRPGLITVLJAR NLDKNTVGYLQWHCSSPLJQVGRAAAAAATVLFGGAGPTETMFVARSIADH KOLIHDVSFDPHGRRMATCSSDQSVKVMDKSSGGMHCTASWKT HGSGWRVTWAHPBFGQVLJASCSFDRTAAWWEILVGSDDKKRT QSHWVRRTTLUDSRTSVTDVKFAPKHMGLMLATCSADGIVRTYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSRRAHSPMIAVGSD DSSRNAMAKVQIFFYNENTRYAKARETLMTVTDPVHDIAFARDH GRSFHILLAIATKDVRIFTILKPVRKEUTSGGPYFFFEITMFVARSIAADH KOLIHDVSFDPHGRRMATCSSDQSVKWDKSSGGMHCTASWKT HGSGWRVWBNSNTTGTVLASSGGDCWLWKANTMONMKCTGIL KGNGSPWGSSGOQTSNPSLGSNIPSLQNSLNGSSAGRKHS HEAGCEVWLGYGPRAAAAAAATVLFGGGAGPTETMFVARSIAADH KOLIHDVSFDPHGRRMATCSSDQSVKWDKSSGGMHCTASWKT HGSGWRVTWAHPFFGQVLASCSCSCWKWDKSSGGMHCTASWKT HGSGWRVTWAHPFFGQVLASCSCSCWKWDKSSGGMHCTASWKT HGSGWRTWAHPFFGQVLASCSCSCWKWDKSSGGMHCTASWKT HGSGWRTTHAMPTFTQVLASCGDCWLWKANTMONMKCTGIL KGNGSPWGSSGOQTSNPSLGSNIPSLGSNIPSSRAHSPMIAVGSD DSSRNAMKVQIFFYNENTRYAKARETLMTVTDPVDIAFARSIAADH KOLIHDVSFDPHGRRMATCSSDGSVKWDKSSGGDMCTASWKT HGGSWRTTLADGRTSTTTTWFTATAWEETUGGSTDKLRG QSHWVKRTTLUDGSTSTVTVFR PKYTAKWEETUGGSTDKLRG QSHWVKRTTLUDGSTSTVTVFR PKYTAKWEETUGGSTDKLRG QSHWVKRTTLUDGSTSTVTVFR PKYTAKWEETUFFTMFVARSIAADH KOLIHDVSFDPHGRRMATCSSDGSVKWDKSSGGDMCTASWKT HGGGWG	.]		1• · · • • · · ·	RANQKLVEYIGKAKGAESHLRAILKSRKPSRWLQTFLSSSQYVT
LERNRRRR 6486 10 581 LVLQAGGAHLSPSRVTQGIYYMLAFSEMPKPPDYSELSDSLTLA GGTGRPSGPLHRAMRMNIFRQRMGHIGVGLIVLLASAAAPTYVEE ISSTYMRLALEHIQQHEEFLEGTTWTHISLKAQLLSLPFWWWTV IFLVPYLQMFLEHSVGTRADPKTVGYGIPTCLAVICNRQAFV KASNQISRLQLIDT 6487 352 863 SFLKPLRGKMSVTLHTUVGDIKLEVFCERTPKTCENFLALCASN YYMGCIFHRNIKGFWQTGDPTGTGRGGNSIWGKKFEDEVSEVL KHAVRGVVSMANNGPNTNGSGFFITTGKQPHLDMKYTVFGKVID GLETLDELEKLPVNEKTYRPLNDVHIKDTHANPFAQ 6488 878 241 TALQEFGTSGPPLSLRRALPSGTGRFKELFGARGPSMPBSPRVF MBPPNLYPVKLYVYDLSKGLARRLSFIMLGKLGEMHTSIVVH KOBFFFGSGGISSCPGGTLLGPPDSVVDVOSTSTVTEBIFLEVL SSLGESLFRGBAYNLFEHNCNTFSNEVAQFLTGRKIPSYITDLP SEVLSTPFGQALRFLLDSIQIPPGGSSVGPROGS KVAKMATALSEEELDNDDYYSLLNVRRERSSEELKAAYRRLCML YHPDKHRDPELKSQAEELFPLUVQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRTPABIREEFERLQRRERRRLQQRTNPKGT ISVGVDAITDLEDRYDGEVSDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINPALRRVTSAKGMGELFFGAG DLQGPLFGLKLFFRILTFRFCYTTNCALOPSSRGIRPGLITVLAR NLDKNTVGYLOMHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDBCCSGARTPSTAWTSAAVKLRBACLSGPGSGSKQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWILGGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDPHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HGSGWRVTWAHPEFGQVLASCSFDRTAAWMEILVGESNDKLRG QSHWVKRTTLUDGSTSVTDVKFAPKHMGLMATCSADGIVRIYE APDVNNLSQWSLOHEISCKLSCSCISWMPSSSRAHSPMLAVGSD DSSPNAMAKVQIFEYNENTRKYAKABTLMTVTDPVHDIAFADNL KNDLHTVALSSGSDQGTSNPSLGSNIFSLONSLNGSSAGRKHS HEAGCEVWILGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLHTMSQWSLOMFTTLASSCDCCVULKKANYMONKCTGIL KGNGSPVRQSSGQGTSNPSLGSNIFSLONSLNGSSAGRKHS HEAGCEVULGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLHTMSQWSLOMFTTLASSCDCCVULKKANYMONKCTGIL KGNGSPVRQSSGQGTSNPSLGSNIFSLONSLNGSSAGRKHS HEAGCEVNLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLHTMSQWSLOMFTTLASSCSTCOXVRANYMONKCTGIL KGNGSPVRQSSGQGTSNPSLGSNIFSLONSLNGSSAGRKHS HEAGCEVNLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLHTMSQWSLQHEISCKLSCSCISWPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTTDPVHDIAFAPNL GRSPHILAIATKVTFTLKPYRKETSGGPTKFEHHVAQFD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTTDPVHDIAFAPNL GRSPHILAIATKVTFTTLKPYRKETSGGPTKFEHHVAQFD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTTDPVHDIAFAPNL	i			CVETYLEDEGQLDLVVKYLQGVYQEVGAKVLQRTNGDRIRFILD
6486 10 581 LVLQAGGAHLSPSRVTQGIYYMLAFSEMDKPPDYSELSDSLTLA GGTGRFSGELHRAWMMNHFRQRMGWIGUSLLASAARYYYFE ISTYMRALEHIQQHPEPELEGTWTHSLKQLLSLFPWWTVV IFLVPYLQMFLFLYSCTRADPKTVGYCIIPICLAVICNRHQAFV KASNQISRLQLLDT 6487 352 863 SFLKFLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN YYNGCIFHRNINGFWVQTGDPTGTGRGGNIWGKKFEDEYSEYL KHNVRGVUSMANNGPNTUGSGPFJTYGKQPHLDMKTVPGKVUL GLETLDELEKLPVNEKTYRPLNDVHIKDTTHANPFAQ 6488 878 241 TALQEFGTSGPFLSIRFALPSGTGRFKPLFGARGPSWPFSPRVP MBPPNLYPVKLYVYDLSKGLARRLSPTMLGKQLEGWHTSIVVH KOEFFFGSGGISSCPPGGTLLGPPDSVVDGSTEVTEBIFLEYL SSLGESLFRGBANNLFBHRNCTTFSNEVAQFLTGRKIPSVITDLP SSULSTPFGGALRPLDSIQIOPPGGSSVGRPMGQS KVAKMATALSEEELDNEDYYSLLNVYRREASSEELKAAYRRLCML YHPDKHRDPELKSQAERLFNLVHQAYSVLSDPQTRAIVDIYGKR GLEMEGWEVVERRRTPABIRBEFFRLQRERBERRLQORTNPKGT 1SYGVDATDLFDRYDDEVENDVSGSFPQIEINFMINSQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTFRCFVTTINCALQFSSKGIRPGLITVLAR NLDKNTVGYLGWHGSSPLLGVGPRHNTRACAPEPSFRPFLHVP TWDAECSGARTFSTAWTSAAVKLREACLSGPGSGSHOLLLLTPR SKRTTGGG 6490 3 1183 HEAGCEVWLGYGFRAAAAAATVLFGGAGFTETMFVARSIAADH KOLIHDVSFDFHGRRMATCSSDQSVKVWKSESGOMHCTASWKT HGSVWRVTWAHPEFGGVLASCSFDRTAAVWERIVSDPHDIAFAPNL GRSFHILAIATKDVRITTLKPVKRELTSSGGFTKFEIHIVAQFD NINSGWRVSVNAITOTTVLASSGGTJKREIHVAQFD NINSGWRVSVNAITOTTVLASSGGTTKFEIHVAQFD NINSGWRVSVNAITOTTVLASSGGTTKFEIHVAQFD NINSGWRVSVNAITOTTVLASSGGTTKFEIHVAQFD NINSGWRVSVNAITOTTVLASSGGTTKFEIHVAQFD NINSGWRVSVNAITOTTVLASSGGTTKFEIHVAQFD NINSGWRVSVNAITOTTVLASSGGTTKFEIHVAQFD NINSGWRVSVNAITOTTVLASSGGTTKFEIHVAQFD NINSGWRVSVNAITOTTVLASSGGTTKFEIHVAQFD NINSGWRVSVNAITOTTVLASSGGTTKFEIHVAQFD NINSGWRVSVNAITOTTVLASSGGTTKFEIHVAQFD NINSGWRVSVNAITOTTVLASSGGTTKFEIHVAQFD NINSGWRVSVNAITOTTVLASSGGTTKFEIHVAQFD NINSGWRVSVNAITOTTVLASSGGTTKFEIHVAAGFSHCHTASWKT HSGSWRVTWAHPEFGGVLASCSFDRTAAWEIVGSENDKLRG GSFHILAIATKWRTTLDSRTSVTDWKFARKGMLATCSSAGIVRITYE APDVMNLSQWSLQHEISCKLSCSCISWNSSSRGHTTASWKT HSGSWRVTWAHPEFGGVLASCSFDRTAAWEIVGSENDKLRG GSHWLATTLLDSRTSVTDWKFARKGILMLATCSSAGIVRYTY BAPDVMNLSQWSLQHEISCKLSCSCISWNSSSRAHSPMLAGSD DSSPNAMAKVQIFFYNENTKKYKARETIMTVTDPVHDIAFAPNL GSSPRAMAKVQIFFYNENTKKY				
GGTGRSGGLHRAWRMMNFRQRMGWIGVGLYLLASAARYYYVB ISETYNRLALEHIQQHPEBPLGTTWHSLKAQLLSIPFWWTV IFLVPYLQNFLLYSCTRADPKTVGYCIIPICLAVICNEHQAFV KASNQISRIQLIDT SFLKPLRGKMSVTLHTDWGDIKIBVFCERTPKTCENFLALCASN YYNGCIFHRNIKGFWVQTGDPTGTGRGSNSIWGKKFEDEYSEYL KHNVRGVVSMANNGENTNGSGFFITYCKCHPLDMKTTVFGKVID GLETLDELBKLPVMKTTVPLDWHIKDTIHANPFAQ 6488 878 241 TALQEFGTGGPLSLERALPGGTGRFKFLFGARGPSWFPSPRVF MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKLEGIWHTSIVVH KDEFFFGSGGISSCPFGTLLGPPDSVVDVGSTEVTEBIFLEYL SSLGESLFFGGANIFBHINCNTFSNEVAQPITGRKIPSVITDLP SEVLSTPFGGALRPLDSIQIQPPGSSVGRPRQGS 6489 1457 375 KVAKMATALSEELDNEDYYSLLNVRREASSEELKAAYRRLCML YHPDKHRDPELKSQAELFFNLVHQAYEVLSDPGTRAIYDIYGKR GLEMBGWEVVERRFTPABIRBETQREERERLQQRTNPKGT ISYGVDATDLFDRYDEEVEDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGLSTQNGNGGGSINFALRKTSAKWGELBFGAG DLQGPLFGLKLFRNLTPRCFVTTUTCALQFSSKGIRFGLTTULAR NLDKNTVGFLOWHCSSPLLQVGRPHRATSAKOGSLEFGAG DLQGPLFGLKLFRNLTPRCFVTTUTCALQFSSKGIRFGLTTULAR NLDKNTVGFLOWHCSSPLLQVGRPHRATSAKOGSGGGLLLTPR TSCAGATTSTAMVSAAVKLREACLSGPGSGGHQLLLLTPR SKRRTGGG 6490 3 1183 HERGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDGVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLUDSRTSVTDVKFAPKHMGLMALATCSADGIVRIYE APDVWNLSQWSLQHEISCKLSCSSISWPSSSRAHSPMIAVGSD DSSPNAMAKVQIFFYNRNTRKYAKAETLMTVTDPVHDLAFAPNL GRSFHILAIATKDVR IFTLKPVRKELTSSGGPTKFEIHIVAQFD NINSQVWRVSNN ITGTVLASSGDGCVRLWKANYMDNWCTGIL KONGSPVNOSSQQGTSNPSLGSNIPSLGNGSAGRKHS HGGCVWLGYGPRAAAAAATVLFGGAGFTETMFVARSIAADH KDLHDVSFDFHGRRMATCSSDGSVKVWKSSSGGWHCTASWKT HSGSWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLUDSRTSVTDVKFAGGAGFTETMFVARSIAADH KDLHDVSFDFHGRRMATCSSDGSVKVWKSSSGGWHCTASWKT HSGSWRVTWAHPEFFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLUDSRTSVTDVKFAGGAGFTETMFVARSIAADH KDLHDVSFDFHGRRMATCSSDGSVKVWKSSSGGWHCTASWKT HSGSWRVTWAHPEFFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLUDSRTSVTDVKFAGGAGFTETMFVARSIAADH KDLHDVSFDFHGRRMATCSSDGSVKVWKSSSGGWHCTASWKT HSGSSWRVTWAHPEFFGQVLASCSFDRTAAWEEIVGSEDDILGG QSHWVKRTTLUDSRTSVTDVKFAGGAGFTETMFVARSIAADH KDLHDVSFDFHGRRMATCSSDGSVKVWKSSSGGWHCTASWKT HSGSSWRVTWAHPEFFGQVLASCSFDRTAA		ļ		
ISSTYNRLALEHIQQHPEEPLEGTTWTHSIKAQLLSLPFWVMTV IFLVPYLQMFLFLYSCTRADPKTVQCIIPICLAVICNRHQAFV KASNQISRLQLIDT 6487 352 863 SFLKPLRGRMSVTLHTDWGDLKIEVFCERTPKTCENFLALCASN YYNGCIFHRNIKGFWQTGDFFGGGNSIWGKKFDEYSEYL KHNVRGVVSMANNGPNTNGSQFFITYGKQFHLDMKTTVFGKVID GLETLDELEKLPVNEKTYRPLNDVHIKDITHANPFAQ 6488 878 241 TALQEFOTGGPISLERPALPSGFFRFLFQARGPSWPPSPRVFP MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGUMHTSIVVH KOEFFFGSGGISSCPPGGTLLGPPDSVVDGSTEVTEBIFLEYL SSLGESLFFGBAYNLFBHRNCTTFSNEVAQFLTGRKIPSYITDLP SEVLSTPFQGALRPLLDSIQIQPPGGSSVGRPNGQS 6489 1457 375 KVAKMATALSEELDNEDYYSLLNVRERASSEELKAAYKRLCML YHPDKHRDPELKSQAELIFNLVHQAYEVLSDPCTRAIYDIYGKR GLEMBGWEVVERRRTPABIREFFRLQREREBRRLQQRTNPKGT ISVGVDATDLFDRYDEEYSDVSGSSFPQLEINKMHISGSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRUTSAKGWGELEFGAG DLQGPLFGLKJFRNLTPRCFYTTNCALQFSSKGIRFGLITVLAR NLDKNTVGYLQWHCSSPLJQVQRPRNTRACADEPSFRPFLHVP SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KOLLHDVSFDFHGRMATCSSDQSVKVWDKSESGDHCTASWKT HSGSVWRVWAHPEFGGVLASCSFDRTAAVWEIVGSDGJKLFR GSFWHILAIATKURI FTLKPVKEITSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDGCVRLWKANYMDNWKCTGIL KONGSPVNGSSQQGTSNPSLGSNIPSLGRHGMASSAGRHS HEAGCEVWLGVRFRAAAAATVLFGGAGFTETMFVARSIAADH KOLLHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KONGSPVNGSSQQGTSNPSLGSNIPSLGNINGSSGRHS GSFHILAIATKURI FTLKPVKLTSSGGPTKFFIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KONGSPVNGSSQQGTSNPSLGSNIPSLGSNIGSSSGRHS HEAGCEVWLGVGFRAAAAATVLFGGAGFTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWLCASWKT HSGSWWRVWAHPEFGGVLASCSFDRTAAVWEIVGSEDDKLRG QSHWLAKRTTLUDSRTSVTDWKFRLTSSGGPTKFFIHVVAQFD NHNSQVWRVSWNITGTVLASSGDGCGSGGSGHSLAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWLCTASWKT HSGSWWRVTWAHPEFGGVLASCSFDRTAAVMEIVGSEDDKLRG QSHWVKRTTLUDSRTSVTDWKFAARAFILMFUNGMLATCSSDGIVKIYE APDVWNLSGWSLQREISCKLSCSCISWPSSSRAHSPMIAVGSD DSSPNAMAKVQIFFYNENTRKYAKETITHTVDPVHDIAFAPNL GRSFHILAIATKDVRIFTIKFYAKELTSSGGFTKFEHIVAQFD DSSPNAMAKVQIFFYNENTRKYAKETITHTVDPVHDTAFAPNL	6486	10	581	LVLQAGGAHLSPSRVTQGIYYMLAFSEMPKPPDYSELSDSLTLA
IFLVPYLQMPLFLYSCTRADPKTVGYCIIPICLAVICNRHQAFV				GGTGRFSGPLHRAWRMMNFRQRMGWIGVGLYLLASAAAFYYVFB
6487 352 863 SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN YYNGCIFHRNI KGFMVQTGDPTGTGRGGNSIMGKKFEDEYSEYL KHNVRGVSMANNGPBTNGSQFFITYGKQPHLDMKYTVFGKVID GLETLDELEKLPVNEKTYRPLNDVHIKDITIHANPFAQ 6488 878 241 TALQEFGTSGPPLSLRFALPSGTGRFKPLPGARGFSWPSPRVP MBPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH KDEFFFGSGGISSCPPGGTLLGPPDSVVDWGSTEVTEBIFLEYL SSLGESLFRGEAYNLFENKCNTFSNEVAQFLTGRKIPSYITDLP SEVLSTPFGQALRPLLDSTQIQPFGGSSVGRPNGQS 6489 1457 375 KVAKMATALSEELDNEDYYSLINVRREASSEELKAAYRLCML YHPDKHRDPELKSQAERLFUNHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTBABIREBFERLQRERBERRLQGRINPKGT ISVGVDATDLFDRYDESYBDVSSFPQTEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKKWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR NLDKKTVGYLQMHCSSPLLQVFRHTNTACAPEPSFRPPLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HERGCEVMLGYGFRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVNDKSESGDMCTASWKT HGGSWRVTWAHPEFSQVLJKRSFDFTAAVWEBIYGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGIMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSRAHSPMIAVGSD DSSPNAMAKVQIFEVNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATMDVRIFTLKPYRELTSSGGFTKFEHHIVAGFD NINSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQTENBELGSNIFSLDNSLNGSSAGRKHS KOLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWCTASWKT HSGSWWRVWARHPEFGGVLASCSFDFTAAWWEELVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLAATCSADGIVRIYE APDVWNLSQWSQQPTRAAAAAAATVLFGGGAPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWCTASWKT HSGSUWRVWARHPEFGGVLASCSFDRTAAWEELVGGSNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLAATCSADGIVRIYE APDVWNLSQWSQQCHSISCSCSCTSWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYARGETLMTVTDPVHIJAFAPNL GRSFHILAIATHDVRIFTKFYARGETLMTVTDPVHIJAFAPNL GRSFHILAIATHDVRIFTKFYARGETLMTVTDPVHIJAFAPNL GRSFHILAIATHDVRIFTKFYARGETLMTVTDPVHIJAFAPNL GRSFHILAIATHDVRIFTKFYARGETLMTVTDPVHIJAFAPNL GRSFHILAIATHDVRIFTKFYARGETLMTVTDPVHIJAFAPNL GRSFHILAIATHDVRIFTKFYARGETLMSGFTKFETHIVAFP	I			ISETYNRLALEHIQQHPEEPLEGTTWTHSLKAQLLSLPFWVWTV
SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN YYNGCIFHRNIKGFWQTGDPTGTGRGGNSIWGKFEDEYSEYL KHNVRGVVSMANDSPNTINGSQFFITYGKQPHLDMKYTYPGKVID GLETLDELEKLPVNEKTYRPLNDVHIKDITHANPFAQ GLETLDELEKLPVNEKTYRPLNDVHIKDITHANPFAQ TALQEFGTGPPLSLRFALPSGTGRFKFLPGARGFSWPPSFRVP MEPPNLYPVLKIVYDLSKARLSP PHLGKQLEGIWHTSIVVH KDEFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTEBIFLEYL SSLGESLFRGEAYNLFHHNCNTESNEVAGFHTGRKIPSYTTDLP SEVLSTPFGGALRPLLDSIQDPGGSSVGRPMGGS SULSTPFGGALRPLLDSIQDQTPGSSVGRPMGGS SEVLSTPFGGALRPLLDSIQDQTPGASSVGRPMGGS SEVLSTPFGGALRPLLDSIGTQPPGSSVGRPMGGS ISVGPDATATUDIYGKR GLEMEGWEVVVERRTETABLEGFSRLQRERERRLQQRTNPKGT ISVGVDATDLFDRYDEEYEDVSGSFFPGIEINKMHISQSIEAPL TATDTAILGGSLSTQNGNGGGSINFBLRGYTTVLAR NLDKNTVGYLQWHCSSPLQVGRPRATARTISASKGWGELEFGAG DLQGPLFGLKFPNLTFCTVTINCALQFSSRGIRPGLITVLAR NLDKNTVGYLQWHCSSPLQVGRPRATARCAEPSFRPFLHVP TRDAECSGARTPSTAWTSAAVKLREACLSGFGSGSHQLLLLTPR SKRTGGG SEXPLUSAGART STAWTSAAVKLREACLSGFGSGSHQLLLLTPR SKRTGGG SEXPLUSAGART STAWTSAAVKLREACLSGFGSGSHQLLLLTPR SKRTGGG SEXPLUSAGART STAWTSAAVKLREACLSGFGSGSHQLLLLTPR SKRTGGG GSTAWTSAGAVKT HEGSVWRVTWAHPEFGQVLASCSFDRTAAVWEBIVGESDAKKT HEGSVWRVTWAHPEFGQVLASCSFDRTAAVWEBIVGESDAKKT HEGSVWRVTWAHPEFGQVLASCSFDRTAAVWEBIVGESDAKKT HEGSVWRVTWAHPEFGQVLASCSGTSWPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKABTLMTVTDPVDIAPAPNL GRSFHILAITATKDVRIFTLKVAKABTLMTVTDPVDIARPAPNL KGNGSPVRNGSQQGTSNPSLGSNIPSLGNINGSSAGRKHS HEAGCEVWLGYGPRAAAAAATVLFGGAGFTETMFVARSTAADH KDLIHDVSFDFHGRRMATCSDGSVTRARSTMYMDWKCTGIL KGNGSPVRGSVGRYGFGRAAAAAATVLFGGAGFTETMFVARSTAADH KDLIHDVSFDFHGRRMATCSDGSVRWDKSESGDWICTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESDKLRG QSHWVRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHETSCKLSCCISWNPSSGRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSSVWRVTWAHPEFGQVLASCSGCISWNPSSGRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSSVWRVTWAHPEFGQVLASCSGCISWNPSSGRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSSVWRVTWAHPEFGQVLASCSGCISWNPSSGRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSSVWRTWAHPEFGQVLASCGGTETMFVAGATHAPAPNL GRSSVWRTWAHPEFGGVLASCGGSTRAFFTHATVGRS	İ .			
YYNGCIFHRNIKGFMVQTGDPTGTGGGNSIWGKKFEDEYSEYL KHNVRGVYSMANNGPNTNGSQFFITYGKQPHLDMKYTUFGKVID GEETLDELEKLPVMEKYTYPLNDVHIKDITHANPPAQ 6488 878 241 TALQEFGTSGPPLSLRFALFSGTGRFKPLPGARGPSWPPSPRVP MBPPNLYPVKLYYVDLSKGLARRLSPIMLGKQLEGIWHTSITVYH KUBFFFGSGGISSCPPGGTLGPPDSVVDVGSTEVTERIFLEYL SSLGESLFRGEAYNLFEHNCNTFSNEVAQFLTGRKIPSYITDLP SEVLSTPFGQALRPLLDSIQIQPPGGSSVGRPNQQS 6489 1457 375 KVAKMATALSEELDNBDYSLLNVRREASSEELKAAYRRLCML YHPDKHRDPELKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTBABIREEFFERLQREREERRLQGRTNPKGT ISVGVDATDLFDRYDEEFSVGSSFFOJEINKMHISGSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTINCALQFSSRGIRPGLITVLAR NLDKNTVGVLQWHCSSFLDQVQRPHRNTRACAPBPSFRPFLHVP THDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HERGCEVWLGYGFRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDPHGRRMATCSDQSVKWWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFORTAAWWEBIVGESNDKLRG QSHWVRTTLVDSRTSVTDVKFAPKHMGLMATCSADGIVRIYE APDVMNLSQMSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDDVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVKREITSSGGPTKFEHIVAQFD NINSQVWRVSWNITGTVLASSGDGGCVRLWKANYMDNWKCTGIL KCNGSPVNGSPQOGTSNPSLGSNIPSLQNILSGPTMFFTHIVAQFD NINSGVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KCNGSPVNGSSQOGTSNPSLGSNIPSLQNINGSSAGRKHS KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSUWVRTTLANPSFGQVLASCSFORTMAVWEBIVGESNDKLRG QSHWVRTTLVDSRTSVTDVKFAPKHMGLMATCSADGIVRIYE APDVMNLSGWSLQHEISCKLSCSCISWNPSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSSVWRVTWAHPEFGQVLASCSFORTMANWEEITVGESNDKLRG QSHWVRTTLVDSRTSVTDVKFAPKHMGLMATCSADGIVRIYE APDVMNLSGWSLQHEISCKLSCSCISWNPSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSSVWRVTWAHPEFGQVLASCSFORTAAVWEBIVGESNDKLRG QSHWVRTTLVDSRTSVTDVKFAPKHMGLMATCSADGIVRIYE APDVMNLSGWSLQHEISCKLSCSCISWNPSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLTMTVTDTPVHDIAFAPNL GRSSPHILAIATATUVRIFTLKFUKVELTSSGGPKFEHILVAQFD DSSPNAMAKVQIFEYNENTRKYAKAETLTMTVTDTPVHDIAFAPNL GRSSPHILAIATATUVRIFTLKFUKELTSSGGPKFEHILVAQFD				
KHNVRGVUSMANNGFNTNGSQFFITVGKQPHLDMKYTVFGKVID GLETLDELEKLPVNEKTYRPLNDVHIKDITIHANPFAQ 6488 878 241 TALQEFGTSGPPLSLRFALPSGTGRFKPLPGARGPSWPPSPRVP MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH KDEFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTERIFLEYL SSLGESLFRGEAYNLFBINCNTFSNEVADPLTGRK, IESYITDLP SEVLSTPFQQALRPLLDSIQIQPPGGSSVGRPMQQS 6489 1457 375 KVAKMATALSEEELDNEDYYSLLNVRREASSEELKAAYRRLCML YHPDKHRDPBLKSQAGRHDLWDAYSULSDPQTRAIYDIYGKR GLEMEGWEVVERRTPABIREEFERLQRERBERRLQQRTMPKGT 15VGVDATDLFDRYDESYDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTERCFVTINCALQFSSRGIRFGLITVLJAR NLDKNTVGYLQWHCSSPLLQVGPPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HERGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVRRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWBPSSSRAHSPMIAVGSD DSSPNAMAKVQIFFYNENTRKYAKABETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQWRVSWNTTGTVLASSGDCCVRLWKANYMDNWKCTGIL KONGSPVNGSQQGTSWPSLGSNIPSLGSNIPSLGSNCKIS GSHWKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWBSSSGRHKIS KONGSPVNGSQQGTSWFSLGSNIPSLGSNIPSLGSRGKHIS GSSWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWBSSSGRHHDAAVGSD DSSPNAMAKVQIFFYNENTRKYAKABETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHTVAQFD DSSPNAMAKVQIFFYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGFTKFEIHTVAQFD DSSPNAMAKVQIFFYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGFTKFEIHTVAQFD	6487	352	863	
GLETLDELEKI, PVNEKTYPLNDVHI KDITIHANPFAQ 6488 878 241 TALQEFGTSGPPLSLRFALPSGTGRFKPLFGARGPSWPPSSRVP MBPPNLYPVKLYVYDLSKGLARRLSP INLGKQLEGIWHTS IVVH KDEFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTERIFLEYL SSLGESLFRGEAYNLFENNCNTFSNEVAGFLITGKKI PSYITDLP SEVLSTPFGQALRPLLDSIQIQPPGGSSVGRPNQGS 6489 1457 375 KVAKMATALSEEELDNEDYYSLLNVRREASSEELKAAYRRLCML YHPDKHRDPELKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRTPABLIREEFELQREREBRRLQQRTHPKGT ISVGVDATDLFDRYDEEFEDVYSSLNVRREASSEELKAAYRRLCML YHDDKHRDPELKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRTPABLIREEFELQREREBRRLQQRTHPKGT ISVGVDATDLFDRYDEEFEDVYSGSSFPQTEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFYTTITCALQFSSRGIRPGLITTVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDABCSGARTPSTAWTSAAVKLRBACLSGPGSGSHQLLLLTPR SKRRTGGG SKRRTGGG HEAGCEWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWPSSSSRAHSPMLAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGFTKFEIHTVARFIAADH KDLIHDVSFDFHGRRMATCSSDGVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWPSSSRAHSPMLAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKAEATLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKAEATLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKAEATLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKAEATLMTVTDPVHDIAFAPNL GRSSPHILAIATKDVRIFTLKPVRKELTSSGGFTKFEIHTVAQFD	1			
6488 878 241 TALQEPGTSGPPLSLRFALPSGTGRFKPLPGARGPSWPPSPRVP MBPPNLYPVKLYVYDLSKGLARRLSP INLGKQLEGIWHTSITVH KDEFFFSGGISSCPPGGTLLGPPDSVVDVGSTEVTEIFLEYL SSLGESLFRGEAYNLFEHNCNTFSNEVAQFLTGRKIPSYITDLP SEVLSTPFGQALRPLLDSTGIQPPGGSSVGRPNGQS 6489 1457 375 KVAKMATALSEELDNEDYYSLLNVRREASSELKAAYRRLCML YHPDKHRDPBLKSQAERLFNLUNGAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTPABIREEFERLQREREBRRLQQRTMPKGT ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVYSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTINCALQFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLUQVRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KOLIHDVSFDPHGRMATCSSDQSVKWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAWEEIVGESNDKLRG QSHWVRTTLVDSRTSVTDVKFAPKHNGLMLATCSADGTVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMLAVGSD DSSPNAMAKVQIFFYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQTSNPSLGSNIPSLQNSLMGSSAGRKIS 6491 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKWWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEE UVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGTVRIYE HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEE UVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGTVRIYE APDVWNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMLAVGSD DSSPNAMAKVQIFFYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPYKELTSSGGPTKFEIHIVAQFD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPYKELTSSGGPTKFEIHIVAQFD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPYKELTSSGGPTKFEIHIVAQFD	ł			
MBFPNLYPVKLYVYDLSKGLARRLSPTMLGKQLEGTWHTSTVVH KDBFFFGSGGISCPPGGTLLGPDSVVDVGSTEVTERIFLEYL SSLGESLFRGBAYNLFRHNCNTFSNEVAQFLTGRKIPSYITDLP SEVLSTPFGQALRPLLDSIQIQPPGGSSVGRPNGQS 6489 1457 375 KVAKMATALSEEELDNEDYYSLLNVRREASSEELKAAYRRLCML YHPDKHRDPBLKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTPABIREEFERLQREREBRRLQQRTNPKGT ISVGVDATDLFDRYDBEYBDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLITVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVNMLSQMSLQHEISCKLSCSCISWNPSSRAHSPMLAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVKELTSSGGPTKFEIHTVAQFD NHNSQWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSFVNGSSQQGTSNPSLGSNIPSLGNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKWDKSESGDWHCTASWKT HSGSVWRVTWAHPBFGQVLASCSFDRTAAVWEE UGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVWNLSQWSLQHEISCKLSCSCISWNPSSRAHSPMLAVGSD DSSPNAMAKVQIPFYNENTRYYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFYKELTSSGGPTKFEIHTVAGSD DSSPNAMAKVQIPEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFYKELTSSGGPTKFEIHTVAGSD DSSPNAMAKVQIPEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFYKELTSSGGFTKFEIHTVAGSD DSSPNAMAKVQIPEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFYKELTSSGGFTKFEIHTVAGFD		<i>j</i>		
KDEFFFGSGISSCPPGGTLLGPPDSVVDVGSTEVTEEIFLEYL SSLGESLFRGBAYNLERHNCTFSBEVAQFLITGRKIPSYITDLP SEVLSTPPGQALPPLLDSIQIQPPGGSSVGRPNGQS 6489 1457 375 KVAKMATALSEEELDNEDYYSLLNVRREASSEELKAAYRRLCML YHPDKHRDPBELKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVBRRRTEABIREFERLQREREERRLQQRTNPKGT ISVVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGLSTQNCNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVD TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEE IVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKABETLMTVTDPVHDLAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEHIVAQFD NHNSQWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIFSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWBKSESGDWCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEELVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEELVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAGFD	6488	878	241	
SSLGESLFRGEAYNLFEHNCNTFSNEVAQFLTGRKIPSYITDLD SSVLSTFFGQALRPLLDSIQTQPPGGSSVGRPNGGS KVAKMATALSEELDNEDYYSLLNVREASSEELKAAYRRLCML YHPDKHADPBLKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRTPABIREEFERLQREREERRLQQRTNPKGT ISVGVDATDLFDRYDESYSFPQIEINKHHISQSIEAPL TATDTALLSGSLSTQNGNGGGSINFALRRYTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLITVLAR NLDKNTVGYLQWHCSSPLLQVORPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLDDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKABITLMTVTDPVHDLAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEHIVAQFD NHNSQWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGFTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAWWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMILSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFVRKELTSSGGFTKFEHIVAGFD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFVRKELTSSGGFTKFEHIVAGFD				
SEVLSTPFGQALRPLLDSIQIQPPGGSSVGRPNGQS 6489 1457 375 KVAKMATALSEEELDNEDYYSLLNVTREASSEELKAAYRRLCML YHPDKHRDPELKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTPABIREEFERLQAEREBRRLQQRTNPKGT ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGFTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFBGRMATCSSDQSVKWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETIMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFVRKELTSSGGPTKFEIHIVAQFD DSSPNAMAKVQIFEYNENTRKYAKAETIMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFVRKELTSSGGPTKFEIHIVAQFD			,	
6489 1457 375 KVAKMATALSEEELDNEDYYSLLNVRREASSEELKAAYRRLCML YHPDKHRDPELKSQAERLFHLUHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTPABIREEFERLQREREBRELQQRTNPKGT ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLIFPRCFVTTNCALQFSSRGIRPGLITVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRRELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLGNILNGSSAGRKHS HEAGCEVWLGYGPRAAAAAATVLFGGAGFTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVCESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATHDVRIFTLKPVRKAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATHDVRIFTLKPVRKAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATHDVRIFTLKPVRKAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATHDVRIFTLKPVRKAKAETLMTVTDPVHDIAFAPNL	1		•	
YHPDKHRDPELKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTPABIREEFERLQRERBERRLQQRTNPKGT ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLITVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APPDVMNLSQWSLQHEISCKLSCSCISWNPSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSQQGTSNPSLGSNIPSLQASLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD				SEVLSTPFGQALRPLLDSIQIQPPGGSSVGRPNGQS
GLEMEGWEVVERRRTPABIREEFERLQREREERRLQQRTNPKGT ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKKWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTTACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPPEFGQVLASCSFDRTAAVWEBIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFFYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDDSTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD	0489	1457	a 375	
ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL TATDTAILGGSLSTQNGNGGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGFTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIFSLQNSLNGSSAGRKHS HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD	}			
TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKABETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD				GLEMEGWEVVERRRTPABIREEFERLQREREERRLQQRTNPKGT
DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLRBACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD	,			15VGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL
NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD	1			
TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD				
SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD	1			
6490 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD	1			
KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD	6400	3		
HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD	0490	3	1183	
QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD	1			KULIHUVSFUFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
APDVMNLSQWSLQHEISCKLSCSCISWNPSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD				
DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD				- · · · · · · · · · · · · · · · · · · ·
GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD	}			
NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD				
KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD				
6491 3 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD				
KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD	(401			
HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD	6491	3	1183	HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH
QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD				KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD				
DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD	,	1		
GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD				APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL]		
NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL		ļ		GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD
				NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	
Ì	amino acid	•	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	ļ		KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS
6492	34	2573	IPFLKSCCCCLFDFPPPPLDQVQEEECEVERVTEHGTPKPFRK
•			FDSVAFGESQSEDEQFENDLETDPPNWQQLVSREVLLGLKPCEI
,			KRQEVINELFYTERAHVRTLKVLDQVFYQRVSREGILSPSELRK
ł	}		IFSNLEDILQLHIGLNEQMKAVRKRNETSVIDQIGEDLLTWFSG
			PGEEKLKHAAATFCSNQPFALEMIKSRQKKDSRFQTFVQDAESN
1			PLCRRLQLKDIIPTQMQRLTKYPLLLDNIATYTEWPTEREKVKK
			AADHCRQILNYVNQAVKEAENKQRLEDYQRRLDTSSLKLSEYPN
			VEELRNLDLTKRKMIHEGPLVWKVNRDKTIDLYTLLLEDILVLL
	j		QKQDDRLVLRCHSKILASTADSKHTFSPVIKLSTVLVRQVATDN
			KALFVISMSDNGAQIYELVAQTVSEKTVWQDLICRMAASVKEQS
			TKPIPLPQSTPGEGDNDEEDPSKLKEEQHGISVTGLQSPDRDLG
			LESTLISSKPQSHSLSTSGKSEVRDLFVAERQFAKEQHTDGTLK
			EVGEDYQIAIPDSHLPVSEERWALDALRNLGLLKQLLVQQLGLT
1			EKSVQEDWQHFPRYRTASQGPQTDSVIQNSENIKAYHSGEGHMP
ł			FRTGTGDIATCYSPRTSTESFAPRDSVGLAPQDSQASNILVMDH
	· ·		MIMTPEMPTMEPEGGLDDSGEHFFDAREAHSDENPSEGDGAVNK
			EEKDVNLRISGNYLILDGYDPVQESSTDEEVASSLTLQPMTGIP
]			AVESTHQQQHSPQNTHSDGAISPFTPEFLVQQRWGAMEYSCFEI
i			QSPSSCADSQSQIMEYIHKIEADLEHLKKVEESYTILCQRLAGS
		·	ALTDKHSDKS
6493	557	1147	TPARMAYQGSSTSDCMSKTLDSASAHFAASAVVSAPVPSRSEVA
ŀ			KEQNTGHNNINGVVQPSGTSKTLYSTNMALSSSPGISAVQLVRT
ļ			VGHTTTNHLIPALCTSSPQTLPMNNSCLTNAVHLNNVSVVSPVN
ļ)		VHINTRTSAPSPTALKLATVAASMDRVPKVTPSSAISSIARENH
			EPERLGLNGIAETTVAMEVT
6494	2425	1052	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
			LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG
:			VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL
			EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEYITQEGHKL
			ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVIESVNLLVSAN
· '			GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS
			VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK
		,	PLIWIESVIEKHSHSRIEYMIKAKSQFKRRSTANNVEIHIPVPN
	1 .		DADSPKFKTTVGSVKWVPENSEIVWSIKSFPGGKEYLMRAHFGL
	}	,	PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL
	<u> </u>		PWVRYITQNGDYQLRTQ
6495	2425	1052	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
			LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG
			VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL
			EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEYITQEGHKL
			ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVIESVNLLVSAN
,			GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS
			VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK
			PLIWIESVIEKHSHSRIEYMIKAKSQFKRRSTANNVEIHIPVPN
			DADSPKFKTTVGSVKWVPENSBIVWSIKSFPGGKEYLMRAHFGL
			PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL
			PWVRYITQNGDYQLRTQ
6496	247	559	LRAVSLLPLQLVLPBYSIHSLFCIMFLCAQEWLTLGLNVPLLFY
			HFWRYFHCPADSSELAYDPPVVMNADTLSYCQKEAWCKLAFYLL
			SFFYYLYCMIYTLVSS
6497	1053	352	ANTQICRLCPRRHLHPPCGAKMGNGTEEDYNFVFKVVLIGESGV
			GKTNLLSRFTRNEFSHDSRTTIGVEFSTRTVMLGTAAVKAQIWD
			TAGLERYRAITSAYYRGAVGALLVFDLTKHQTYAVVERWLKELY
	[DHAEATIVVMLVGNKSDLSQAREVPTEEARMFAENNGLLFLETS
	<u></u>		ALDSTNVELAFETVLKEIFAKVSKQRQNSIRTNAITLGSAQAGQ
			**···

SEQ Predicted and nucleotide location nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence se	.d, B=
No: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence Serie, T=Threonine, V=Valine, Codon, /=possible nucleotide deletion, _=po	
location corresponding to first amino acid residue of amino acid residue of amino acid sequence 8-Serine, T=Threonine, V=Valine, Codon, /=possible nucleotide deletion, M=Department of Sequence 8-Serine, T=Threonine, V=Valine, W=Typtophan, Y=Typtosine, X=Unknown, Codon, /=possible nucleotide insertion) 8-PFOEKRACCISL 9-PFOEKRACCISL 9-PFOEKRACCISL 9-PFOEKRACCISL 9-PFOEKRACCI	TIIC,
corresponding to first amino acid sidue of amino acid residue of amino acid sequence	
to first amino acid residue of amino acid residue of amino acid sequence sequence sequence 6498 2636 272 SIRLCPWGTHLRGPTTMRLSSLLALLRPALPLILGESI LRVSWIGGEGEDPCVEAVGERGGPQNPDSRARLDQSDE VPYYRDPNKPYKKVLRTYIQTELGSRERLLVAVLTSR AVAVMRTVAHHPPRLLYFTGGRGRARAPAGMQVVSHGDE SETLRHLHTHPGADYDWFIMODDTYVQAPRLAALAGH LYLGRAEEFIGAGEQARYYCGLGFGSVLGSCNGSPFLAK KEGSSAFLSAFAVHPVSEGTLMYRLHKRFSALELERAY QAQIRNLTVLITEGEGAGLSWPVGLPAPFTPHSRFEVLG QHTFSCANGAPKCPLQGASRADVGDADLETALEQLNRRY QKQRLLNGYRRFDPARGMEYTLDLLLECVTQRGHRRAL LRPLSRVEILPMPYVTEATRAVQLVLPLLVAEAAAAPAPF NVLEPFEHALLTLLLYGPREGGRADPDFLGVKAAAA PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTT PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPGRSPED DPPSPPBADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGGEEERALEGLEVMDVFLRFSGLHLFRAVEPGLVG CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEDEQAM 6499 3 2040 SCSADTRPSGQAWPTVGLRAAAAAPAFF ADGLFLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKARLGFFAELCEFYSRDPDGLIFCALKRECNRPSGLEFG LRDAWNGVVNGTWKLEGEALEQAI ISOAQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRRPCNRPSGLEFG LRDAWNGVVNGTWKLEGEALEQAI ISOAQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEGGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLMQLVEKLKAA LKEACPNSSASNASGAAAPTLPAAHPSTLTHPQRRIDTL PEPARITSPDKKPRMPMDTSVYESPYSPBEELKDKKLF	
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, w=tryptophan, Y=Tyrosine, X=Unknown, w=tryptophan, Y=Tyrosine, X=Unknown, w=tryptophan, Y=Tyrosine, X=Unknown, w=tryptophan, Y=Tyrosine, X=Unknown, w=tryptophan, Y=Tyrosine, X=Unknown, w=tryptophan, Y=Tyrosine, X=Unknown, w=tryptophan, Y=Tyrosine, X=Unknown, w=tryptophan, Y=Tyrosine, X=Unknown, w=tryptophan, Y=Tyrosine, X=Unknown, w=tryptophan, Y=Tyrosine, X=Unknown, w=tryptophan, Y=Tyrosine, X=Unknown, w=tryptophan, Y=Tyrosine, X=Unknown, y=tryptophan, y=tryptophan, y=tryp	
residue of amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion) BPGFGEKRACCISL 6498 2636 272 SLRLCPWGTHLAGPTTMRLSSLLALLRPALPLILGESI LRVSWIGGEGEDPCVEAVGERGGPONPDSRARLDQSDE VPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSF AVAVNRTVAHHFPRLLYFTGGRGRARAPAGMQVVSHGDE SETLRHLHTHFGADYDWFFIMQDDTYVQAPRLAALAGH LYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPH DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELM KEGSSAFLSAFAVHVSSETLMYRLHKRFSALELERRY QAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLG QHTFSCADGAPKCPLQGASRADUGDALETALEQLNRRY QKQRLLNGYRRFDARGMEYTLDLLLECVTQRGHRRAI LRPLSRVEILDMPYVTEATRVQLVLPLLVABAAAAPAPA NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAA PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTT PEVLMRCRNMAI SGWQAFFPVHRQEFNPALSFQRSPEG DPPSPFGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGGEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQQAN GKAHCGPAELGGEVMDVFLRFSGLAMALFEQQAN GKAHCGPAELGETSPLALGFETF GHPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEEH ADGLFLRQCLRSLGGVYLSLVHDVRFHHFPIERQLNG GKAHCGPAELGEFYSRDPDGLPCNLRKPRONGPSGLPQ LRDAWNDVVRQTWKLEGEALEQAIISQAPQVEKLLAT PWYHSLTREAERKLYSGAQTGKFLLRPRREQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKIKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPBELKDKKLF	
amino acid sequence Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) BEGGEKRACCISL SIRLCPWGTHLAGPTTMRLSSLLALLRPALPLILGISI LRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLDQSDE VPYYRDPKPYKKVLRTRYIQTELGSERRLLVAVLTSF AVAVNRTVAHHFPRLLYFTGGRGARAPAGMQVSHGDE SETLRHLHTHFGADYDWFFIMQDDTYVQAPRLAALAGE LYLGRAEBEFIGAGEQARYCHGGFGYLLSRSLLLRLRPF DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELA KEGSSAFLSAFAVHVSSETLMYRLHKRFSALELERRY QAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLG QHTFSCADGAPKCPLQGASRADUGDALETALEGLNRRY QKQRLLNGYRRFDPARGMEYTLDLLLECVTQRGHRRAI LRPLSRVEILDMPRYTEATRVQLVLPLLVABAAAAPAPA NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAA PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTT PEVLMRCRMMAISGWQAFFPVHRQEFNPALSPQRSPEG DPPSPFGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGGEEERALEGLEVMDVFLRRSGLHLFRAVEPGLVG CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQQAN GCAPTPVRQUSGRAQLAMALFEQQAN GKAHCGPAELGEFYRDDVLSVHDVRFHHFPIERQLNG GKAHCGPAELGEFYSDDPGLPCNLRKPRONRSGLAGGKTAAGAFTTSPLALGPETP GHPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEEH ADGIFLLRQCLRSLGGYVLSVHDVRFHHFPIERQLNG GKAHCGPAELGEFYSDDPDGLPCNLRKPRONRPSGLEPQ LRDAMVRDVVRQTWKLEGEALEGAIISQAPQVEKLLAT PWYHSLTREAERKLYSGAQTTGKFLLRPRREGGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLWSYLKIKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPBELKDKKLF	ston
Sequence Seposible nucleotide insertion	
BPGPGEKRACCISL 6498 2636 272 SIRLCPWGTHLAGPTTMRLSSILALLRPALPLILGLSI LRVSWIQGEGEDPCVBAVGERGGPQNPDSRARLDQSDE VPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSE AVAVNRTVAHHFPRLLYFTGQRGARAPAGMQVVSHGDE SETLRHLHTHFGADYDWFFIMQDDTYVQAPRLAALAGH LYLGRAEEFIGAGEQARYCHGGFGYYLLSRSLLIRLRPH DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELL# KEGSSAFLSAFAVHPVSEGTLMYRLHKRFSALELERAY QAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLG QHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRY QKQRLLNGYRRFDPARGMEYTLDLLLECVTQRGHRRAY LRPLSRVEILBMPYVTEATRVQLVLPLLVABAAAAPAF NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAA PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTT PEVLNRCRMMAISGWQAFFFVHFGEFNPALSPQRSPEG DPPSPPGADPSRGAPLGFFFFDGFDRGASAEGCFYNADYLAA ELAGGZEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSELYHRCRLSNLEGLGGRAQLAMALFEQEQAN 6499 3 2040 SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETF ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDSLPCNLKKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVBYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHRPQRRIDTL PEPARITSPDKPRPMMDTSVYESPYSDPEELKDKKKLF	
LRVSWIQGEGEPCVEAVGERGEPONPDSRARLDQSDE VPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSR AVAVNRTVAHHFPRLLYFTGORGARAPAGMQVVSHGDE SETLRHLHTHFGADYDWFFIMQDDTYVQAPRLAALAGH LYLGRAEBFIGAGEQARYCHGGFGYLLSRSLLLRLRPH DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELA KEGSSAFLSAFAVHPVSEGTLMYRLHKRFSALELERAY QAQIRNLTVLTTEBEAGLSWPVGLPAPFTPHSRFEVLG QHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRY OKQRLLMGYRRFDPARGMEYTLDLLLECVTQRGHRRAL LRPLSRVEILPMPYVTBATRVQLVVLPLLVABAAAPAF NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAA PGTRLAWLAVRABAPSQVRLMDVVSKKHPVDTLFFLTT PEVLNRCRMMALISGWQAFFPVHPQEFNPALSPQRSPPG DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSBELYHRCRLSNLEGLGGRAQLAMALFEQEQAN 6499 3 2040 SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETF ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGBALEQAIISQAPQVEKLIAT PWYHSSLTRBEAERKLYSGAQTDCKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVBYLKLKA LKEACPNSSASMASGAAAPTLPAHPSTLTHPQRRIDTIT PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKKLF	
LRVSWIQGEGDPCVEAVGERGGPQNPDSRARLDQSDE VPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTTS AVAVNRTVAHHPPRLLYFTGQRGARAPAGMQVVSHGDE SETLRHLHTHFGADYDWFFIMQDDTYVQAPRLAALAGH LYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPF DILSARPDEWLGRCLIDSLGVGCVSQHQQQYRSFELA KEGSSAFLSAFAVHPVSEGTIMYRLHKRFSALELERRY QAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLG QHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRY QKQRLLMGYRRFDPARGMEYTLDLLLECVTQRGHRRAI LRPLSRVEILPMPYVTEATRVQLVLPLLVAEAAAAPAF NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAA PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLT PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPG DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFQEQAN 6499 3 2040 SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGEFE ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAWWRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVBYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTIT PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKKLF	GCSLSL
AVAVNRTVAHHFPRLLYFTGQRGARAPAGMQVVSHGDE SETLRHLHTHFGADYDWFFIMQDDTYVQAPRLAALAGH LYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPH DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELA KEGSSAFLSAFAVHPVSEGTLMYRLHKRFSALELBERAY QAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLG QHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRY QKQRLLNGYRFPDARGMEYTLDLLLLECVTQRGHRRAI LRPLSRVEILFMPYVTEATRVQLVLPLLVABAAAPAPAF NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAA PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFITT PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPG DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN ADGLFLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEGGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKRPPMPMDTSVYESPYSDPEELKDKKLF	DFKPRI
SETLRHLHTHFGADYDWFFIMQDDTYVQAPRLAALAGH LYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPH DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELA KEGSSAFLSAFAVHPVSEGTLMYRLHKRFSALELERAY QAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLG QHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRY QKQRLLNGYRRFDPARGMEYTLDLLLECVTQRGHRRAI LRPLSRVEILPMPYVTEATRVQLVLPLLVAEAAAAPAF NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAA PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTT PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPG DPPSPPGADPSGAPIGGRFDRQASAEGCFYNADYLAA ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN GHPPVRPQVSGGPGAMPDPAAHLPPFYGSISRAEAEEH ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRGTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
LYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPH DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELA KEGSSAFLSAFAVHPVSEGTLMYRLHKKFSALELBRAY QAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLG QHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRY QKQRLINGYRRFDPARGMEYTLDLLLECVTQRGHRRAI LRPLSRVEILPMPYVTEATRVQLVLPLLVABAAAAPAF NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAA PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTT PEVLMRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPG DPPSPFGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGGEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN 6499 3 2040 SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETF GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEEH ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCFFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVGTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELA KEGSSAFLSAFAVHPVSEGTLMYRLHKRFSALELERAY QAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLG QHTFSCADGAPKCPLQGASRADVGDALETALEQLMRRY QKQRLLNGYRRFDPAGMEYTLDLLLECVTQRGHRRAL LRPLSRVEILPMPYVTEATRVQLVLPLLVAEAAAAPAF NVLEPREHALLTLLLVYGPREGGRAPDPFLGVKAAAA PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTT PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPG DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN GHPPVRPQVSGGPGAMPTVGLRAAAGAFRTGSPLALGPETF ADGLFLLRQCLRSLLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVBYLKKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
KEGSSAFLSAFAVHPVSEGTLMYRLHKRFSALELERAY QAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLG QHTFSCADGAPKCPLQGASRADVGDALETALEQLMRRY QKQRLLMGYRRFDPARGMEYTLDLLLECVTQRGHRRAI LRPLSRVEILPMPYVTEATRVQLVLPLVAEAAAAPAF NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAA PGTRLAMLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTT PEVLMRCRMMAISGWQAFFPVHFQEFNPALSPQRSPPG DPPSPPGADPSRGAPIGGRFDRQASAEGCFYMADYLAA ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN 6499 3 2040 SCSADTRPSQQAWPTVGLRAAAGAFRTGSPLALGPETF GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEEH ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
QAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLG QHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRY QKQRLLNGYRRFDPARGMEYTLDLLLECVTQRGHRRAI LRPLSRVEILPMPYVTEATRVQLVLPLLVABAAAAPAF NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAA PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTT PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPG DPPSPFGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN GCSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEET ADGLFLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
QHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRY QKQRLLNGYRRFDPARGMEYTLDLLLECVTQRGHRRAL LRPLSRVEILPMPYVTEATRVQLVLPLLVABAAAAPAF NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAA PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTT PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPG DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN 6499 3 2040 SCSADTRPSQQAWPTVGLRAAAGAFRTGSPLALGPETF GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEET ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
QKQRLLNGYRRFDPARGMEYTLDLLLECVTQRGHRRAI LRPLSRVEILPMPYVTEATRVQLVLPLLVABAAAAPAF NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAA PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTT PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPG DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN 6499 3 2040 SCSADTRPSQQAWPTVGLRAAAGAFTGSPLALGPETF GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEET ADGLFLLRQCLRSLGGYVLSLVHDVFFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
LRPLSRVEILPMPYVTEATRVQLVLPLLVABAAAAPAF NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAA PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTT PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPG DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN GHPPVRPGVSGGPGAMPDPAAHLPFFYGSISRAEAEET ADGLFLLRQCLRSLGGYVLSLVHDVFFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	-
NVLEPREHALLTLLLVYGPREGGRAPDPFLGVKAAAA PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTT PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPG DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGQEEEEALEGLEVMDVFLRPSGLHLFRAVEPGLVQ CSPRLSELYHRCRLSNLEGLGGRAQLAMALFEQEQAN CSPRLSELYHRCRLSNLEGLGGRAQLAMALFEQEQAN GCSPRTPSGQAWPTVGLRAAAGAFRTGSPLALGPETF GHPPVRPQVSGGPGAMPDPAAHLPPFYGSISRAEAEEH ADGLFLLRQCLRSLGGYVLSLVHDVFFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGBALEQAIISQAPQVEKLIAT PWYHSSLTREBAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVBYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTT PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPG DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN 6499 3 2040 SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETP GHPPVRPQVSGGPGAMPDPAAHLPPFYGSISRAEAEEH ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGBALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPG DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN 6499 3 2040 SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETP GHPPVRPQVSGGPGAMPDPAAHLPPFYGSISRAEAEEH ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTRBEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
DPPSPFGADPSRGAPIGGRFDRQASAEGCFYNADYLAA ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQ CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN 6499 3 2040 SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETF GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEEH ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGBALEQAIISQAPQVEKLIAT PWYHSSLTRBEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVBYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPBELKDKKLF	
CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQAN 6499 3 2040 SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETF GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEEH ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
6499 3 2040 SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETF GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEEH ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	KFSLRD
GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEEH ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	ST
ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNG GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPQ LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	LKLAGM .
LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIAT PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
PWYHSSLTRBEAERKLYSGAQTDGKFLLRPRKEQGTYA KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVBYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPBELKDKKLF	
KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKA LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTL PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	
PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLF	1
I DEPOTE DO A DO CONTROL DA LA CONTROL DE LA	
EMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGG	
LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLA	
VNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKWYA	
RKFSSRSDVWSYGVTMWEALSYGQKPYKKMKGPEVMAF	
MECPPECPPELYALMSDCWIYKWEDRPDFLTVEQRMRA	CYYSLA
SKVEGPPGSTQKAEAACA	; <u> </u>
6500 1773 726 TGPTHASADAWGLVRSVTEWCANVRGNPCAAALSCPQA	
MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHH	
QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSL	
TWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAY	
YRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLG	
DLEYVGMEGGIVLSVESMKRLNSLINIPEKCPEQGGMI KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEA	
QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPY 6501 1 570 LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLT	
IHSRLLDHRPVIOGETRYFVKEFEEKRGLREMRVLENL	
TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQRE	
HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAM	-
YAEMEKDLAKFSTF	
6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQS	~
KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEK	
SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLM	YQAVKE
AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQ:	YQAVKE LATEGS
KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYK	YQAVKE LATEGS GTPSGT
EQARRDALKQRAEQSISEEPGWEEEEERLMGISPISPK	YQAVKE LATEGS GTPSGT FCLEEK
AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESSE:	YQAVKE LATEGS GTPSGT FCLBEK /HQLEQ.
QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGE	YQAVKE LATEGS GTPSGT FCLBEK /HQLEQ . EAKVPV

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1			
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 :	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			IHSKPLTPAGHTGGPEPRPPARVETLRBEAPTDLRVFELNSDSG
1			KSTPSNNGKKGSSTDISEDWEKDFDLDMTEEEVQMALSKVDASG
			EVSGPGGSEGSEPNGPGCESSPQPAQLSPQEGPCSCLR
6503	213	1650	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE
1			KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS
			SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
1			AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
j			KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ
			EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV
1			AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT
]		QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP
1			IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG
			KSTPSNNGKKGSSTDISEDWEKDFDLDMTEEEVQMALSKVDASG
	' ' '		EVSGPGGSEGSEPNGPGCESSPQPAQLSPQEGPCSCLR
6504	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG
1			SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITQ
1 .			WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
ļ	ŀ		DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAOA
}			PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
1	1		REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
l l	ļ	į	DDDFHIYVYDLVKKS
6505	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG
1		Í	SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITQ
1	· ·		WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
			DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA
			PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
1	j	Ì	REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
			DDDFHIYVYDLVKKS
6506	ī	1350	EVSPPTSCCLTVAVADPGVSEGFRGFGAGCEMPGRGRCPDCGST
1			ELVEDSHYSQSQLVCSDCGCVVTEGVLTTTFSDEGNLREVTYSR
1			STGENEQVSRSQQRGLRRVRDLCRVLQLPPTFEDTAVAYYQQAY
	' ' '	ļ · .	RHSGIRAARLQKKEVLVGCCVLITCRQHNWPLTMGAICTLLYAD
			LDVFSSTYMQIVKLLGLDVPSLCLAELVKTYCSSFKLFQASPSV
1			PAKYVEDKEKMLSRTMQLVELANETWLVTGRHPLPVITAATFLA
1			WQSLQPADRLSCSLARFCKLANVDLPYPASSRLQELLAVLLRMA
	1		EQLAWLRVLRLDKRSVVKHIGDLLQHRQSLVRSAFRDGTABVET
1.			REKEPPGWGQGQGEGEVGNNSLGLPQGKRPASPALLLPPCMLKS
			PKRICPVPPVSTVTGDENISDSEIEQYLRTPQEVRDFQRAQAAR
	†		QAATSVPNPP
6507	1878	929	RSHASRLPELPSGCLVLQVQELVQMSGMEATVTIPIWQNKPHGA
		<u> </u>	ARSVVRRIGTNLPLKPCARASFETLPNISDLCLRDVPPVPTLAD
1			IAWIAADEEETYARVRSDTRPLRHTWKPSPLIVMQRNASVPNLR
			GSEERLLALKKPALPALSRTTELQDELSHLRSQIAKIVAADAAS
	1]	ASLTPDFLSPGSSNVSSPLPCFGSSFHSTTSFVISDITEETEVE
1		ł	VPELPSVPLLCSASPECCKPEHKAACSSSEEDDCVSLSKASSFA
			DMMGILKDFHRMKQSQDLNRSLLKEEDPAVLISEVLRRKFALKE
			EDISRKGN
6508	862	342	WEARKRPORWPSERREVRVPPPHLORGRSGLEPGTFRKMAAARP
İ]	SLGRVLPGSSVLFLCDMQEKFRHNIAYFPQIVSVAARMLKNTTL
	1		DLLDRGLQVHVVVDACSSRSQVDRLVALARMRQSGAFLSTSEGL
	1	1	ILQLVGDAVHPQFKEIQKLIKEPAPDSGLLGLFQGQNSLLH
6509	2	1053	FVWNPRGGRKRROAAVTQAATRASGTPSPRDGTMTQGKLSVAN
	_		KAPGTEGOOOVHGEKKEAPAVPSAPPSYEEATSGEGMKAGAFPP
	1	1	APTAVPLHPSWAYVDPSSSSSYDNGFPTGDHELFTTFSWDDQKV
ì			RRVFVRKVYTILLIQLLVTLAVVALFTFCDPVKDYVQANPGWYW
1			ASYAVFFATYLTLACCSGPRRHFPWNLILLTVFTLSMAYLTGML
L	·	L	

CEC	Predicted	Dwodieto 3	
SEQ ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			SSYYNTTSVLLCLGITALVCLSVTVFSFQTKFDFTSCQGVLFVL
·-			LMTLFFSGLILAILLPFQYVPWLHAVYAALGAGVFTLFLALDTQ
		1	LLMGNRRHSLSPEEYIFGALNIYLDIIYIFTFFLQLFGTNRE
6510	37	1156	PCALDGCPQRGAVHPLLSSAMGLLAFLKTQFVLHLLVGFVFVVS
-			GLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLVMLLEWW
			SCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCBRF
1	}		GVLGSSKVLAKKELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVV
1			EGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSMEVAAAKGLPVL
ĺ			KYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGIL
			YGKKYEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIY
			NQKGMFPGEQFKPARRPWTLLNFLSWATILLSPLFSFVLGVFAS
6511	2541	1425	GSPLLILTFLGFVGAGNGHCR
8511	4541	1425	GEEQPLAAAPTECLEQVIGGAGDPGTWASFPSPLPGPAPLKGGK;
	·		TMATNFSDIVKQGYVKMKSRKLGIYRRCWLVFRKSSSKGPQRLB KYPDEKSVCLRGCPKVTEISNVKCVTRLPKETKRQAVAIIFTDD
			SARTFTCDSELEAEEWYKTLSVECLGSRLNDISLGEPDLLAPGV
			QCEQTDRFNVFLLPCPNLDVYGECKLQITHENIYLWDIHNPRVK
		}	LVSWPLCSLRRYGRDATRFTFEAGRMCDAGEGLYTFQTQEGEQI
1			YQRVHSATLAIAEQHKRVLLEMEKNVRLLNKGTEHYSYPCTPTT
			MLPRSAYWHHITGSQNIAEASSYAGEGYGAAQASSETDLLNRFI
			LLKPKPSQGDSSEAKTPSQ
6512	159	807	FGKKSTWFPLSRSLRVASGRSCKLGHGGYTGSGPGFGEPRDSGA
Ì			EVPSGSGRATGCERGGVRGARQGRAPGSSIWRKEPRMVCTRKTK
		,	TLVSTCVILSGMTNIICLLYVGWVTNYIASVYVRGQEPAPDKKL
,			EEDKGDTLKIIERLDHLENVIKQHIQEAPAKPEEAEAEPFTDSS '
6513	2	756	LFAHWGQELSPEGRRVALKQFQYYGYNAYLSDRLPLDRP
0313	2	/56	FVSPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTA
			LFPDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQV AAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQ
			GVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPV
,			LQQDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSF
	٠,		SPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALF
			PDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAA
;	• •		PYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGV
<u>:</u>			PLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQ
'			QDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSP
ــــــــــــــــــــــــــــــــــــــ	·		EPGFSLAQLNLIWQLTDTRQLVHSFTEGR
6514	985	302	VGIPGPTISSAAEMEDLLDLDEELRYSLATSRAKMGRRAQQESA
			QAENHLNGKNSSLTLTGETSSAKLPRCRQGGWAGDSVKASKFRR
			KASERIEDFRLRPQSLNGSDYGGDIPIIPDLEBVQEEDFVLQVA
			APPSIQIKRVMTYRDLDNDLMKYSAIQTLDGEIDLKLLTKVLAP
		•	EHEVRERNPSWQDDVGWDWDHLFTEVSSEVLTEWDPLQTEKEDP AGQARHT
6515	1345	305	GRVGSRRRGAAVPGGCGAGSTQLEVSASASCGALGSADMNPIVV
	-515	343	VHGGGAGPISKDRKERVHQGMVRAATVGYGILREGGSAVDAVEG
			AVVALEDDPEFNAGCGSVLNTNGEVEMDASIMDGKDLSAGAVSA
			VQCIANPIKLARLVMEKTPHCFLTDQGAAQFAAAMGVPEIPGEK
	}	!	LVTERNKKRLEKEKHEKGAQKTDCQKNLGTVGAVALDCKGNVAY
	İ		ATSTGGIVNKMVGRVGDSPCLGAGGYADNDIGAVSTTGHGESIL
	i		KVNLARLTLFHIEQGKTVEEAADLSLGYMKSRVKGLGGLIVVSK
			TGDWVAKWTSTSMPWAAAKDGKLHFGIDPDDTTITDLP
6516	1	1402	FRRLRYLGQDATAAARDLRTRGLQGYCPSATARQQVLVSALQQL
	ĺ		KGRRSEHRNENQEMPYSTNKELILGIMVGTAGISLLLLWYHKVR
	İ		KPGIAMKLPEFLSLGNTFNSITLQDEIHDDQGTTVIFQERQLQI
	į		LEKLNELLTNMEELKEEIRFLKEAIPKLEEYIQDELGGKITVHK
Ll			ISPQHRARKRRLPTIQSSATSNSSEEAESEGGYITANTDTEEQS

<u> </u>	Predicted	Dunald at 1. 3	
SEQ	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
I NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			FPVPKAFNTRVEELNLDVLLQKVDHLRMSESGKSESFELLRDHK
Ì		ļ	EKFRDEIEFMWRFARAYGDMYELSTNTQEKKHYANIGKTLSERA
			INRAPMNGHCHLWYAVLCGYVSEFEGLQNKINYGHLFKEHLDIA
1			IKLLPEEPFLYYLKGRYCYTVSKLSWIEKKMAATLFGKIPSSTV
1	İ	İ	QEALHNFLKAEELCPGYSNPNYMYLAKCYTDLEBNQNALKFCNL
6517	3	1414	ALLLPTVTKEDKEAQKEMQKIMTSLKR
0317	3	1414	GRVWGGSSSLNAMVYVRGHAEDYERWQRQGARGWDYAHCLPYFR
}			KAQGHELGASRYRGADGPLRVSRGKTNHPLHCAFLEATQQAGYP
			LTEDMNGFQQEGFGWMDMTIHEGKRWSAACAYLHPALSRTNLKA
1			EAETLVSRVLFEGTRAVGVEYVKNGQSHRAYASKEVILSGGAIN
	1	İ	SPQLLMLSGIGNADDLKKLGIPVVCHLPGVGQNLQDHLEIYIQQ
1			ACTRPITLHSAQKPLRKVCIGLEWLWKFTGEGATAHLETGGFIR
		·	SQPGVPHPDIQFHFLPSQVIDHGRVPTQQEAYQVHVGPMRGTSV
	· ·	-	GWLKLRSANPQDHPVIQPNYLSTETDIEDFRLCVKLTREIFAQE ALAPFRGKELQPGSHIQSDKEIDAFVRAKADSAYHPSCTCKMGQ
			PSDPTAVVDPQTRVLGVENLRVVDASIMPSMVSGNLNAPTIMIA EKAADIIKGQPALWDKDVPVYKPRTLATOR
6518	242	1098	PAWNPGSEPRTRVRPRARSFPLPPPRAPRRRHRLLRAVPGPSR
5510	232	1036	RHRCRRAPPPPSTMGDAGSERSKAPSLPPRCPCGFWGSSKTMN
l			LCSKCFADFQKKQPDDDSAPSTSNSQSDLFSEETTSDNNNTSIT
1			TPTLSPSQQPLPTELNVTSPSKEECGPCTDTAHVSLITPTKRSC
			GTDSQSENEASPVKRPRLLENTERSEETSRSKQKSRRRCFQCQT
			KLELVQQELGSCRCGYVFCMLHRLPEQHDCTFDHMGRGREEAIM
İ			KMVKLDRKVGRSCORIGEGCS
6519	3	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS
		1113	AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPOSYGSPAS
	• •		WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSOPGPRKLL
			VPPTLLHAQPHHLLLPAAAAAASANAKSRRPKEKREKERRRHGL
1			GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKERBKKKHK
			VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKK
			ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG
	. 4-		KNLDTKNYDSKIPENSBFPFVSLKEPRVQNNLKRLDTLBFKQLI
1			HIEHQPNGGASVIHCLQ
6520 :	3	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLOLSSRDPPGSLS
			AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS
			WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL
			VPPTLLHAQPHHLLLPAAAAAASANAKSRRPKEKREKERRRHGL
,	,		GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK
			VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKHK
			ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG
			KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI
			HIEHQPNGGASVIHCLQ
6521	184	1798	KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP
	•		IRRTVNSTRETPPKSKLAEGEEEKPEPDISSEESVSTVEEQENE
			TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKEKK
			VKKTIPSWATLSASQLARAQKQTPMASSPRPKMDAILTEAIKAC
			FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI
			KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE
			DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA
			LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS
			AIAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE
			KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE
			DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA
			PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS
			KKPATSARKE
6522	1042	391	NKWLRPSPRSHRTPESGRVLSLFRLPPPGMALSGSTPAPCWEED

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	504	\=possible nucleotide insertion)
			ECLDYYGMLSLHRMFEVVGGQLTECELELLAFLLDEAPGAAGGL
1			SRARSGLKLLLELERRGOCDESNLRLLGOLLRVLARHDLLPHLA
			RKRRPVSPERYSYGTSSSSKRTEGSCRRRQSSSSANSQQGSP
İ			PTKRQRRSRGRPSGGARRRRRGPQPHPSSSQSPPDLPLKAK
6523	2	1097	ASCQTRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI
0525	1 -	1097	RSRKLGIFRRCWLVFKKASSKGPRRLEKFPDEKAAYFRNFHKVT
			ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
			KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
ļ			WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER
			LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE
			IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF MDTSTCKVVHDLE
6524	2	1097	
0324	4	1031	ASCQTRRRTÄALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI
			RSRKLGIFRRCWLVFKKASSKGPRRLEKFPDEKAAYFRNFHKVT
1			ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
i			KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
] .			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
1			WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER
1			LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE
1.			IYSLQGNHENRHSDLTGKSCKTSENRFLBENAPLVMYGITHHLF
6525		1050	MDTSTCKVVHDLE
0545	1	1859	GESPFSEBESIEFNPSSSGRSARTVSSNSFCSDDTGWPSSQSVS
			PVKTPSDAGNSPIGFCPGSDEGFTRKKCTIGMVGEGSIQSSRYK
	•	•	KESKSGLVKPGSEADFSSSSSTGSISAPEVHMSTAGSKRSSSSR
	:		NRGPHGRSNGASSHKPGSSPSSPREKDLLSMLCRNQLSPVNIHP
			SYAPSSPSSSNSGSYKGSDCSPIMRRSGRYMSCGENHGVRPPNP
	,		EQYLTPLQQKEVTVRHLKTKLKESERRLHERESEIVELKSQLAR
	,		MREDWIEEECHRVEAQLALKEARKEIKQLKQVIETMRSSLADKD
٠ .			KGIQKYFVDINIQNKKLESLLQSMEMAHSGSLRDELCLDFPCDS
1.		·	PEKSLTLNPPLDTMADGLSLEEQVTGEGADRELLVGDSIANSTD
			LFDEIVTATTTESGDLELVHSTPGANVLELLPIVMGQEEGSVVV
	•		ERAVOTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS
]. ·]	·		MESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANR
. ,	.		LMRELDFAACVEERLDGVIPLARGGVVRQYWSSSFLVDLLAVAA
	*		PVVPTVLWAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR
F 522			IKT
6526	2	2034	SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN
		·	GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD
)			NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP
		ľ	KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGEP
		İ	LQIDHLVFVVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK
1			KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLPSINRLRH
1 . 1		l	FINDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK
'			GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD
] [TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP
1			LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN
1			TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL
[[•		KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI
			PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY
			PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV
}	İ		GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV
			LKEIYQTQGIFLDQPLQ
6527	1	922	GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCQRGDLS
1	[FIFNGDAAPSESFVVLDNEQKVYQRIHHEESEMETEEEVDILMS
			SDIYSATLSTKSISFTRAQTGWLFREDKTERVGNFLADFYLVNG

C 070	Dece 41 about	D	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LVLESRKRREHLSEEDILRNKAIMESLSKGGNIMEQNFEPIRRQ
			SLTPPPQNTITWEEYISAENGKAPHLGRELVCKESKKTFKATIA
			MSQEFPLGIELLLNVLEVVAPFKHFNKLREFVQMKLPPGFPVKL
			DIPVFPTITATVTFQEFRYDEFDGSIFTIPDDYKEDPSRFPDL
6528	1	1073	LTGPÄÄAEPRCAADAGMKRALGRRKGVWLRLRKILFCVLGLYTÄ
			IPFLIKLCPGIQAKLIFLNFVRVPYFIDLKKPQDQGLNHTCNYY
Į i			LQPEEDVTIGVWHTVPAVWWKNAQGKDQMWYEDALASSHPIILY
			LHGNAGTRGGDHRVELYKVLSSLGYHVVTFDYRGWGDSVGTPSE
			RGMTYDALHVFDWIKARSGDNPVYIWGHSLGTGVATNLVRRLCE
			RETPPDALILESPFTNIREEAKSHPFSVIYRYFPGFDWFFLDPI
1			TSSGIKFANDENVKHISCPLLILHAEDDPVVPFQLGRKLYSIAA
1			PARSFRDFKVQFVPFHSDLGYRHKYIYKSPELPRILREFLGKSE
L	<u> </u>	<u> </u>	PEHQH
6529	363	2215	THIRYNKIGVVKTMSCGNEFVETLKKIGYPKADNLNGEDFDWLF
	,		EGVBDESFLKWFCGNVNEQNVLSERELEAFSILQKSGKPILEGA
			ALDEALKTCKTSDLKTPRLDDKELEKLEDEVQTLLKLKNLKIQR
1		·	RNKCQLMASVTSHKSLRLNAKEEEATKKLKQSQGILNAMITKIS
Į.			NELQALTDEVTQLMMFFRHSNLGQGTNPLVFLSQFSLEKYLSQE
ŀ			EQSTAALTLYTKKQFFQGIHEVVESSNESQFFNFLKIQTPSICD
1	·		NQEILEERRLEMARLQLAYICAQHQLIHLKASNSSMKSSIKWAE
-			ESLHSLTSKAVDKENLDAKISSLTSEIMKLEKEVTQIKDRSLPA
			VVRENAQLLNMPVVKGDFDLQIAKQDYYTARQELVLNQLIKQKA
1			SFELLQLSYEIELRKHRDIYRQLENLVQELSQSNMMLYKQLEML
			TDPSVSQQINPRNTIDTKDYSTHRLYQVLEGENKKKELFLTHGN
	,	:	LEEVAEKLKQNISLVQDQLAVSAQEHSFFLSKRNKDVDMLCDTL
			YQGGNQLLLSDQELTEQFHKVESQLNKLNHLLTDILADVKTKRK
			TLANNKLHQMEREFYVYFLKDEDYLKDIVENLETQSKIKAVSLE
Last			D. ,
6530	128	2986	GAAHHGAIVQVHPLLPGSSTIMIHDLCLVFPAPAKAVVYVSDIQ
		·	ELYIRVVDKVBIGKTVKAYVRVLDLHKKPFLAKYFPFMDLKLRA
1			ASPIITLVALDEALDNYTITFLIRGVAIGQTSLTASVTNKAGQR
1.	. `		INSAPQQIEVFPPFRLMPRKVTLLIGATMQVTSEGGPQPQSNIL
	,	1	FSISNESVALVSAAGLVQGLAIGNGTVSGLVQAVDAETGKVVII
I		,	SODLVQVEVLLLRAVRIRAPIMRMRTGTQMPIYVTGITNHQNPF
1			SFGNAVPGLTFHWSVTKRDVLDLRGRHHEASIRLPSQYNFAMNV
			LGRVKGRTGLRAVVKAVDPTSGQLYGLARELSDEIQVQVFEKLQ
1			LLNPEIEAEQILMSPNSYIKLQTNRDGAASLSYRVLDGPEKVPV
1	ļ [']		VHVDEKGFLASGSMIGTSTIEVIAQEPFGANQTIIVAVKVSPVS
	i		YLRVSMSPVLHTQNKEALVAVPLGMTVTFTVHFHDNSGDVFHAH
1			SSVLNFATNRDDFVQIGKGPTNNTCVVRTVSVGLTLLRVWDAKH
			PGLSDFMPLPVLQAISPELSGAMVVGDVLCLATVLTSLEGLSGT
			WSSSANSILHIDPKTGVAVARAVGSVTVYYEVAGHLRTYKEVVV
			SVPQRIMARHLHPIQTSFQEATASKVIVAVGDRSSNLRGECTPT
			QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG
			QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA
1	1	,	EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS
			PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSQGPLSTTLTFSSP
		\	VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHFLDSYQVMFFTLF
			ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS
			SPTSPNALPPARKASPPSGLWSPAYASH
6531	845	1425	PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS
1			SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA
			QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL
1			NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS
1			SGLLVLPQAGLLTPHPS
6532	2	954	AAGPPSEVVNQDSLFPEPEPGPAPQVLLGPQGPGLIKGVAPPTL

SEQ	Predicted	Predicted end	I have noted gomestic and a second
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid'	I .	Codon, /=possible nucleotide deletion,
		sequence	Codon, /=possible nucleotide deletion,
	sequence		\-possible nucleotide insertion)
1 .	}	į	ITDSTGTHLVLTVTNKNAHSPGLSRGSPQQPSSQPGSPAPAPSA
ľ			QMDLEHPLQPLFGTPTSLLKKEPPGYEEAMSQQPKQQENGSSSQ
	ľ	}	QMDDLFDILIQSGEISADFKEPPSLPGKEKPSPKTVCWSPLAAQ
			PSPSAELPQAAPPPPGSPSLPGRLRDFLESSTGLPLLTSGHDGP
	<u> </u>	•	EPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHFVPEPSSTMGL DLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFSTDFLDGHD
	j	İ	LOLHWDSCL
6533	1798	373	<u> </u>
0555	1/30	373	STISWLARVEPPRRSSGVGAARLRFPGGSRPLRARACVLALAVL
			ALLERNNADSMSAHSMLCERIAIAKELIKRAESLSRSRKGGIEG
			GAKLCSKLKAELKFLQKVEAGKVAIKESHLQSTNLTHLRAIVES
			AENLEEVVSVLHVFGYTDTLGEKQTLVVDVVANGGHTWVKAIGR KAEALHNIWLGRGQYGDKSIIEQAEDFLQASHQQPVQYSNPHII
			FAFYNSVSSPMAEKLKEMGISVRGDIVAVNALLDHPEELQPSES ESDDEGPELLQVTRVDRENILASVAFPTEIKVDVCKRVNLDITT
'			LITYVSALSYGGCHFIFKEKVLTEQAEQERKEQVLPOLEAFMKD
		,	KELFACESAVKDFQSILDTLGGPGERERATVLIKRINVVPDOPS
			ERALRLVASSKINSRSLTIFGTGDTLKAITMTANSGFVRAANNO
	1		GVKFSVFIHOPRALTESKEALATPLPKDYTTDSEH
6534	47	596	KATRFISAAFVVLNKQGVSPAKLPHTSWSWSLQTLSFLFSGDLA
0334		370	EKSLQCFPCSAMLLELIPLLGIHFVLRTARAQSVTQPDIHITVS
,		,	EGASLELRCNYSYGATPYLFWMERTVEEAFILLVCLKPWRVASS
			LEKKEKEDESFQLLLGSRYNVLKAHCLLPLIRWLTSGDSLLSAQ
			PHCPQGL
6535	250	964	LIKTFFRDVAIQRDLLPKEKNLETLLTLAFLEIDKAFSSHARLS
0333	450	704	ADATLLTSGTTATVALLEDGIELVVASVGDSRAILCRKGKPMKL
			TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD
			LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSOEIW
1	;		DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN
]]	· ` `		SEINFSFSRSFASSGRWA
6536	242	1174	SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS
]	- -	···	LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS
:			LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV
1 .1	· .		GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI
[· .		INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK
[:	٠	•	IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW
			DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC
]	ĺ		PI
6537	1638	921	NRFNPPPTQGPDPSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV
'			FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV
	j		DESDPDVDFPNSFHAFOTAEGIRKAHPDKDWFHLVGLLHDLGKV
			Silvering Silvering Property and Chrystel
			LALFGEPOWAVVGDTFPVGCRPOASVVFCDSTFODNPDLODPPV
			LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYOPHCGLDRVLMSWGHDGEARGGOWGGGGRWGTVGGGG
			STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG
6538	3345	2412	STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR
6538	3345	2412	STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE
6538	3345	2412	STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV
6538	3345	2412	STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK
6538	3345	2412	STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAHVLFMQBNKYKEAIGFYEPIVK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL
6538	3345	2412	STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYEFGISRVIKSLEPYN
6538	3345	2412	STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYEFGISRVIKSLEPYN KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC
6538	3345	2412	STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYEFGISRVIKSLEPYN KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW
			STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYEFGISRVIKSLEPYN KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW NK
6539	218		STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYEFGISRVIKSLEPYN KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW NK FLGAASPHPHFSSLAPHPDQFEFTPVQDELEAMELWGPGV
			STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYEFGISRVIKSLEPYN KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW NK FLGAASPHPHFSSLAPHPDQFEFTPVQDELEAMELWGPGV LERLWLLLLRRPEDAMAECPTLGEAVTDHPDRLWAWEKFVYLDE
6539	218		STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG AEAVPAGDTLSPQSTCTR PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL SYDDPNRKMYHLCIVNLVIGTLYCAKGNYEFGISRVIKSLEPYN KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW NK FLGAASPHPHFSSLAPHPDQFEFTPVQDELEAMELWGPGV

000	T possible to		
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6541	1165	536	RTLVQRRILMLLRKPARGRDLRGRGRGTPRGGRKGLLPTPDEFP
		ŀ	RFEGGRKPDSWDGNREPGPGHEHFRDTPRPDHPPHDGHSPASRE
			RSSSLQGMDMASLPPRKRPWHDGPGTSEHREMEAPGGPSEDRGG
			KGRGGPGPAQRVPKSGRSSSLDGEHHDGYHRDEPFGGPPGSGTP
			SRGGRSGSNWGRGSNMNSGPPRRGASRGGGRGR
6542	3	3775	SWPRGRGETGGHPGALRTRTMQKSVRYNEGHALYLAFLARKEGT
			KRGFLSKKTAEASRWHEKWFALYQNVLFYFEGEQSCRPAGMYLL
			EGCSCERTPAPPRAGAGQGGVRDALDKQYYFTVLFGHEGQKPLE
			LRCEEEQDGKEWMEAIHQASYADILIEREVLMQKYIHLVQIVET
			EKIAANQLRHQLEDQDTEIERLKSEIIALNKTKERMRPYQSNQE
]]	DEDPDIKKIKKVQSFMRGWLCRRKWKTIVQDYICSPHAESMRKR
			NQIVFTMVEAESEYVHQLYILVNGFLRPLRMAASSKKPPISHDD
]	VSSIFLNSETIMFLHEIFHQGLKARIANWPTLILADLFDILLPM
	;		LNIYQEFVRNHQYSLQVLANCKQNRDFDKLLKQYEANPACEGRM
			LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSKLE
	·		ELSRVMHDEVSDTENIRKNLAIERMIVEGCDILLDTSQTFIRQG
			SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFLICTRS
			SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSGQVFGHLDF
			KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDNIRCNGLM
			TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCKVPQIR
			YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVLGKLSD
· ·		·	IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCRKFSSP
- 1			PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPTTTTOS
			PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRVDLCNK
			LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPSTPRHLR
	·	,	YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNNTERTC
			DKEFIIRRTATNRVLNVLRHWVSKHAODFELNNELKMNVLNLLE
			EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDIIQMTDC
l			MKAECFESLSAMELAEQITLLDHVIFRSIPYBEFLGQGWMKLDK
			NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIEKWVAV
	•		ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKQTKALMD
"		,	KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAFIEEGT
			PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPKVAQYL
			LDKDLIIDEDTLYELSLKIEPRLPA
6543	1857	950	FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCTHPLDL
ł			LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASLCRQMT
			YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLAGGFVG
			TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEGLRRLF
			SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIFTHFVA
		•	SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVETAKLGP
			LAFYKGLVPAGIRLIPHTVLTFVFLEQLRKNFGIKVPS
6544	630	79	PSPCFIRSRLDGQPWMAGLEAWLSONFSLHOPOSRVRVRRASIS
			EPSDTDPEPRTLNPSPAGWFVQQHPELELMSSFRERFGRNWLQY
			RSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRPSPPQEEAR
			GPQESPQKMSEEVRAEPOEEEEEKEGKEEKEGEMAPLPEAHLG
1			EGKOKECP .
6545	176	560	
-5.5	4,0	200	PPHSHAALLPAAMTPLLTLILVVLMGLPLAQALDCHVCAYNGDN CENDMPCDAMAAYCMTTDTTVTTDTDMAAGACACACACACACACACACACACACACACACACACAC
			CFNPMRCPAMVAYCMTTRTYYTPTRMKVSKSCVPRCFETVYDGY
6546	1667	364	SKHASTTSCCQYDLCNGTGLATPATLALAPILLATLWGLL
0240	1657	364	HLLNGLDEVAAFFVADLGAIVRKHFCFLKCLPRVRPFYAVKCNS
ļ			SPGVLKVLAQLGLGFSCANKAEMELVQHIGIPASKIICANPCKQ
ļ			IAQIKYAAKHGIQLLSFDNEMELAKVVKSHPSAKMVLCIATDDS
ŀ	`		HSLSCLSLKFGVSLKSCRHLLENAKKHHVEVVGVSFHIGSGCPD
			I DONVACETADADE GERCEPET CHEMING DE COCEDORISME CA DE
			PQAYAQSIADARLVFEMGTELGHKMHVLDLGGGFPGTEGAKVRF
			EEIASVINSALDLYFPEGCGVDIFAELGRYYVTSAFTVAVSIIA KKEVLLDQPGREEENGSTSKTIVYHLDEGVYGIFNSVLFDNICP

T TRO	I best distance		
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
·	residue of	amino acid	
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence	Bedaeuce	\=possible nucleotide insertion)
-	50425.100		TPILQKKPSTEQPLYSSSLWGPAVDGCDCVAEGLWLPQLHVGDW
			LVFDNMGAYTVGMGSPFWGTQACHITYAMSRVAWEALRROLMAA
			EQEDDVEGVCKPLSCGWEITDTLCVGPVFTPASIM
6547	1	541	LHSKYLAPALCSQPGMMRCCRRCCCRQPPHALRPLLLLPLVLL
"	_		PPLAAAAAGPNRCDTIYQGFAECLIRLGDSMGRGGELETICRSW
			NDFHACASQVLSGCPEEAAAVWESLQQEARQAPRPNNLHTLCGA
			PVHVRERGTGSETNQETLRATAPALPMAPAPPLLAAALALAYLL
•			RPLA
6548	2	219	FVSRLSVRDVRFPTFLGGHGADAMHTDPDYSAAYVPIETDAEDG
1	_		IKGCGITFTLGKGTEVGELKILSRFQNA
6549	73	1490	ETGRVCEDARPACGSRSRRRKEAAPGIPTPSPSSSSPTSSRPA
]	1.75	ARAFSKAPARLSRPRAREEPPDPGRRYIQEEIIQARKHKLIKMC
			SSVAAKLWFLTDRRIREDYPOKEILRALKAKCCEEELDFRAVVM
1: 1	•		DEVVLTIEQGNLGLRINGELITAYPQVVVVRVPTPWVQSDSDIT
1			VLRHLEKMGCRLMNRPQAILNCVNKFWTFQELAGHGVPLPDTFS
	,		YGGHENFAKMIDEAEVLEFPMVVKNTRGHRGKAVFLARDKHHLA
1 .			DLSHLIRHEAPYLFQKYVKESHGRDVRVIVVGGRVVGTMLRCST
1			DGRMQSNCSLGGVGMMCSLSEQGKQLAIQVSNILGMDVCGIDLL
1 1		'	MKDDGSFCVCEANANVGFIAFDKACNLDVAGIIADYAASLLPSG
		•	RLTRRMSLLSVVSTASETSEPELGPPASTAVDNMSASSSSVDSD
			PESTERELLTKLPGGLFNMNQLLANEIKLLVD
6550	2293	922	FRVSRDGAPDCGIEQMGLAMEHGGSYARAGGSSRGCWYYLRYFF
			LFVSLIQFLIILGLVLFMVYGNVHVSTESNLQATERRAEGLYSQ
			LLGLTASQSNLTKELNFTTRAKDAIMQMWLNARRDLDRINASFR
			QCQGDRVIYTNNQRYMAAIILSEKQCRDQFKDMNKSCDALLFML
	•	•	NQKVKTLEVEIAKEKTICTKDKESVLLNKRVAEEQLVECVKTRE
1 1			LQHQERQLAKEQLQKVQALCLPLDKDKFEMDLRNLWRDSIIPRS
			LDNLGYNLYHPLGSELASIRRACDHMPSLMSSKVEELARSLRAD
1 1			IERVARENSDLQRQKLEAQQGLRASQEAKQKVEKEAQAREAKLQ
1 .1			AECSRQTQLALEEKAVLRKERDNLAKELEEKKREAEQLRMELAI
			RNSALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEEFKRKI
			LESQRPPAGIPVAPSSG
6551	157	748 .	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
1 .1		•	ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN
1 1			ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER
] ' ,			EVIQKAIBENNNFIKMAKEKLAQKMESNKENRBAHLAAMLERLQ
			EKDKHAEEVRKNKELKEBASR
6552	157	748	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
			ADTVDLNWCVISDMEVIBLNKCTSGQSFEVILKPPSFDGVPEFN
{			ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER
{			EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ
<u> </u>			EKDKHAEEVRKNKELKEEASR
6553	2 ,	1807	FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD
] [EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV
1			RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD
]	LGVLGSFIHREBYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS
			LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG
	Ī		SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS
	İ	ļ	YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEELYAEIRDKN
1		Į	FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA
j i	ļ		RGSLANHTSIABLIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN
[[ſ		YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT
			YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE
[QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF
1	I		EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSQL
1			EDGGTEYVIATTKLMNGTSWIEALMEKPF

0.70	T = 1,1 = 1		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
,	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bequeince	\=possible nucleotide insertion)
6554	119	1244	FEMGSQVSVESGALHVVIVGGGFGGIAAASQLQALNVPFMLVDM
	1		KDSFHHNVAALRASVETGFAKKTFISYSVTFKDNFRQGLVVGID
1		:	LKNQMVLLQGGEALPFSHLILATGSTGPFPGKFNEVSSQQAAIQ
1			AYEDMVRQVQRSRFIVVVGGGSAGVEMAABIKTEYPEKEVTLIH
1			SQVALADKELLPSVRQEVKEILLRKGVQLLLSERVSNLEELPLN
1	1		EYREYIKVQTDKGTEVATNLVILCTGIKINSSAYRKAFESRLAS
	į		SGALRVNEHLQVEGHSNVYAIGDCADVRTPKMAYLAGLHANIAV
			ANIVNSVKQRPLQAYKPGALTFLLSMGRNDGVGQISGFYVGRLM
			VRLTKSRDLFVSTSWKTMRQSPP
6555	1552	498	IHMALLRKINQVLLFLLIVTLCVILYKKVHKGTVPKNDADDESE
			TPEELEEEIPVVICAAAGRMGATMAAINSIYSNTDANILFYVVG
1			LRNTLTRIRKWIEHSKLREINFKIVEFNPMGLKGKIRPDSSRPE
			LLQPLNFVRFYLPLLIHQHEKVIYLDDDVIVQGDIQELYDTTLA
			LGHAAAFSDDCDLPSAQDINRLVGLQNTYMGYLDYRKKAIKDLG ISPSTCSFNPGVIVANMTEWKHORITKQLEKWMOKNVEENLYSS
			SLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFL
			QEAKLLHWNGRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS
6556	241	1449	ASLCKGCFFVTHVLVIILPSLQSPPTFGFLLDIDGVLVRGHRVI
			PAALKAFRRLVNSQGQLRVPVVFVTNAGNILQHSKAQELSALLG
į			CEVDADQVILSHSPMKLFSEYHEKRMLVSGQGPVMENAQGLGFR
			NVVTVDELRMAFPLLDMVDLERRLKTTPLPRNDFPRIEGVLLLG
			EPVRWETSLQLIMDVLLSNGSPGAGLATPPYPHLPVLASNMDLL
			WMAEAKMPRFGHGTFLLCLETIYQKVTGKELRYEGLMGKPSILT
Í			YQYAEDLIRRQAERRGWAAPIRKLYAVGDNPMSDVYGANLFHQY
			LQKATHDGAPELGAGGTRQQQPSASQSCISILVCTGVYNPRNPQ
		•	STEPVLGGGEPPFHGHRDLCFSPGLMEASHVVNDVNEAVQLVFR
6557	2500		KEGWALE
655/	2598	1534	RMCGRTSCHLPRDVLTRACAYQDRRGQQRLPEWRDPDKYCPSYN
			KSPQSNSPVLLSRLHFEKDADSSERIIAPMRWGLVPSWFKESDP
		•	SKLQFNTTNCRSDTVMEKRSFKVPLGKGRRCVVLADGFYEWQRC QGTNQRQPYFIYFPQIKTEKSGSIGAADSPENWEKVWDNWRLLT
		. :	MAGIFDCWEPPEGGDVLYSYTIITVDSCKGLSDIHHRMPAILDG
1			BEAVSKWLDFGEVSTQEALKLIHPTENITFHAVSSVVNNSRNNT
,		;	PECLAPVOLVVKKELRASGSSQRMLQWLATKSPKKEDSKTPQKE
			ESDVPQWSSQFLQKSPLPTKRGTAGLLEQWLKREKEEEPVAKRP
	;	. '	YSQ
6558	21	1138	FHGRRRGGRKMELGSCLEGGREAAEEEGEPEVKKRRLLCVEFAS
1		ŧ	VASCDAAVAQCFLAENDWEMERALNSYFEPPVEESALERRPETI
			SEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWNID
1			GLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSS
			NYEIITGHEEGYFTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLC
			VHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEAPES
			ATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWD
			TQMNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKL
6559	3	364	DCGRFPSDHWGLLCNLDIIL
""		364	GPELSGLPTRPKKLKANQTPIAMDCCASRSCSVPTGPATTICSS DKSCRCGVCLPSTCPHTVWLLBPTCCDNCPPPCHIPQPCVPTCF
			LLNSCQPTPGLETLNLTTFTQPCCEPCLPRGC
6560	3	1435	TATSGGIWLRRKWRCHWPRPLPOSCVGTEGGLOVRDTSSRIAKG
			GVDHTKMSLHGASGGHERSRDRRRSSDRSRDSSHERTESOLTPC
		İ	IRNVTSPTRQHHVEREKDHSSSRPSSPRPOKASPNGSISSAGNS
			SRNSSQSSSDGSCKTAGEMVFVYENAKEGARNIRTSERVTLIVD
			NTRFVVDPSIFTAQPNTMLGRMFGSGREHNFTRPNEKGEYEVAB
			GIGSTVFRAILDYYKTGIIRCPDGISIPELREACDYLCISFEYS
			TIKCRDLSALMHELSNDGARRQFEFYLEEMILPLMVASAQSGER
			ECHIVVLTDDDVVDWDEEYPPQMGEEYSQIIYSTKLYRFFKYIE
			·

SEQ	Predicted	Predicted end	Imino agid gogment gentalista al
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
J .	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			NRDVAKSVLKERGLKKIRLGIEGYPTYKEKVKKRPGGRPEVIYN
1			YVQRPFIRMSWEKEEGKSRHVDFQCVKSKSITNLAAAAADIPQD
			QLVVMHPTPQVDELDILPIHPPSGNSDLDPDAQNPML
6561	3	1086	PGRRFRRKESSSSRWFPADCLLGLRGPASSLLSPEPSPSWPSHS
1			PCPMAALTDLSFMYRWFKNCNLVGNLSEKYVFITGCDSGFGNLL
1			AKQLVDRGMQVLAACFTEEGSQKLQRDTSYRLQTTLLDVTKSES IKAAAQWVRDKVGEQGLWALVNNAGVGLPSGPNEWLTKDDFVKV
1			INVNLVGLIEVTLHMLPMVKRARGRVVNMSSSGGRVAVIGGGYC
			VSKFGVEAFSDSIRRELYYFGVKVCIIEPGNYRTAILGKENLES
			RMRKLWERLPQETRDSYGEDYFRIYTDKLKNIMQVAEPRVRDVI
			NSMEHAIVSRSPRIRYNPGLDAKLLYIPLAKLPTPVTDFILSRY
1			LPRPADSV
6562	1	1562	MSTLYDIRAHKAQLLRFFASSDSNKALEQRRTLHTPKLEHLDRV
1 . 1			LYEWFLGKRSEGVPVSGPMLIEKAKDFYEQMQLTBPCVFSGGWL
			WRFKARHGIKKLDASSEKQSADHQAAEQFCAFFRSLAAEHGLSA
			EQVYNADETGLFWRCLPNPTPEGGAVPGPKQGKDRLTVLMCANA
			TGSHRLKPLAIGKCSGPRAFKGIQHLPVAYKAQGNAWVDKEIFS
			DWFHHIFVPSVREHFRTIGLPEDSKAVLLLDSSRAHPQEAELVS
1		•	SNVFTIFLPASVASLVQPMEQGIRRDFMRNFINPPVPLQGPHAR
	•		YNMNDAIFSVACAWNAVPSHVFRRAWRKLWPSVAFAEGSSSEBE
1			LEAECFPVKPHNKSFAHILELVKEGSSCPGQLRQRQAASWGVAG
1			REAEGGRPPAATSPAEVVWSSEKTPKADQDGRGDPGEGEEVAWE
İ			QAAVAFDAVLRFAERQPCFSAQEVGQLRALRAVFRSQQQVRRRR GALGAVVKVEALQEGPGGCGATAQSPLPCSSTAGDN
6563	1319	2694	LARPAQPVLLREPEGAGPPVPAGHLVHHLQGGHLRERAHPDLEA
			HEHPLPCDQMFWRQMGGHLRMVEANSRGVVWGIGYDHTAWVYTG
			GYGGGCFQGLASSTSNIYTQSDVKCVHIYENQRWNPVTGYTSRG
·]			LPTDRYMWSDASGLQECTKAGTKPPSLQWAWVSDWFVDFSVPGG
			TDQEGWQYASDFPASYHGSKTMKDFVRRRCWARKCKLVTSGPWL
}			EVPPIALRDVSIIPESPGAEGSGHSIALWAVSDKGDVLCRLGVS
l · . · l			ELNPAGSSWLHVGTDQPFASISIGACYQVWAVARDGSAFYRGSV
1 .1	,		YPSQPAGDCWYHIPSPPRQRLKQVSAGQTSVYALDENGNLWYRQ
1			GITPSYPQGSSWEHVSNNVCRVSVGPLDQVWVIANKVQGSHSLS
	·		RGTVCHRTGVQPHEPKGHGWDYGIGGGWDHISVRANATRAPRSS
6564	1	975	SQEQEPSAPPEAHGPVCC
6264	Δ.	9/5	APGSCALWSYCGRGWSRAMRGCQLLGLRSSWPGDLLSARLLSQE KRAAETHFGPETVSEEEKGGKVYQVPESVAKKYDVMNDMMSLGI
:			HRVWKDLLLWKMHPLPGTQLLDVAGGTGDIAFRFLNYVOSOHOR
]			KQKRQLRAQQNLSWEEIAKEYQNEEDSLGGSRVVVCDINKEMLK
			VGKQKALAQGYRAGLAWVLGDAEELPFDDDKFDIYTIAFGIRNV
			THIDQALQEAHRVLKPGGRFLCLEFSQVNNPLISRLYDLYSFQV
			IPVLGEVIAGDWKSYQYLVESIRRFPSQEEFKDMIEDAGFHKVT
			YESLTSGIVAIHSGFKL
6565	1464	999	RSAVANGLTKRRMGLKLNGRYISLILAVQIAYLVQAVRAAGKCD
	1		AVFKGFSDCLLKLGDSMANYPQGLDDKTNIKTVCTYWEDFHSCT
	ļ	j	VTALTDCQEGAKDMWDKLRKESKNLNIQGSLFELCGSGNGAAGS
			LLPAFPVLLVSLSAALATWLSF
6566	3	1385	KYESAQPGGTQPEPGLGARMAIHKALVMCLGLPLFLFPGAWAQG
	.		HVPPGCSQGLNPLYYNLCDRSGAWGIVLEAVAGAGIVTTFVLTI
	. [ILVASLPFVQDTKKRSLLGTQVFFLLGTLGLFCLVFACVEKPDF
			STCASRRFLFGVLFAICFSCLAAHVFALNFLARKNHGPRGWVIF
	į		TVALLLTLVEVIINTEWLIITLVRGSGEGGPQGNSSAGWAVASP
	•		CAIANMDFVMALIYVMLLLLGAFLGAWPALCGRYKRWRKHGVFV
			LLTTATSVAIWVVWIVMYTYGNKQHNSPTWDDPTLAIALAANAW
			AFVLFYVIPEVSQVTKSSPEQSYQGDMYPTRGVGYETILKEQKG QSMFVENKAFSMDEPVAAKRPVSPYSGYNGQLLTSVYQPTEMAL
			A SHIT A STANKE SHIDE A WAYKE A SA LOCATION TO A LOCATION OF THE A SA LO

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ľ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			MHKVPSEGAYDIILPRATANSQVMGSANSTLRAEDMYSAQSHQA
	}		ATPPKDGKNSQVFRNPYVWD
6567	125	863	TKRSNLKAYACSIHHIRTMSYVFVNDSSOTNVPLLOACIDGDFN
			YSKRLLESGFDPNIRDSRGRTGLHLAAARGNVDICQLLHKFGAD
	1		LLATDYQGNTALHLCGHVDTIQFLVSNGLKIDICNHQGATPLVL
•			AKRRGVNKDVIRLLESLEEQEVKGFNRGTHSKLETMOTAESESA
ĺ			MESHSLLNPNLQQGEGVLSSFRTTWQEFVEDLGFWRVLLLIFVI
Ì	İ		ALLSLGIAYYVSGVLPFVENQPBLVH
6568	3	1183	HASDRLLVLPDNYSHFSQASANLQGPSRTTELFHPTLASISSPM
			LEGAELYFNVDHGYLEGLVRGCKASLLTQQDYINLVQCETLEDL
	1		KIHLQTTDYGNFLANHTNPLTVSKIDTEMRKRLCGEFEYFRNHS
			LEPLSTFLTYMTCSYMIDNVILLMNGALOKKSVKEILGKCHPLG
1	1		RFTEMEAVNIAETPSDLFNAILLIETPLAPFFQDCMSENALDELN
1,	[·		IELLRNKLYKSYLEAFYKFCKNHGDVTAEVMCPILEFEADRRAF
	,		IITLNSFGTELSKEDRETLYPTFGKLYPEGLRLLAOAEDFDOMK
			NVADHYGVYKPLFEAVGGSGGKTLEDVFYEREVQMNVLAFNROF
1			HYGVFYAYVKLKEQEIRNIVWIAECISQRHRTKINSYIPIL
6569	205	1532	RRRGPORLGHGRPTPLLCRWRTAGPSHWEKOARAFOGLRPVDPR
		i	RMSWLFPLTKSASSSAAGSPGGLTSLQQQKQRLIESLRNSHSSI
}			AEIQKDVEYRLPFTINNLTININILLPPQFPQEKPVISVYPPIR
		,	HHLMDKQGVYVTSPLVNNFTMHSDLGKIIQSLLDEFWKNPPVLA
		•	PTSTAFPYLYSNPSGMSPYASQGFPFLPPYPPQEANRSITSLSV
		i	ADTVSSSTTSHTTAKPAAPSFGVLSNLPLPIPTVDASIPTSONG
1			FGYKMPDVPDAFPELSELSVSQLTDMNEQEEVLLEQFLTLPQLK
l.			QIITDKDDLVKSIEELARKNLLLEPSLEAKRQTVLDKYELLTOM
1			KSTFEKKMQRQHELSESCSASALQARLKVAAHEAEEESDNIAED
			FLEGKMEIDDFLSSFMEKRTICHCRRAKEEKLQQAIAMHSQFHA
!			PL
6570	330	1304	ARLPRLTFLREGFLYVLLSHWVFVGAPRPPASDSWKKGLVPSAP
`		:	PASRKMGSKALPAPIPLHPSLQLTNYSFLQAVNTFPATVDHLQG
			LYGLSAVQTMHMNHWTLGYPNVHEITRSTITEMAAAQGLVDARF
			PFPALPFTTHLFHPKQGAIAHVLPALHKDRPRFDFANLAVAATQ
		**	EDPPKMGDLSKLSPGLGSPISGLSKLTPDRKPSRGRLPSKTKKE
			FICKFCGRHFTKSYNLLIHERTHTDERPYTCDICHKAFRRQDHL
	,		RDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA
		<u> </u>	SSAAKCSGETVICGGT
6571	169	656	APDMNRKKLQKLTDTLTKNCKHLFRGFDKDNDGCVNVLEWIHGL
1		,	SLFLRGSLEEKMKYCFEVFDLNGDGFISKEEMFHMLKNSLLKQP
			SEEDPDEGIKDLVEITLKKMDHDHDGKLSFADYELAVREETLLL
		·	EAFGPCLPDPKSQMEFEAQVFKDPNEFNDM
6572	49	1646	TPERAQPGALLGAAGCCVCGGRWWPRSHERGYFSSAKMGSKRRN
1			LSCSERHQKLVDENYCKKLHVQALKNVNSQIRNQMVQNENDNRV
			QRKQFLRLLQNEQFELDMEEAIQKAEENKRLKELQLKQEEKLAM
			ELAKLKHESLKDEKMRQQVRENSIELRELEKKLKAAYMNKERAA
1			QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEENAAEDKRNKA
			KAQYYLDLEKQLEEQEKKKQEAYEQLLKEKLMIDEIVRKIYEED
			QLEKQQKLEKMNAMRRYIEEFQKEQALWRKKKREEMEEENRKII
			EFANMQQQREEDRMAKVQENBEKRLQLQNALTQKLEEMLRQRED
			LEQVRQBLYQEEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA
i]		LKELVLQAAKEEEENFRKTMLAKFAEDDRIELMNAQKQRMKQLE
			HRRAVEKLIEERRQQFLADKQRELEEWQLQQRRQGFINAIIEEE
	ļ		RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSBI
			CEEK
6573	767	275	GGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK
			LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL
			TRKLSQRPTVEELRERKILIRFSDYVEVADAQDYDRRADKPWTR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
]	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 .	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	,	\-possible nucleotide insertion)
			LTAADKVSRGECWRVGGRTVCWVSLGSPLGSV
6574	204	1159	LESSVPVSVGVFWACGVSWTGAAGLQDGALSDTMARNAEKAMTA
1			LARFRQAQLEEGKVKERRPFLASECTELPKAEKWRRQIIGEISK
1			KVAQIQNAGLGEFRIRDLNDEINKLLREKGHWEVRIKELGGPDY
			GKVGPKMLDHEGKEVPGNRGYKYFGAAKDLPGVRELFEKEPLPP
Ì		ĺ	PRKTRABLMKAIDFEYYGYLDEDDGVIVPLEQEYEKKLRAELVE
			KWKAERBARLARGEKEEEEEEEEEINIYAVTEEESDEEGSQEKG
	1		GDDSQQKFIAHVPVPSQQEIEEALVRRKKMELLQKYASETLQAQ
			SEEARRLLGY
6575	117	820	SPALASQSGGITERKMLEPQENGVIDLPDYEHVEDETFPPFPPP
			ASPERQDGEGTEPDEESGNGAPVPVPPKRTVKRNIPKLDAQRLI
		1	SERGLPALRHVFDKAKFKGKGHEAEDLKMLIRHMEHWAHRLFPK
	İ		LQFEDFIDRVEYLGSKKEVQTCLKRIRLDLPILHEDFVSNNDEV
	1	1 1	AENNEHDVTSTELDPFLTNLSESEMFASELSISLTEEQQQRIER
_ ,	'	 .	NKQLALERRQAKLP
6576	1	1060	PEPQALVGQKRGALRLLVARLVLTVSAPAEVRRRVLRPVLSWMD
:			RETRALADSHFRGLGVDVPGVGQAPGRVAFVSEPGAFSYADFVR
			GFLLPNLPCVFSSAFTQGWGSRRRWVTPAGRPDFDHLLRTYGDV
1		•	VVPVANCGVQEYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGCL
İ		,	YLKDWHLCRDFPVEDVFTLPVYFSSDWLNEFWDALDVDDYRFVY
			AGPAGSWSPFHADIFRSFSWSVNVCGRKKWLLFPPGQEEALRDR
]	;	•	HGNLPYDVTSPALCDTHLHPRNQLAGPPLEITQEAGEMVFVPSG .
			WHHQVHNLVMCCFSCPLSGAFLQEDGSTTSPLSQPELGWNGVAH
			G
6577	2271	. 987	SDRMASDDFDIVIEAMLEAPYKKEEDEQQRKEVKKDYPSNTTSS
			TSNSGNETSGSSTIGETSNRSRDRDRYRRRNSRSRSPGRQCRHR
	;		SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF
		:	
			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF
			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPEERDARTVFCMQLAARIRPRDLEDFFSAV
			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVBFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL
			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVBFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG
			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRILG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA
			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM
6578	377	1489	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRILG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA
6578	377	1489	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM
6578	377	1489	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA
	377	1489	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL
	377	1489	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG
	377	1489	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVBFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLABGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA
	377	1489	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPEERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELQALRDF AQLGSAHFWGMMTLGGLPGFAIGYVTGLQIKFTSPLTHNVSGTA
	377	1489	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLABGAGIQLPSTAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFİG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI
:			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPEERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELQALRDF AQLGSAHFWGMMTLGGLPGFAIGYVTGLQIKFTSPLTHNVSGTA
	377	711	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLGELQALRDF AQLGSAHFWGMMTLGGLFGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK KTPEEPSPKDSEKSAMGV
:			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLIGELQALRDF AQLGSAHFWGMMTLGGLPGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK KTPEEPSPKDSEKSAMGV RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI
:			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLGELQALRDF AQLGSAHFWGMMTLGGLFGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK KTPEEPSPKDSEKSAMGV
:			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLIGELQALRDF AQLGSAHFWGMMTLGGLPGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK KTPEEPSPKDSEKSAMGV RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI
:			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLIGELQALRDF AQLGSAHFWGMMTLGGLPGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK KTPEEPSPKDSEKSAMGV RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM
:			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPPLSVVFIG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLIGELQALRDF AQLGSAHFWGMMTLGGLPGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK KTPEEPSPKDSEKSAMGV RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM DVGQIGFHRQKDVKIVTVBKKVNEILNRLEKTKVERFPDLAAEK
:			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPEERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFİG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELQALRDF AQLGSAHFWGMMTLGGLPGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK KTPEEPSPKDSEKSAMGV RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM DVGQIGFHRQKDVKIVTVEKKVNETLNRLEKTKVERFPDLAAEK ECRDREERNEKKAQIQEMKKREKEEMKKKREMDBLRSYSSLMKV ENMSSNQDGNDSDEFM
6579	2	711	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFİG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELQALRDF AQLGSAHFWGMMTLGGLPGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK KTPEEPSPKDSEKSAMGV RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM DVGQIGFHRQKDVKIVTVEKKVNETLNRLEKTKVERFPDLAAEK ECRDREERNEKKAQIQEMKKREKEEMKKKREMDELRSYSSLMKV ENMSSNQDGNDSDEFM LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP
6579	2	711	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFİG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELQALRDF AQLGSAHFWGMMTLGGLPGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK KTPEEPSPKDSEKSAMGV RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM DVGQIGFHRQKDVKIVTVBKKVNEILNRLEKTKVERFPDLAAEK ECRDREERNEKKAQIQEMKKREKEEMKKKREMDBLRSYSSLMKV ENMSSNQDGNDSDEFM LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP RPPQEQVGPLMVKVEEKEEKGKYLPSLEMFRQRFRQFGYHDTPG
6579	2	711	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFİG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELQALRDF AQLGSAHFWGMMTLGGLFGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK KTPEEPSPKDSEKSAMGV RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI EDIPKEVLMDCAHLVKANSIQGCKMNNVNVYTPWSNLKKTADM DVGQIGFHRQKDVKIVTVBKKVNEILNRLEKTKVERFPDLAAEK ECRDREERNEKKAQIQEMKKREKEEMKKKREMDBLRSYSSLMKV ENMSSNQDGNDSDEFM LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP RPPQEQVGPLMVKVEEKEEKGKYLPSLEMFRQRFRQFGYHDTPG PREALSQLRVLCCEWLRPEIHTKEQILELLVLEQFLTILPQBLQ
6579	2	711	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRILG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFİG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELQALRDF AQLGSAHFWGMMTLGGLPGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK KTPEEPSPKDSEKSAMGV RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM DVGQIGFHRQKDVKIVTVBKKVNEILNRLEKTKVERFPDLAAEK ECRDREERNEKKAQIQEMKKREKEEMKKKREMDBLRSYSSLMKV ENMSSNQDGNDSDEFM LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP RPPQEQVGPLMVKVEEKEEKGKYLPSLEMFRQRFRQFGYHDTPG PREALSQLRVLCCEWLRPEIHTKEQILELLVLEQFLTILPQELQ AWVQEHCPESAEEAVTLLEDLERELDEPGHQVSTPPNEQKPVWE
6579	2	711	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLABGAGIQLPSTAAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELQALRDF AQLGSAHFWGMMTLGGLPGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK KTPEEPSPKDSEKSAMGV RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSVNSSAYT IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM DVGQIGFHRQKDVKIVTVBKKVNEILNRLEKTKVERFPDLAAEK ECRDREERNEKKAQIQEMKKREKEEMKKKREMDBLRSYSSLMKV ENMSSNQDGNDSDEFM LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP RPPQEQVGPLMVKVEEKEEKGKYLPSLEMFRQRFRQFGYHDTPG PREALSQLRVLCCEWLRPEITTKEQILELLVLEQFLTILPQBLQ AWVQEHCPESAEEAVTLLEDLERELDEPGHQVSTPPNEQKPVWE KISSSGTAKESPSSMQPQPLETSHKYESWGPLYIQESGEEQEFA
6579	2	711	SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRILG VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAAAAQAAALQLNGAVPLGA LNPAALTALSPALNLASQCLQLSSLFTPQTM PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFİG MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELQALRDF AQLGSAHFWGMMTLGGLPGFAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK KTPEEPSPKDSEKSAMGV RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM DVGQIGFHRQKDVKIVTVBKKVNEILNRLEKTKVERFPDLAAEK ECRDREERNEKKAQIQEMKKREKEEMKKKREMDBLRSYSSLMKV ENMSSNQDGNDSDEFM LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP RPPQEQVGPLMVKVEEKEEKGKYLPSLEMFRQRFRQFGYHDTPG PREALSQLRVLCCEWLRPEIHTKEQILELLVLEQFLTILPQELQ AWVQEHCPESAEEAVTLLEDLERELDEPGHQVSTPPNEQKPVWE

Predicted Predicted Predicted Namino acid segment containing signal peptide No:				
No:	SEQ	Predicted	Predicted end	
corresponding to first amino acid amino acid residue of amino acid amino acid amino acid amino acid sequence sequence	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
L=Leucine, M=Methionine, N=Asparagine, amino acid residue of residue of amino acid sequence P=Profine, Q=Glutamine, R=Asparine, S=Serine, T=Threonine, V=Valine, amino acid sequence V=Typtophan, Y=Tyrosine, X=Juhknown, *=Stop Codon, /=possible nucleotide deletion, V=possible nucleotide insertion) CASCGKAFSNSNLTHERTHTGEKPYCTKCGKAFSNSNLTH	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence Septence, T-Threnomine, V-valine, w-Txyptophan, Y-Tyrosine, X-Unknown, *-Stop Codon, /-possible nucleotide deletion, \-\possible nucleotide deletion, \-\possible nucleotide deletion, \-\possible nucleotide insertion) CASCAKAFSNSSNITHARRHTMGEKPVCTKCCKAFFGHSSNITH HYTHILUDRPYDCKCCKAFFGSSDLLKHORMHTERAPYCCKOCK AFFSKKSLIRRHTHITGERPYCONECKSFSGHADSSIGRLM TGEKPYKCKECGKAFMISSNFKKHRITHTGEKPYCMECKSFSGHADSSIGRLM TGEKPYKCKECGKAFMISSNFKKHRITHTGEKPYCMECKSFSGHADSSIGRLM TGEKPYKCKECGKAFMISSNFKKHRITHTGEKPYCMECKSFSGHADSSIGRLM TGEKPYKCKECGKAFMISSNFKKHRITHTGEKPYCHECKTFC SKSNLSSHGRWITHGERAPY TGEKPYKCKECGKAFMISSNFKKHRITHTGEKPYCHECKTFC SKSNLSSHGRWITHGERAPY TGEKPYKCKECGKAFMISSNFKKHRITHTGEKPYCHECKTFC SKSNLSSHGRWITHGERAPY TGEKPYKCKECGKAFMISSNFKKHRITHTGEKPYCHECKTFC SKSNLSSHGRWITHGERAPY TGEKPYKCKECGKAFMISSNFKKHRITHTGEKPYCHECKTFC SKSNLSSHGRWITHGERAPY CONSTRUCTION TORK TORK TORK TORK TORK TORK TORK TORK		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence Sequence Codon, /-possible nucleotide deletion, V-				
residue of amino acid sequence (Codon, -possible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide deletion) (-possible nucleotide deletion, -possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide insertion) (-possible nucleotide) (-possible nucleot		1	amino acid	
amino acid sequence Cadon, /-possible nucleotide deletion,		amino acid	residue of	
Sequence Sequence		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
CARCKARPSNSSNLTKHRRITTGERPYYCTKGKARFHSSNLTH HYRTHUDRPYDCCKGKARGGGSBLKHKQMHTERPAYCKDCK KAPSGKGSLIRHYHIHTGEKPYQCHECKSPSQHAGLSSHGKL TGEKCYKCKECKGKAPHGSSNTNKHRITTGERPYCCHCGK KAPSGKGSLIRHYHIHTGERPYCCHECKSPSQHAGLSSHGKTL TGEKCYKCKECKGKAPHISSNTNKHRITTGERPYCCHCKTPC SKSNLSKHKQNVITGEGSAP RVFLKDLSTFWARSNTASIAQARKLVEQLKMEANIDTIKVSKA AADLMAYCHAHKDDELITPYPASCNIP PREKKIPCAIL 6582 1428 718 CFITTKITHGSTFVASCNITASIAQARKLVEQLKMEANIDTIKVSKA AADLMAYCHAHKDDELITPYPASCNIP PREKKIPCAIL GRIFTHINNYRSKLDLSSNLFQHTSGMOVQLFLSSLS QDSKLVYIQLLMONINLHQEPREPLYVSWANINSEKKSSLLSSI QDSKLVYIQLLMONINLHQEPREPLYVSWANINSEKKSSLLSSI QDSKLVYIQLLMONINLHQEPREPLYVSWANINSEKKSSLLSG QDSKLVYIQLLMONINLHQEPREPLYVSWANINSEKKSSLLSG QDSKLVYIQLLMONINLHQEPREPLYVSWANINSEKKSSLLSG QDSKLVYIQLLMONINLHQHEPREPLYSWANINSEKKSSLLSG QDSKLVYIQLLMONINLHQHEPREPLYSWANINSEKKSSLLSG SQSSSWCGKCRCFAPLI 487 41 RIFSMTSGRLRWCTWEPATALWSASLKLGTSSMHFSPRSISYR LSEMSLYPERILBYTALFRS PDSBERATSCPRLHJWCRAPL RSPSPLGRLQVLPRSPLHWTHNSGEVLGLQVQRSRSSTGPA SQASGSAVQGGWCIF LSMMLSPLPSNTRGLSTATLWSAGEKKKYGKASSSTGPA SQASGSAVQGGWCIF FLEMAAGJSSSQNTSVVVVPKNTTKKYNINANAADKVYNT RSPSPLGRLQVLPRSPLHWYNYNTTLARRETTALTABAREEKER KYNT TVLKEPREBOPWLLRVNGSGRKFKGIKKGGVFRNTSYITTC CPGGAPAPPYNNYNYTTLARRETTALTABAREEKER KYNT TVLKEPREBOPWLLRVNGSGRKFKGIKKGGVFRNTSYITTC CPGGAPAPPYNNYNYTTLARRETTALTABAREEKER SDASDAGBEGGFYCHAKKKAPLAKGGRKKKKSDDEAPPDS DDCDPROGEVTYNBOGSSSSGREPESKARAPQCEEGGKOVDGOS DSESSEREKEPPERVAKKARGARKYGGKKKSDDEAPPDS DDCDPROGEVTYNBOGSSSSGREPESKARAPQCEEGGKOVDGOS DSESSEREKEPPERVAKKARGARAPPPOBKKRRKNSSBSDBSS ESDIDSEASSAPPAKKXTYPEKRRKPOGGSRONSPOTPSAB GSTSSTLRAAASKLBGGKRVSBMPAARKLLDTOFQSLLSKST PQPPSGKTTPNGGVQVTEDAVRATHLTARRENTINDONGTOKAT TRINSTIDDFVGCDEFARASSCVIPKSPPAARUSBCDBSDSS ESDIDSEASSAPPAKKXTYPEKRRKPOGGSRONSPOTPSAB GSTSSTLRAAASKLBGGKRVSBMPAAKRLBTUKKSRKYFE HIGKSTDIAVRGVGTERDAVRATTAGROPVETHENTINTSYLTYT TVLQWMTNAGABGAVYTTGAGNOFSYEVTHEIDTKYSKKAVPF HIGKSTDIAVRGVGTARATTARNDDAVTQVBARAPTAVNUNG GSRALCGNIAGHGKKKTARAPTAVATAGGGGGARTATAVRS GAPEGOGPSALERIS GTYGSGVERRITANDDAVTQVBARAPTAVATAGGGGGARGAATAGGARGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA		amino acid	sequence	
HYRTHLUIPPYDCKOKAPOGSBLLIKHQRMITTERAPYCKOKA KAPSKGSLIRHY HITGERYPYCKPCKS F9GHADLSSHORLI TGEKOYKKKECKAPHISSINTNKHHRIHTGEKPYNCHICGKTPC SKSNLSKHORVITGEGRAP RYPLKDIGSTPYRASINTASTAQARKLVEQLKMEANIDRIKVSKA AADLMAYCGAHAKEDELLITYPASENPTRKKFTCAIL 6582 1428 718 CFITTIKIGSPVSYTISPILVIRKEESELIKHNEGOVJHTYSSFIN ORB I I FWILMWYFRIDLIPSILIGELLITSHCNEGVQLIFLSSFIN ORB I I FWILMWYFRIDLIPSILIGELLITSHCNEGVQLIFLSSFIN ORB I I FWILMWYFRIDLIPSILIGELLITSHCNEGVQLIFLSSFIN ORB I I FWILMWYFRIDLIPSILIGELLITSHCNEGVQLIFLSSIL ORSKLYVIQLAMIN HILMGERREPTYVSWBNINNSEKSELISER QOETSILVETIRG I QHNNUKRI HILMGERREPTY LIKELSKLOKEND I I FRYSKORLERKOTTUPPATALMSASILRIGTSMHFSPRSISLD ESMUSSEKCROGAPLI RISSHCRICHTY BYSISSELIKHTSCPHILHUMKCRAFT RISSHCRICHTY BYPHILMYTHS CHANGER HILMCKCRAP RSSPICRICHTY BEPLINFHTHINGSEVLICLOQVASRSGTGPAC SOAGSGAVQCGMWCIF FINDALGPSSGNINTERVYRVPKNHTKKYNI HAPPAAADLVNFAT WOQARLERDLSNKKI YQBEEMPESGAGSEFINKI REEARRKXYG TVILKEFRPEDOPHILLEVNGKSGRK FGI KRGOVTENTS YYI FTI CFIGAFAF PYNINNYN TYLLRIRHTITABABAEBKERRIKVINI FSI MQQRKLODDODEDBEEKEKGRKASEUR HIDLEDDLSM SDASBAGSEGGRYPKAKKARA PLAKKGGKKKKKKKSSDBEFENS SDASBAGSGGGOVYPKAKKARA PLAKKGGKKKKKKKSSDBEFENS DDGDFEOQEVDYMSDGSSSSGBEPBSKAKAPQGEEGG KOVDOG DSSESSEREKPPEDEKKRESKSKAKGGKKKKKKSSDBEFENS SDASBAGSGGGOVYPKAKKARA PLAKTOPGSLISKGNS FGAS GGSTSSTIRAAASIRLOGKRYSSINTNOKHHFISKI FSI MQQRKLOGKDODDODEDBEEKEKROGKGSSRONS POTTPSS DDGDFEOQEVDYMSDGSSSGBEPBSKAKAPQGEEGG KOVDOG DSSESSEREKPPEDEKKRESKSKANGGKKKKKKKKKSSDBEFENS ESDI DSRASSAFFMAKKKTYPKKERKPOGGSSRONS POTTPSS SDASBAGTEGOVYTAKATOR TORKHTYTOR TORKHTYCH TYTHOTH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TYTHOTH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHTYCH TORKHT		sequence		1. '
KAPSGKGSLIRNYLITTGEKPYQCHECKSPSQHAGLSSHQKIF TGEKPYKCKECKAPHISINTMEHISITTGEKPYKCHCGKTPC SKSNLSKHQNVITGEGSAP RVPLKRUCKAPHISINTMEHISITTGEKPYKCHCAKTPC SKSNLSKHQNVITGEGSAP RVPLKDLSTPMASNINTASIAQARKLVEQLKMEANIDRIKVSKA AADLMAXCBAHAKBDELLITPVPASCNIP PREKKPCAIL 6582 1428 718 CFITTKITIGSPVSVPYLSPLVURKELESLLENGGQVIHTSSFIN ORD IL PWILLVMPRRILDLESNLENGGQVIHTSSFIN ORD IL PWILLVMPRRILDLESNLENGGQVIHTSSFIN ORD SKLVYIQLLADNINLINGGPREPLVVSHRNIPNSEKKSSLLSSEL QOSKLVYIQLLADNINLINGGPREPLVVSHRNIPNSEKKSSLLSSEL QOSKLVYIQLLADNINLINGGPREPLVVSHRNIPNSEKKSSLLSSEL QOSKLVYIQLLADNINLINLSQMEYGMRQSHLYRE ILFLSLVSLGREN DIE PAFDHEYGIA YNSUSSELLERLQKIDAP PSASVENCRKCRGAPLI 878SPLGRILQVIPRSPLHVHTHINSGKEVLGLQVQRSRSGTJFAC SQASGAVQGONCIP RSPSPLGRILQVIPRSPLHVHTHINSGKEVLGLQVQRSRSGTJFAC SQASGAVQGONCIP LSPMALGSPHAVHTHINSGKEVLGLQVQRSRSGTJFAC SQASGAVQGONCIP LSPMALGSPHAVHTHINSGKEVLGLQVQRSRSGTJFAC SQASGAVQGONCIP LSPMALGSPHAVHTHINSGKEVLGLQVQRSRSGTJFAC SQASGAVQGONCIP LSPMALGSPHAVHTHINSGKEVLGLQVQRSRSGTJFAC SQASGAVQGONCIP LSPMALGSPHAVHTHINSGKEVLGLQVQRSRSGTJFAC SQASGAVQGONCIP LSPMALGSPHAVHTHINSGKEVLGLQVQRSRSGTJFAC SQASGAVQGONCIP LSPMALGSPHAVHTHINSGKEVLGLQVQRSRSGTJFAC SQASGAVQGONCIP LSPMALGSPHAVHTHINSGKEVLGLQVQRSRSGTJFAC SQASGAVQGONCIP LSPMALGSPHAVHTHINSGKEVLGLQVQRSRSGTJFAC SQASGAVQGONCIP LSPMALGSPHAVHTHINSGKEVLGLQVQRSRSGTJFAC SQASGAVGGONCIP LSPMALGSPHAVHTHINSGKEVLGLQVQRSRSGTGTPAC SQASGAVGGONCIP LSPMALGSPHAVHTHINSGKEVLGLQVQRSRSGTSTSTIT, TLANGKKKKKKSDDEAPFRS SDASDASGEGGRVYBAKKARQLANGGKKKKKKSDDEAPFRS SDASDASGEGGGRVYBAKKARQLANGGKKKKKKSDDEAPFRS SDASDASGEGGGRVYBAKKARQLANGGKKKKKKKSDDEAPFRS SDASDASGEGGGRVYBAKKARQLANGGKKKKKKKSDDEAPFRS SDASDASGEGGGRVYBAKKARQLANGGKKKKKKASDEAPFRS SDASDASGEGGGRVBAKARQDESSEKARAPQCEGGGRANGTASGE SDASGASGAVGANQTANTATKSTATUKANTA FSIMAGARGAAVATATTATATATATATATATATATATATATATATATA				CAECGKAFSNSSNLTKHRRTHTGEKPYVCTKCGKAFSHSSNLTL
TGEKPYKCKECKAPNISSNYPKICHERITHGEKPYWCHHCGKTPC SKSNLSKHQRVITHGEGEAP RYPLKDLESTPRASNNTASIAOARKLUPGLKMEAN IDRIKVSKA AADLMAYCEAHAKEDPLLITYPVASSNPPERKKYPCALL 6582 1428 718 CPITKITGSPVSVYJLSPILVRKELESLLENEGDQVIHTSSPIN QHEIIFWILWWIPKILDESNLPGLIITSEHCNBGVQLISLSIS QDSKLVYIQLIGUDNINHGEPBEPLLYVSWRYPNSEKKSSLLSLS QDSTSTLVETIRGSIQINNVLEPINLLSQMKPGMKRQRSLYRE ILFELSUSJGRRIDI I BAPTNYSTQIAYMLSSELIZERLQKIDAP PSASVEMCRKCRGAPLI 6583 487 41 RIFSMTSGLRKWRCTWRPATALMSASLRLGTSSMHFSPRSISLD LSMMLSPLPSNTRGLSFTALFRSPOSEHATSCPELHURCKAPL RSPSIGRLQVJRSPSJHVSTTINSKEVJLQVVQRSRSSTGPAC SOAGSGAVQGWNCIF RSPSIGRLQVJRSPSJHVSTTINSKEVJLQVVQRSRSSTGPAC SOAGSGAVQGWNCIF WOQALLERDLSNKKIYQEBEMPESGASSFNRKURERARKKYG IVLKERPREDOPHLRVWRGKRGKKKSIKDGVRSSYTGPAC WOQALERDLSNKKIYQEBEMPESGASSFNRKURERARKKYG IVLKERPREDOPHLRVWRGKSGKKKSKIKKGKDDEAPEDS SDASASGEGGRVPKAKKARALARGKKKKKKTRSSDEAPEDS SDASASGEGRVPKAKKARALARGKKKKKKKSDDEAPEDS DDGDPSGQEVJTMSDGSSSSQEPESKARAPQOZESFKKVORKDEA SDADASGEBGRVPKAKKARALARGKKKKKKKSDDEAPEDS DDGDPSGQEVJTMSDGSSSSQEPESKARAPQOZESFKKVORKDGS DSSESEBERBYPBEDKEEDESHARGRIKKKRGDDEAPEDS DDGDPSGQEVJTMSDGSSSSQEPESKARAPQOZESFKKVORKDGS SDASASASGEGRVPKAKKARALARGKRKKKKRKSDDEAPEDS DDGDPSGGVTMSDGSSSSQEPESKARAPQOZESFKKVORCH STANDARASKERGTVFAKKKTPFRREKKSGDDEAPEDS DDGDPSGGVTMSDGSSSSQEPESKARAPQOZESFKKVORCH SSADASGERGERVPKAKKARASELDJORVYTENSY TYTO CPPGAFEAPPVINWYNFTPLARREKKSGDDEAPEDS DDGDPSGGVTMSDGSSSSQEPESKARAPQOZESFKVORCH STANDARASKLUDGRKVARVARASELDGORKVORKKGSDEAPEDS DDGDPSGGVTMSDGSSSSQSSCPESKARAPQOZESFKVORCH SSADASGERGERVPKAKKARASELDGORKVORKKGSBCDAPEDS DDGDPSGGVTMSDGSSSSQSSCPPSKARAPCQDSLSSCKTYNSYTESPK GSSTATLRAASKLUDGRVARVALARGAPGTFKTATDGTPCSJSSCKTT PQPPSGKTTNSGDVQVTEDAVRYLTKRFMTTDLKKFYDSSGSDDMC HKKERPARAMANGUNGTHEAPPROPHSLAVYNTRABSRDDMC HKKERPARADSRUDGVTEDAVRYLTARKFMTTADDGSGSLAVYNTROSPKORT PQPSGFMTNTAMPGGSGSSGGANGROPPSTOMA HKERGRAAACKADATARTALSGCTURARDSRDDMC HKKERPARAMANGUNGTHEAPPROPHDLYNDREDALTATARTYPSGGBLANDFARVYNTROSPK GAPEQOPSALERSISTINGVSGTVARANDSGCDALTATARTYPSG GAPEQOPSALERSISTINGVSGTVARANDSGCDALTATARTYPSG GAPEQOPSALERSISTINGVSGTVARANDSGCDALTATARTYPSG				·
SENSILSKHORVHTOEGEAP 8581 228 476 RVPIKDLESTPHASNITHAS TAQARKLVEQLKMEAN TORIKVSKA AADLMAYCEAHAKEDPLLTPVPASENPTREKKPFCAIL 6582 1428 718 CFTTKTHGSPVSVFYLSPLVIRKELESLLKREGGQVITTSSFIN OHE II FWTLWWFRILDLESNLFGLLKREGGQVITTSSFIN OHE II FWTLWWFRILDLESNLFGLLKREGGQVITTSSFIN OHE II FWTLWWFRILDLESNLFGLLKREGGQVITTSSFIN OHE KYNTYQLKUNDIN INLHQEPREDLYVSKRIFNSEKKSSLLSER QOETSTUVET IRGS IQHNNULFINLSQUMKGMKGRSLYRE ILFLGLVKIDAP PASAVEMCRIKGRSI QIENKLYNINGLSKALLSER LOKTDAP PASAVEMCRIKGROPATALWSALSILGTSSMHSPRSISDL LSRENGVGROWNE IN ILFLGLVSLGERNID I BAPTNEYGI AVNALSSELLERLQKIDAP PASAVEMCRIKGROPATALWSALSILGTSSMHSPRSISDL LSRENGLQVQRSRSGTGPAC SQAGGGAVQGMCTF 6584 4189 1750 FLPWARLGPSSQNVTEYVVRVPRNTTKKYNIMAFNAADKVNFAT WRQAALERDLSNKKI YQBEEMPESGAGSFNKILGRERRKKYG INLERERRKKYG IVLKEFRREDOPHLIRWRGKSPLL RSPSILGELQVQURSSPLIVATHINSGKVLIGLQVQRSRSGTGPAC SQAGGGAVQGMCTF 6584 189 1750 FLPWARLGPSSQNVTEYVVRVPRNTTKKYNIMAFNAADKVNFAT WRQAALERDLSNKKI YQBEEMPESGAGSFNKALRERRRKKYG IVLKEFRREDOPHLIRWRGKSREKKGRKASSLEVENSKYLNE FSINQORRLKDODOODBEEEKEKKGRKKASSLEVENSKYLNE FSINQORRLKDODOODBEEEKEKKGRKASSLEVENSKYLNE FSINQORRLKDODOODBEEEKEKKGRKASSLEVENSKYLNE FSINQORRLKDODOODBEEKEKKGRKASSLEVENSKYLNE FSINQORRLKDODOOBBEEKEKKGRKASSLEVENSKYLNE FSINGORRLKDOODBEEKEKKGRKASSLEVENSKYLNE FSINGORRLKDOODBEEKEKKGRKASSLEVENSKYLNE FSINGORRLKDOODBEEKEKKGRKASSLEVENSKYLNE FSINGORRLKDOODBEEKEKKGRKASSLEVENSKYLNE FSINGORRLKDOODBEEKEKKGRKASSLEVENSKYLNE FSINGORRLKAKKGGSDDAFEDS DEGESGAFPANKKKTPTOKEKKGRSGNASRFOTPSAS GSTSSTLARAASKLEGGKRVSKAKKASLDSESSSSS ESDIDSEASSAFPMAKKKTP FRERKRYGGGSSGNASRFOTPSAS GSTSSTLARAASKLEGGKRVSKAKKASLUNG FTOKKYNTATAGSLEKKKYTTAGLKKAKTOSSESSINGS FTOKATAG TAGA				
APPLICATEST APPLICATION		}		TGEKPYKCKECGKAFNHSSNFNKHHRIHTGEKPYWCHHCGKTFC
AADLMAYCEAHAKEDPILITPVEASENP PEKKPPCAIL 6582 1428 718 CPTTKTHCSPVEYPLSSPVLIKELESLENSEGVLYHTSSPTIM QPIITWTLVMYPRILDENILDGILLTSEHCNEGVQLPLSSLS QDSKLVYIQLEMDINIHGEPREELIVYSKRWFNSEKKSLLSER QOSTSTUZFIRGSIQINNIVLEYINLSQQWKFMSEKKSLLSER QOSTSTUZFIRGSIQINNIVLEYINLSQQWKFMSEKKSLLSER QOSTSTUZFIRGSIQINNIVLEYINLSQQWKFMSEKKSLLSER QOSTSTUZFIRGSIQINNIVLEYINLSQGWKFMSEKKSLLSER QOSTSTUZFIRGSIQINLEYINLSSLELGRIQKIDAP PSASVEMCRICKGRAPITALWSASILGTSSMHSPRSIGP LSMMLSPLPSHTGISTTALFSPOSEHATSCPELHLWRCRAPL RSPSELGRLQVUDRSPLHVWTINSGKSVLGUQVGRSSGTGPAC SQAGSAQVQGOMCIF 6584 189 1750 PLDMAALCPSGONVIETYVVEVBRYTTKKYNIMAPNAADKVYBAT MNQARLERDLSNKTIYQBEEMPESGAGSBYNKLREBARKKXG IVLKSPRSEDQFWLLRVNGKSGKKYKGIKKGYCTENTSYTIFTQ CPDGAFRAFFVINNYNTFILARHRILTABEAGEEWERNKVLNIK FSIMQGRRLKDGDODBEEEKKKGKKASSDLERIHDLEDDLEWS SDASDASGEGGGRVBKAKKAPLAKGGRKKKKKGSDDPAEPES DDGDFGGQGVUDWSDGSSSGSGEPESKAAPTQOKREGORSPESSSS ESDIDSEASSFMAKKAPLAKGGRKVESPBAAKKIRDSDPAEPES DDGDFGGGGVUDWSDGSSSGSGEPESKAAPTQOKREGORSPESSSS ESDIDSEASSFMAKKAPLFREKRYGGGSGRNSRFOTFSAS GGSTSSTLRAAASKLEGGKRVSEMPAAKKIRDTOPQSLSGKST PQPPGGKTTINSDQOVYTEDAMPRITIKRWTHOLLKKFQTKK TILSSBQVAVLAQILKRLAPERKNINDKMHFSILXE 6585 3 1678 1678 1678 1678 1678 1678 1678 1678 1678 1678 1678 1678 1678 1678 1679 167				
CFTTKTHCSPVSUPPLISPLURKELESLLENBEGDOVTHTSSPIN OHD I FWTU-WYRFRLID-PSNLDGLLITSSELDCUD-LISSLS ODSKLVYIQLLWDNINLHQEPREPLYVSWRNFNSEKKSSLLSEE QOETSTLVETIRGSIQIRNVLEPINLISQWRFMRKROSILYRE ILPELSUSJCBREND ID RAPFINDSTOFIA NINLSSEBLIERLQKIDAP PSSAVEWCRKCRGAPLI FISHTSGRIKMENTEN DIE RAPFINSTGISTISSHHSPRSISJP LSMMLSPJPSNTRGISSPTALFRSPDSSHATSCPELHLWRCRAPL RSSPIGRELQVJRSP PHANTHINSCKEVLGLQVQRSRSGTOPAC SQAGSGAVQGAWCIF RSSPIGRELQVJRSP PHANTHINSCKEVLGLQVQRSRSGTOPAC SQAGSGAVQGAWCIF PLANGARKKKTHNIMAFNAADKVNFAT WOMAALERDIJSNKI TYGEEBMPESGAGSFINK KLREARRKKYZ IVLKEFREEDOPWLLRVNGKSGRKFKSI KKGGVIENTSY TIFTQ CPDGAFEAPPVINWNTFILARHRITLREARE EBWERRIKVLINK FSIMQQRRLDODODDEBEKSKRGRKFKSI KKGGVIENTSY TIFTQ CPDGAFEAPPVINWNTFILARHRITLREARE EBWERRIKVLINK FSIMQQRRLDODODDEBEKSKRGRKFKSI KKGGVIENTSY TIFTQ CPDGAFEAPPVINWNTFILARHRITLREARE EBWERRIKVLINK FSIMQQRRLDODODDEBEKSKRGRKFKSI KKGGVIENTSY TIFTQ CPDGAFEAPPVINWNTFILARHRITLREARE EBWERRIKVLINK FSIMQQRRLDODODDEBEKSKRGRKFKSI KKGGVIENTSY TIFTQ CPDGAFEAPPVINWNTFILARHRITLREARE EBWERRIKVLINK FSIMQQRRLDODODDEBEKSKRGRKFKSI KKGGVIENTSY TIFTQ CPDGAFEAPPVINWNTFILARHRITLREARE EBWERRIKVLINK FSIMQQRRLDODODDEBEKSKRGRKFKSI KKGGVIENTSY TIFTQ CPDGAFEAPPVINWNTFILARHRITLREARE EBWERRIKVLINK FSIMQQRRLDODODDEBEKSKRGRKFKASELLRIHDLEDDEMS SDADASGEBGRVFVKAKKAF LANGKRKKKKKGSDDEAPFDD DEGBFERSKEK FRANKAL FRANKATSH FSIMQQRRLDOD DEGBFERSKRGRAF FRANKAL BURDEN SDADASGEBGRVFVKAKKAF LANGKRKKKKKGSDDEAPFDD DEGBFERSKEK FRANKAL FRANKATSH STADASGESSA GARS FRANKAL FRANKATSH SADASGESGA SHANKAR BARDAS BEDSAS ESDIDSEE ESDIDSEE SSISSIS ESDIDSER SSISSIS ESDIDSER SSISSIS CHERT FRANKATSH SADAS BEDSAS ESDIDSER ESDIDSER ESDIDSER ENGRAPHA KKKTFPTRANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH SADA HKKTFT FANKATSH	6581	228	476	RVFLKDLSSTPMASNNTASIAQARKLVEQLKMEANIDRIKVSKA
QREITWILWYERRIADLERNIGGILLITSERCKEGYQLPLESLIS QDSKLYVIQLUMDNINLHQEPREPLYVSWRNPRSEKKSSLLSEB QQETSTLVETIRQSIQHNNVLRPINLLSQMKREGMERQRSLYRE ILFLELVSLGRENIDIEAFDNEYGITAYNSLSSELIERQKIDAP PSASVEMCRECTGAPLI RIFSMISGRENBECTWRPATALWSASLRLGTSSMHESPRSISLD ESSPLIGHLQVLERSPLIVHTHNSGKEVLGLQVQRSRSGTGPAC SQAGSGAVQGMCTIP SSPLIGHLQVLERSPLIVHTHNSGKEVLGLQVQRSRSGTGPAC SQAGSGAVQGMCTIP FLDMAALGEBISNNVTSYVRVPKNTTKKYNIMAFNAADKVNFAT WNQAALERDLSNNKTYQEEEMPESGAGSERNRILKERRARKKYG IVLKEFREDEOPPHLERVRGSGRKFGIKKKKKKGVTENTSYYIFTY CPGGAFBAPPVHWWYNFTPLARHRITTABEABEEWRENRKVLNH FSIMQORRLICHOODOBBEEKEKGRRKKGKKGSUDDAPEDS DDCDFEGGEVPYMSDGSSSGEBESKAARSELRIHDLEDDLEMS SDASDASGEGGEVPYRAKKAPILAKGGRKKKKKKGSDDEAPEDS DDCDFEGGEVPYMSDGSSSGEBESKAARSELRIHDLEDDLEMS SDASDASGEGGEVPYRAKKAPILAKGGRKKKKKKSGDDEAPEDS DSESSBERKPPBEDKEBEEKKRAPTROGESSKNONSFOTFSAG GGSTSSTLRAAASKLEGGKKVSSMPAARKREDTGPGSLSGKST POPPSGKTTNNSGDVQVTEDAVRRYLTKRMTTYDLLKKFOTKK TGLSSGCTVAVLAQTLIKKHPBERKMINGKHIFSLKR GGSTSSTLRAAASKLEGGKAVSSMPAARKREDTGPGSLSGKST POPPSGKTTNNSGDVQVTEDAVRRYLTKRMTTYDLLKFOTKK TGLSSGCTVAVLAQTLIKKHPBERKMINGKHFISLKR GGSTSSTLRAAASKLEGGKAVSSMPAARKREDTGPGSLSGKST POPPSGKTTNNSGDVQVTEDAVRRYLTKRMTTYDLLKKFOTKK TGLSSGCTVAVLAQTLIKKHPBERKMINGKHFISLKR GGSTSSTLRAAASKLEGGANDVOOLKUNTYTGPGGDLJVODVVP TDEMAHFDRERIPERVVHAKGAGAPGYPEVTHDITKYSKAKVPB HIGKKTPIAVRFSTVAGSSGSADTYRDRRGFAVKFYTEGGWIDL VGNNTPIFFIRDPILEPSFITHSGKRNPGTHLKOPDMVWDFWSLK PSSLIQVSFLESDRGIPGHRHNNGYGSHTFKLWANAGBAYCK FHYKTDGGIKNLSVEDAARLSGGDPDYGTHAKPDAWVDFWSLK PSSLIQVSFLESDRGIPGHRHNNGYGSHTFKLWANAGBAYCK FHYKTDGGIKLANGDGIFTGKKAVKNPTEVUPDVPGHICALL DKYNARKPKRAIHTPVGGSSHLAARKANL LGPNYLHIPWGCPYRARVANVQRGDMCCADAPVYDVINB EQKRLICENTAGHLKDADGIFTGKKAVKNPTEVUPDYGHICALL DKYNARKPKRAIHTVFTYISPWERAMGVDPQCKWEKFYNNE GAPEOQPSALEHSICYYGSEVRRFNTANDDAVVTQRGSFKKNEKFYENHD DVFSDSSMHDFROKFDFTVGGGLATAAGFGAAGTAGVGG TGSGDQAGGSGRHITVFFTYISPWERAMGVDPQCKWEKFYNNE GAPEOQPSALEHSICYYGSEVRSKMTPGMPRKV GGSGGGGGSGGGGGGGGGGGGGGGGGGGGGGGGGGGG				
ODSKLYJOLIMONINLIOPEREDLYUSHNISEKKSSLLSEE QUETSTLVETIRQSIQHNVLKPINLLSQMKPGKRQRSLYRE ILPLSIVSERRENIDIRAFONETGIAYNSLSSEILERLQKIDAP PSASVEWCRKCFGABLI 6583 487 41 RIFSMTSGKRWCTWRPATALWSASLKIGTSSMHESPRSISIP LSMMLSFLPSNTRGISPTALFRSPDSEHATSCPRLHLWRCRAPL RSPSPLGELQVDERSPLIVHTHNISGKEVLGLQVQRSRSGTGPAC SQAGSQAVQGGNWCIF 6584 189 1750 FLDWARLGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFAT WNQALLERBISDNKKIYQEEMPESGASSEYNRLKRERARRKYG IVLKERREDOPMLLRVNGKSGRKFKGIKKGGVTENKKVLNN FSIMQORRLKODODDEBEEKEKRGRKASSLRIHDLEDDLEMS SDASDASGBEGGRVPKAKKKAPLAKGGRKKKKKKSSDDEAFEDS DDGDFRGQEVDYNNSDGSSSSGBEBEKKKKGSDDEAFEDS SDASDASGBEGGRVPKAKKKAPLAKGGRKKKKKKSSDDEAFEDS SDIDSEASSFFMAKKTIPTPKRERKPSGRSNSRFOTSPAR GGSTSSTLRAAASKLEQGKRVSEMPAKRLBLDTGGSLSGKST PQPPGGKTTPNSGDVQVTEPVRERKPRSGRSSRONSRFOTSPAR GGSTSSTLRAAASKLEQGKRVSEMPAKRLBLDTGGSLSGKST PQPPGGKTTPNSGDVQVTEDVARTVITKKTNTULLKKFOTKK TGLSSEQTVNVLAQILKKLNPERRMINDKMHFSLKE FSIDISEASSFFMAKKTIPTPKRERKPSGRSNSRFOTSPAR GGSTSSTLRAAASKLEQGKRVSEMPAKRLBLDTGGGSLSGKST PQPFGGKTTPNSGDVQVTEDVARTVITKKTNTULDLKKFOTKK TGLSSEQTVNVLAQILKKLNPERRMINDKMHFSLKE FSIDISEASSFFMAKKTIVTYGRGGPLVQDVVF TDEMAHFDRRRIPERVURAKGAGAFGYFEVTHDITTYSKAVVFE HICKETPLAVEFSTVAGSGSADTVEDPRGFAVKFYTEDGMDL VGNNTPIFFIRDFILEPSFTISQKRNPQTHLKDPDWVDFMSLK PESLIKJOSFLESDRGI PDGHRHMYGYGSFFKLVNANGEAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TYPIQVMTFNQASTFFFNPPOLIKWPHKDYPILEVGKLVLNANGEAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TYPIQVMTFNQASTFFFNPPOLIKWPHKDYPILEVGKLVLNANGEAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TYPIQVMTFNQASTFFFNPPOLIKWPHKDYPILEVGKLVLNANGEAVYCK FHYKTDGGIFFFNPPOLIKWPHKDYPILEVGKLVLNANGEAVYCK FHYKTDGGIFFFNPPOLIKWPHKDYPILEVGKLVLNANGE GRADAGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6582	1428	718	CFTTKTHCSPVSVPYLSPLVLRKELESLLENEGDQVIHTSSFIN
OORTSTLVETINGSLOHNVULKPINLLSQQMKPGRRQRSLYRE ILPLSLIVBLERNIDIEAFDNEYGIAYNSLSSILERLQKIDAP PSASVEWCRKCFGAPLI RIFSMTSGRLWRGCTWRPATALWSASLRLGTSSMMPSPRSISDP LSMMLSPLPSNTRGIS-PTALFRSPDSEHATSCPRLHLWRCAPL RSFSPLGRLQVLPRSPLHVHTHNSGEVLGLQVQRSRSSGTGPAC SQAGSGAVQGGNCTF 189 1750 PLDWAALGPSSQWTEYVVRVPKNTTKKYNIMAPNADKVNFAT WNQARLERDLSNKKIYQEEMPESGAGSEPNKLREEARRKXYG IVLKEFRPEDQPHLRVNGKGSGKKFKGIIKKGGVTENTSYYIFTQ CPGAFEAPPVHWWNFTPLARHRTLTAEAEEEWRRKXYGN FSIMQORALEDOPONDEBEEKEKRGRRASSELNIHDLEDDLEMS SDASDASGEGGEVPKAKKKAPLAKGGRKKKKKGSDDEAFEDS DDGDFRGGQUPVNSDGOSSSOSEPPSKAKRGSBLENIHDLEDDLEMS SDASDASGEGGEVPKAKKKAPLAKGGRKKKKKKGSDDEAFEDS DDGDFRGGQUPVNSDGOSSSOSEPPSKAKRGSBESDASFE ESDIDSEASAFMAKKKTPPKRERKPSGGSSRGNSRPGTPSAE GSSTSSTLRAAASKLEQGKRVSSMPAARRLELDTGPQSLSKST PQPPSGKTTNNSGDVQVTEDAVRRYLTKRMTTKDLLKKFQTKK TGLSSEQTVAVLAQLIKRLWPBERMINDKHTSLKE GSTSSTLRAAASKLEQGKRVSSMPAARRLELDTGPQSLSKST PQPPSGKTTNNSGDVQVTEDAVRRYLTKRMTTKDLLKKFQTKK TGLSSEQTVAVLAQLIKRLWPBERMINDKHTSLKE GSTSSTLRAAASKLEQGKRVSSMPAARRLELDTGPQSLSKST PQPPSGKTTNNSGDVQVTEDAVRRYLTKRMTTKDLLKKFQTKK TGLSSEQTVAVLAQLIKRLWPBERMINDKHTSLKE GSTSSTLRAAASKLEQGKRVSSMPAARRLELDTGPQSLSKST PQPPSGKTTNNSGDVQVTEDAVRRYLTKRMTTKDLLKKFQTKK TGLSSEQTVAVLAQLIKRLWPBERMINDKTVTGPRGPLLVODVVF TDEMAHPDRRFIPERVUAKGAGAPGYFEVTHDITKYSKAVVPB HIGKKTPIAVRFSTVAGESGSADTVRDRGFQFLLVODVVF TDEMAHPDRRFIPERPILFPSFIHSQKRNFQTHLKDPDMVMDFNSLK PSSLGVAFFSTVAGESGSADTVRDRGFQVKYKYTTEDGNMDL VGNNTPIFFIRDFILFPSFIHSQKRNFQTHLKDPDMVMDFNSLK PSSLGVAFFSTVAGGSGRGTGDFGCMANGAVYTYTNSF GAPPQOPSALEHSIQYSGEVRRPTANDDMVTQRAPYVNVLNS ERKRLCSNLLAFDENDATAGSKYFSK TYJCQMTFNOASTFFFNYGGTPPD IRASPKKKSKSKLIMBLTGGGGESSGL NLGKKISVPRRAWNQRDGMCMONGGAPMYYFNSF GAPPQOPSALEHSIQYSGEVRRPTANDDMVTQRAPYVNVLNS EQRKBLCSNLARGHKONGATTAGVGE TGSGDQAGGGGKHITVFYFYISPMERAMGVDQCKMELGIDLLA NLGKKISVPROVALEELSLLINNGSSMFKLEQNRVEKFIYRHH DVSDSSMHPGGFGFDFFFFFPPARKKRSSKLIMBLTGGGGESSGL NLGKKISVPROVALEELSLLINNGSSMFKLEQNRVEKFIYNH DVSDSSMHPGGFGFDFFFFFFFFFFYSGFFANKKFSSKLIMBLTGGGGESSGL NLGKKISVPROVALEELSLLINNGSSMFKLEGARTAGATAGVGE TGSGDQAGGGGKHITTVFKYTISPMERAMGVDQAGGGGGAGGAGGAGGFGFV LFPDLVSGLULVUNTELVQSYQ				QHPIIFWTLVWYFRRLDLPSNLPGLILTSEHCNEGVQLPLSSLS
TIPLSIVSLIGREN DI EAPDNEYGIAYNSLSSEILERLQKIDAP PSASYEWCRKCFGAPLI RIFSMISGREWRCTWRPATALWSASLRLGTSSMHPSPRSISLP LSMMLSPLPSNITSGLSPTALFRSPDSEHATSCFRHLWRCRAPL RSPSPLGRIQVLPRSP1LHVHTMISGKERKULGLQVQGRSRSGTSPAC SQAGSGAVQGONGTF EDMAALGESSQNVTSEYVVRVPKNTTKKYNIMAFNAADKVNFAT WNQARLERDLSNKKIYQEEMPESGAGSEFNRKLREBARRKKYG IVLKEFREEDQPWILEKVNGKSGRKFKGIKKGGYTENTSYTIFTQ CPDGAFEAPFVHWAWYNFTPLARHEILTABEAEEEMERRNKYLBH FSIMQQRILKDQDQDEBEEKKKRKKKKSDDEAFEDS DDGDFEQGEVDYWDGGSSSQEPBSKAKAPQQEEGPKGVDEQS DSSEESEEKPPEDDKEEEEKKAPTPQEKKRKDSSEESDSE ESDIDSEASSAFMAKKKTPLAKGGKKKKKKSDDEAFEDS DDGDFEQGEVDYWDGGSSSQEPBSKAKAPQQEEGPKGVDEQS DSSEESEEKPPEEDKEEEEKKAPTPQEKKRKDSSEESDSSE ESDIDSEASSAFWAKKKTPLAKGRWTMTHULDEDDLEWS PQPPSGKTTPNSGDVGYTEDAVRRYITMSTTYKLIKKKFOTKK TGLSSZQTVNVLAQILKRINPERKNINDKHHFSLKE FSTRAAASKLEQGRVSBMPAAKRIRLDTOPQSLSGKST PQPPSGKTTPNSGDVGYTEDAVRRYITMSTTYKLUKNAKSFOTKK TGLSSZQTVNVLAQILKRINPERKNINDKHHFSLKE FSLKGVSPLFSNGRIG PDDHRHMMYGYEHAMADSSEDPASDOM HKEGRAAQKADVLITTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHFDRRRIFPRVVHAKGAGAFGYFEVTHDIYKYSKAKVEF HICKKTPIAVFSTVAGEGSSADVTVRPRGPAVKYTTEDGWMDL VGNNTFIFFIRDPILPPSFILBGKRNPQTHLKOPDMVDFWSLR PSSLKGVSPLFSNGRIG PDDHRHMMYGYAFAVKYTEDGWMDL VGNNTFIFFIRDPILPPSFILBGKRNPQTHLKOPDMVDFWSLR PSSLKGVSPLFSNGRIG PDDHRHMMYGYGAPKYFYTEDGWMDL VGNNTFIFFIRDPILPPSFILBGKRNPQTHLKOPDMVDFWSLR PSSLKGVSPLSNGRIG PDDHRHMMYGYGAPKYFYTEDGWMDL VGNNTFIFFIRDPILPPSFILBGKRNPQTHTKYSKAKVEF GAPEQQPSALHSIGVSGSVRFFTNADDDNVTQVRAFYVNLINE EQKKLCENLAGHLKDAOIFIGKKAVKNFFEVHPDYGSHIQALI- LGBNYLHIPVSCGSVLARFFTNADDNVTQVRAFYVNLINE EQKKLCENLAGHLKDAOIFIGKKAVKNFFEVHPDYGSHIQALI- DKYNAKKSVRDIVMLEBLSLLITNGSKMFKLRGMRVEKFIYSNH- EQKKLCENLAGHLKDAOIFIGKKAVKRSKLIMBLTGGGGESSGL MLGKKISVPRIVMLEBLSLLITNGSKMFKKRSKLIMBLTGGGGGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				QDSKLVYIQLLWDNINLHQEPREPLYVSWRNFNSEKKSSLLSEE
PSASYEWCRKCFGAPLI				
487 41 RIFSWTSGRLEWRCTWRPATALWSASIRLGTSSMHESPRSISID LSMMLSPLPSNTRGLSPTALFRSPDSHATSCPRLHLWRCRAPL RSPSPLGRIQVLERSPLHVHTHINSGKEVLGLQVQRSRSGTGPAC SQAGSGAVQGRMCIF 6584 189 1750 PLPMAALGPSSQNYTSYVVRVPKNTTKKYNIMAFNAADKVNFAT WQARLEDLSNKKIYQBEEMPEGGAGSBFNRKLREBARRKKYQ IVLKEFRPEDQPWLLRVNGKSGRKFKGIKKKGVTENTSYYIFTQ CPDGAFEAFPVHWWYNFTPLARHRILTABEAEEEMERRKKYQ CPDGAFEAFPVHWWYNFTPLARHRILTABEAEEEMERRKKYG SDASDASGEGGRVPKAKKAPLAKGGYKEKKKKGSDDEAFEDS DDGDFEGGEVDYWDGSSSSSGBEPSKAKAPQQEEPKGVDEQS DSSESSEBERBPEEMPEDEBEKKAPPQEBEPKKRKDSDEAFEDS DDGDFEGGEVDYWDGSSSSSGBEPSKAKAPQQEEPKGVDEQS DSSESSEBERPPEEMPEEREKKAPPGEFEKKAPPGAFEDS GSSTSSTLRAAASKLEQGKRVSBMPAAKRILDTOPQSLSGKST PQPPSGKTTPNSGDVQVTDDAVRRYLTRKPMTTCDLKKFQTKK TGLSSSQTVNVLAQTLKRINPERMINDKWHFSLKS GSTSSTLRAAASKLEQGKRVSBMPAAKRILDTOPQSLSGKST PQPSGKTTPNSGDVQVTDDAVRRYLTRKPMTKDLLKKFQTKK TGLSSSQTVNVLAQTLKRINPERMINDKWHFSLKS GSTSSTLRAAASKLEQGKRVSBMPAAKRILDTOPQSLSGKST PQPSGKTTPNSGDVQVTDDAVRRYLTRKPMTKDLLKKFQTKK TGLSSSQTVNVLAQTLKRINPERMINDKWHFSLKS GSTSSTLRAAASKLEQGKRVSBMPAAKRILDTOPQSLSGKST PQPSGKTTPNSGDVQVTDDAVRRYLTRKPMTKDLLKKFQTKK TGLSSSQTVNVLAQTLKRINPERMINDKWHFSLKS GSTSSTLRAAASKLEQGKRVSBMPAAKRILDTOPQSLSGKST PQPSGKSTPNSGDVTDDAVRRYLTRKPMTKCDLKKFQTKK TGLSSSQTVNVLAQTLAQTLKRINPERMINDKWHFSLKS GSTSSTLRAAASKLEQGKRVSBMPAAKRILDTOPQSLSGKST PQPSBGFTNSGDFTDFWGDFARAASCSVLKFTTAMADSGTDAVDOWWDFNSLR PRESLIGVSFTSDFTGDFWGDPARASCSVLKFTTAMADSGTDAVKYTTEDGMMDL VGNNTFIFFIRDFILPFSTLBIQKRNQTHLKOPDFWVDPWNDV TDEMAHFORRI IPFSTLBIDFWGDDFARASCSVLKFTTAMADDNYTQKAPYVNLINE EQRKILCRNIAGHLKDAQIFIQKKAVKNFFEVHPDYGSHIQALL DKYNAKFKORAAHTPVCGYRARVANYCRDGPMCMDDMCQGAPNYYNNLINE EQRKRLCRNIAGHLKDAQIFIQKKAVKNFFEVHPDYGSHIQALL DVKYNSKYRANAITFFTVGGGGTAAGGAGGAAGATAGVGE GSGQAGGSGKHTTYVGGGGGTAAGGAGGAAGATAGVGE TGSGQAGGGKKHTTYVGGGGGTAAGDQAGRGGAAGATAGVGE TGSGQAGGGKKHTTYVGGGGTAAGGAGGAAGATAGVGE TGSGQAGGGKKHTTYTYTGGGGTAAGGAGGAAGATAGVGE TGSGQAGGGKKHTTYTYTYGGGGGTAAGGAGGAAGATAGVGE TGSGQAGGGKKHTTYTYTYGGGGGTAAGGAGGAAGATAGVGE TGSGCAAGGGCKHTTYTYTYGGGGGTAAGGAGGAAGTAGVGAFC LIFPDLVKGDSMDGHDLTFKYTYTGGGGATAGLGGGAAGATTAGVGE TGSGCAAGGGCKHTTYTYTTGGGGGAAGTAGAGAVLAKFA LIFP		1	;	1
LSMMLSPLPSNTRGLS PTALFRS PDSEHATSCPRLHLWRCCAPL RSPSPLGRLQUPRS PLHVHTHNSGKEVLGLVQRSRSGTGPAC SQAGSGAVQGOMCT 6584 189 1750 PLDMAALGPSSONTEYVVVP KINTKKYNIMAFNAADKVNFAT WONGALLERDLSINKIT YQEEMPISGAGSE FINK KLRERARKKYG IVLKEFRPEDQFWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQ CPDGAFEAF PVINNYNTTPLARIRTLTAEAREEMERRIKKYU SDAGDARGEGGRVPIMMSDGSSSGVERERGRKASELRIHLDEDLEMS SDASDASGEGGRVPKAKKAPLAKGGRKKKKKGSDDEAFEDS DDGDFFGGVDVMSDGSSSSQUEPSKRAKKKGSDDEAFEDS DDGDFGGVDVMSDGSSSSQUEPSKRAKKKGSDDEAFEDS DSSEESEEKPPEDKEEEEKKAPTPQEKKRRCDSSESDSE ESDIDSEASSAFFMAKKKTPFKEERFPSGGSRGNSR PGTPSAE GGSTSSTLRAAASKLEGGKRVSSMFAKRLDDTGPSLSGKST PQPPSGKTTPNSGDVQVTEDAVRYLTRKPMTKDLLKKFQTKK TGLSSGTVNVLAGLIKKLMPERKMINDKMHFSLKE 6585 3 1678 GPIRNSRIDDFVGGDFRAEASCSVLHSKPHAMADSRDPASDQMQ HMKEQRAAQKADVLTTGAGRPVGDKLINVITVGPROPLLVQDVVF TDEMAHIPDGREITPERVVHAKGAGAFGYFFVTHDITKYSKKVFE HIGKKTPLAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNNDL VGNNTPIPFIRDPILPFBPPTHZHEKVANAMOGAFGYFFVHDITKYSKKVFE HIGKKPPLAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNNDL VGNNTPIPFIRDPILPFBPTHPDFDLKVAWPHKDYELIPVGKALVER PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCK FHYKTDGGIKALSVEDAARLSGDDPDYGIRDLFNALATGKYPSW TYYQVMTTNQAETFPRPPPDLKWAPHKDYELIPVGKLVLINNR PVMYFAEVBGILAFDFNSNPPGIRASPMANYDNSP GAPEQQPSALBHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQKRLCENIJAGHLKDAQIPTIQKKKYSSKLINBLTGGGGSSSGL NLGKKISVPROWILEBLSLLTINGGSKMFKLRBURGHGSGSGSGL GAPEQQPSALBHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQKRLCENIJAGHLKDAQIPTIQKKKISSKLINBLTGGGGESSGL NLGKKISVPROWILEBLSLLTINGGSKMFKLRGMRVERITENTH DVFNSSSMDHFGKFLPTVGGGLTAGQGFSYSKSNGRGGSQAGG GSGAGGYGSDQHHLGSGSGAGGTGGPAGGAAGGTAAGVGE TGSGDQAGGGGKHTVYFKTISPWERAMGVDPQQKMELGIDLLA YGAKABLPKYKSFWRTAMPYGGYEKASKSMTFOMPKV 6587 75 1117 RRVPSIGMMFECNDEHDITKHFVVCHVDAPGGVCASAGF PQGYGPPSMEGLAMLPSVVQHGFKYVIGTUGVGAGAYVLAKFA LIFPDLVEGLULVINTDNGKSWIDAAATLLGGUGGAYVLAKFA LIFPDLVEGLULVINTDNGKSWIDAAATLGGUGGAGYVLAKFA LIFPDLVEGLULVINTDNGKSWIDAAATLGGUGGAGYVLAKFA LIFPGLVENNAKTRECPWILVVQDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLEQVTQPGKKLTEAFKYPLGGMGYMFSABMTLARS		<u>L</u>		
RSPSPLGRLQVLPRSPLHVHTHNSGKEVLGLQVQRSRSGTGPAC SQAGSCAVQGGMVCIF FLPMAALGPSSQNYTEYVVRVPKNTTKKYNIMAFNAADKVNFAT WNQARLERDLSNKKIYQEEEMPESGAGSFRYBKLREERRKKYG IVLKEPRPBOQPWLLKVMQKSGRKKFKGIKKGGVTENTSYYIFTQ CPDGAPEAPPVHNWYNFTPLARHRTLTAEEAEEEWERRNKVLNH FSIMQQRBLKDQDQDEDEEKKERGRKKKKGGUTENTSYYIFTQ CPDGAPEAPPVHNWYNFTPLARHRTLTAEEAEEEWERRNKVLNH FSIMQQRBLKDQDQDEDEEKKERGRKKKKKGSDEAFEDS DDGDFRGQRVJYMSDGSSSSGERPESKAKAPQGEGFKGVUDGG DSSEESEEKPPEDKKEEEEKKAPTPQEKKRKKKGKSDEAFEDS DDGSFRGGRVJYMSDGSSSSGERPESKAKAPQGEGFKGVUDGG DSSEESEEKPPEEDKEEEEKKAPTPQEKKRRKDSSEESDSSE ESDIDSEASSAFFWAKKKTFPKREERPSGGSSRGNSRFGTPSAE GGSTSSTLRAAASKLEGGKRVSEMPAARKLELDTGPGSLSGKST PQPPSGKTTPNSGDVGVTEDAVRYTKPMTTKDLLKKFGTKK TGLSSECTVNVLAQILKRLNPERKMINDKMHFSLKE FSLIGVSGLTSGRAVARDAGKAGAGAGFYFFVTHAFFWTTKDLKKFGTKK TGLSSECTVNVLAQILKRLNPERKMINDKMHFSLKE FSLIGVSGLTSDRGVTEDAWGTFATADGRPVCHLAKFGTKK TGLSSECTVNVLAQILKRLNPERKMINDKMHFSLKE FSLIGVSFLTSDRGIDGRRHNNGYGSTTFKVTADGRPVCHT TDEMAHPDRERIPERVVHAKGAGAFGYFFVTHDITKKYSKAKVFE HIGKKTPILAVRSTVAGEGSGADTVADPRGPAVKFYTEDGNWDL VGNNTPIFFIRDPILFPSFIHSQKRNPGTHLKDPDMWDFWSLR PESLIGVSFLTSDRGIDFDRGHRHNNGYGSTTFKVNANGRAVYCK FYHKTDGIKNLSVEDAARLSGGDPYGTRDLFNAIATGKYFSW TFYLQWMTFNOAETFPNPFDLTKVWPHKDYPLIFVCKLULINN PVNYFAEVEQIAFDPSNMPPGIEASPDWGNGGGADNYYPNSF GAPEQQPSALBHSIQYSGEVRRNTANDDNIVQNAFYVNVINE EQKRILCENLAGHLKDQJFIFQKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL DKYNAEKPKNAIHTFVQSGSHLAAREKANL DKYNAEKPKNAIHTFVQSGSHLAAREKANL DKYNAEKPKNAIHTFVQSGSHLAAREKANL FDLKCENLAGHLGGGGGSSGLAG SGSAGQYGSDQQHHLGSGSGAGTGGPAGAGGGAAGTAGVGE TGSGDAGGGKHTTVKTYIISPERRAMVDPQQKMELGIDLLA YGAKABLPKYKSFNRTAMPYGGVEKASKRMTYMPKY TGSGDAGGGGKHTTVKTYTISPERRAMVDPQQKMELGIDLLA YGAKABLPKYKSFNRTAMPYGGVEKASKRMTYMPKY POGYOFPSMEGLAAMLDSVVQHEGKKYUGUGAGAGYVLAKRA LIFPDLYBGLIAVNIDAATTLLSGLTSTLDPTVLSH LFSGRBLVNNTELVGSVRQGIGNVVNQAALOLFMMYNSRRDLD INREGTVPNNKTIRCVPUNLVVGDNAATCLSGUFGRAVULAKRA LIFPDLYBAKTLTEDGVGLTDNAAATCLSGUFTSTDPTVLSH LFSGRBLVNNTELVGSVRQGIGNVVNQAALOLFMYNSRRDLD INREGTVPNNKTIRCVPUNLVVGDNAATCLSGUFCNSLLDPTTTF FLKMADSGGLEQVTQPKKLTEROWUNDARATCLSCUFCNSLLDPTTTF FLKMADSGGLEQVTQPKKLTEROW	6583	487	41	RIFSMTSGRLRWRCTWRPATALWSASLRLGTSSMHPSPRSISLP
SQAGSQAVQGOWCIF 5584 189 1750 PIPMAALGPSSQNYTEYVVRVPKNTTKKYNIMAFNAADKVNFAT WNQARLERDLSNKKIYQEEMPESGAGSEFRRKLREBARKKYG IVLKEERPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQ CPDGAFEAFPVHNWYNFTPLARHRTLTABEAEEWERRNKVUNH FSIMQQRRINDQDQDEDEEKEKERGRKASELRIHDLEDDLENS SDASDASGBEGGRVPKAKKKAPLAKGGRKKKKKKGSDDEAFEDS DDGDFRGQEVDYMSDGSSSSQEBEPSKAKAPQQEEGFKVDEGS DSSEESEEKPPEEDKEEEEKKAPTPQEKKRKKSDDEAFEDS DSSEESEEKPPEEDKEEEEKKAPTPQEKKRRKDSSEEDSSE ESDIDSEASSAFFMAKKKTPFKEERKPSGGSSRONSRPGTPSAE GGSTSSTILRAASKLEGGKRVSBMPAARRILDIDTGGSLGKST PQPPSGKTTPNSGDVQVTEDAVRYTITRKPMTTKDLLKKFQTKK TGLSSQTVNVLAQTLKRLNPERKNINDKMFSLKE GFIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HMKEQRAAQKADVLTTGAGMPVGDKLNVITVGPRGPLLVQDVVF TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVPE HIGKKTPIAVRFSTVAGEGSGADTYRDPRGRAVKYTEDGNMDL VGMNTPIFFIRDPILFPSFIHSQKRNPQTHLKDDMVMDFWSLR PSELHQVSFLYSBGIPDGHRHMNGYGSHTFKLVWANKGBAYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TYYIQVMTFNQAETFPRNPPDLIKWPHKDYLIPVGKLVLINN PVNYFFEBVEQILAFPDSNMPPGIEASPDKMQGGAPNYYPNSF GAPEQQPSALHSIQYLSGEVRRFNTANDDNVTQVAFYVNVLNE EQKKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNABKFKNAIHTPVQSGSHLAARSKANL 6586 32 804 PLPEGPAESTSTMPVSGTPAPNKRKSSKLINBELTGGGQESSGL NLGKKISVPRIVMLEBLSLITNRGSKMFKIRQMRVEKFIYENNP DVVSDSSMDHFQKTLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQOHLHGSGSGAGATGAVGG TGSGDQAGGEKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKABLPKYKSFMRTAMPYGGVEKASKMFTQMRVEKFIYENNP DVVSDSSMDHFQKTLPTVGGQLTTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQOHLGSGSGLITKVFVYNGRSFKGNRPAILTY HDVGLMHKLCFNTFFNEDMGEITKHFVVCHVDAPGQQVGASOP PGGYGFSMEGLAMLDSVVQHOFKYVIGLIGVGAGAYVLAKFA LIFPDLVEGLIAVNIDDNGKGNIDMAATKLSGLISTLPDTVLSH LFSGEBLVNNTELVGSVRQQIGNVVNQAALQLFMATMANSRRDLD INREGTVPNAKTLRCPVMLVVQDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLEQVTQPSKKITELGGGVVECNSKLDDTTTT FLKMADSGGLEQVTQPSKLTPLGGGGVVECNSKLDDTTTT FLKMADSGGLEQVTQPSKLTPLGGGGVVECNSKLDDTTTT FLKMADSGGLEQVTQPSKLTPLGGGGVVECNSKLDDTTTT FLKMADSGGLEQVTQPSKLTPLGGGGVVECNSKLDDTTTT		}		1
1750 PLPMAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFAT WRQALLERDLSNKKTYQEEEMPEGGAGSEPNRKLREBARRKYG IULKEFPERDQPWLEVWRGKSGRFKGITKKGGTENTSYYTFTQ CPDGAPEAPPVRNWNFFFLARHRTLTAEBAEEWERRNKVLMH FSIMQQRILKQDQDDEDEEKEKRGRKASELRIHDLEDDLEMS SDASDASGEEGGRVPKAAKKAPLAKGGRKKKKKGSDDEAFEDS DDCDFFGGGVVDKAKKAPLAKGGRKKKKKGSDDEAFEDS DDCDFFGGGVVDKAKKAPLAKGGRKKKKKGSDDEAFEDS DDCDFFGGGVVDKGKSSSQSEPESKAKAPQQEEGPKGVDEGS GSESEEBEKPPEBEKEEEEKKAPTPOEKKRRKGSSEEDSSE ESDIDSEASSAFFMAKKTPPKRERKPGGGSRGNSRPGTPSAB GGSTSSTLFAAASKLEGGKRVSEMPAAKRILDTGFQSISGKST PQPPSGKTTPNSGDVQVTEDAVRTYLTRKFMTTKDLLKKPGTKK TGLSSSQTVNVLAQTLKKLNPERKNINDKHHFSLKE GFIRNSRIDDFVGGDFRABASCSVHAKKPADASROPASDQMQ HKEGRAAGKAUVLTTGAGNVGDKLNVTTVGDRGPLLVQUVVFT TDEMAHFDRERIPERVUHAKGAGAFGYFVFHIDITKYSKAKVEE HIGKKP1AVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNMDL VGNNTPIFPIRDPILFPSFIHGKRNPQTHLKDPDMWDPWSLR PESLHQVSFLPSDRGIPDGHRHMGYGSHTFKLVNANGBAVTCK FHYKTDGGIKNLSVEDAARLSQEDPDVGIRDLFNA LATGKYPSW TFYIQWTFNQAETFPFRPFDLTKVWPHKYPTLPVGKLVLNAN PUMYFABVBOLAFDESNMPJGIEASPDKMLQGRIAAVPTHRR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNTQVRAFYVNVLME EQRKRLCENIAGHLKNQIFTFYBAPDGHTMPYGGTLQALLD DKYNAEKPINATHTFVQSGSHLAAREKANL PLPEQPAESTSTMPVGGTJARQAFSYSKSNGRGGSQAGG SGSAGQYGSDQHHLKJSGSGAGGAAGTAGVGE TGSGQAGGGGGTHTVFYTYISPWERAMGVDPQCKMELGIDLLA YGAKAELPKINSFTHPTVGGQLGTTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQHHHJGSGSGAGGTAGAGTAGVGE TGSGQAGGGGGRHITVFYTYISPWERAMGVDPQCKMELGIDLLA YGAKAELPKINSFTHPTVGGQLGTTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQHHHJGSGSHLAAREKANL PLPEQPAESTSTMPVGGYEKASKRIMELTGGGQCSAGAGTAGVGE TGSGQAGGGGGRHITVFYTYISPWERAMGVDPQCKMELGIDLLA YGAKAELPKINSFNITAMPYGGYEKASKRIMFGMPKY DVFSDSSMHHFQKFLPGKYUTGIGVGGAAGAGTAGVGE TGSGQAGGGGGRHITVFFTYISPWERAMGVDPQCKAGSPF PQGYQFPSMEQLAAALPSVVQHFGFKYUTGIGVGAGAYVLAKFA LIPPDLVGCLULVINDPMKKGNIDMATKLSGSTTT,PDTVJSH LIPSGELVNNTELVQSYRQGIGNVVNQANLQLFKHMNNSRDLDL LNRGTVPNAKTLRCPVMLVVGQNATAKLSGCHTSTT,PDTVJSH LIPSGERLVNNTELVGSYRQGIGNVVNQANLAKLSGLTSTT,PDTVJSH LIPSGERLVNNTELVGSYRQGIGNVVNQANLALRASSMUTRL				RSPSPLGRLQVLPRSPLHVHTHNSGKEVLGLQVQRSRSGTGPAC
WNQARLERDLSNKKTYQEEEMPESGAGSEFNRKLREEARRKKYG IVLKEFREBOPWLLRVNGKSGRKFKGIKKGVTENTSYTIFTQ CPGAFEAPPYNINVNTFTLARITLTBEBAEEEWERNRVLNH FSIMQORRLKDQDODEBEEKEKGRKASELRIHDLEDDLEMS SDASDASGBEGGRVPKAKKAPLAKGGRKKKKKGDDEAFEDS DDGDFEGGEVDIMMSDGSSSSGEEPESKAKAPQOEEGFKGVDEGS DDSEESEBERKPPEEDKEEEEKKAPTPOEKKRKKKGSDEAFEDS ESDIDSEASSAFFMAKKKTPPKREKKPSGGSSRGNSPGTPSAB GGSTSSTLRAAASKLEGGKRVSBEPAKRIRLDTGPQSLSGKST PQPPGKTTPNSGDVQVTEDAVRRYLTKENTTTDLLKKRQTKK TGLSSZCTVNVLAQLILKRLINPERKNINDKHFISLKE 6585 3 1678 GFIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HWKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHIPDRRRIPERPRVHAKKGAFYFVEVHITTKYSKKAVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGPAVKFYTEDONNDL VGNNTPIFFIRDPILFPSFTHSQRRNVGTHLKNDAMFSULK FESLHQVSFLFSBROIPDOHRHMNOYGSHFKLVNANGBAVVCK FHYKTDOGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TPYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIFVGKLVLNRN PVMYFAEURQIAFDPSNNPPGILEASPDKMLQGRLFAYDDTHRIR LGPNYLHIPVNCPYRARVANYQRDGPMCMQNQGGAPNYYPNSF GAPEQOPSALBISIGYSGEVRFNTANDDNVTQWAPYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNABKPRNAIHTTVQSGSHLAAREKANL 6586 32 804 PJEEGPAESTSTPVGTPAFNYKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSMMHFGKFLPTVGGQLGTAGGGFSYSKSNGRGGSQAGG GGSAGGGGGGGGHTNATHTYTYS PMERAMGVDPQQKMELGIDLLA YGGKAGLPKYKSFNRTAMPYGGYEKSKSKMTFQMFVV 4GAKABLPKYKSFNRTAMPYGGYEKSKRKMTFOMPKV 4GAKABLPKYKSFNRTAMPYGGYEKSKSKMTFOMPKV 4GAKABLPKYKSFNRTAMPYGGYEKSKSKMTFOMPKV LIFPDLWELULVUNIDPMGKMIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSVRQQIGNVVNQANLQLFMNMYNSRDLD INREGTVPNAKTLRCPVMLVVQDNAADLQVENSKLDFTTTT FLKMADSGGLPQVTQFGKULVANQADADLQVENSKLDFTTTT FLKMADSGGLPQVTQFGKULVANGADADLQVENSKLDFTTTT FLKMADSGGLPQVTQFGKULVANGADADLQVENSKLDFTTTT FLKMADSGGLPQVTQFGKULVANGADADLQVENSKLDFTTTT FLKMADSGGLPQVTQFGKULVANGADADLQVENSKLDFTTTT FLKMADSGGLPQVTQFGKULTEAPKYFLGGGMYMPSASMITRLARS		ĺ		SQAGSGAVQGGNWCIF
IVLKEFRPEDQPWLLRVMGKSGRKFKGIKKGGVTENTSYYIFTQ CPDGAFEAFPVINWYNFTPLARHTLTABABEEWERRINVLMH FSIMQQRIKLDQDODEBEEWEKEKGRRKASELRIHDLEDDLEMS SDASDASGEEGGRVPKAKKAPLAKGGRKKKKKGSDDEAFEDS DDGDFFGGEVDYMSDGSSSSGEPESKAKAPQGEEGFKGVDEQS CSESEERKPPEEDKEEEEEKKAPTPQEKKRRKDSSEESDSSE ESDIDSEASSAFFMAKKKTPPKRERKPSGGSSGNGRRPGTPSAB GGSTSSTLRAAASKLEQGKRVSEMPAAKRILDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTDLLKKPQTKK TGLSSEQTVNVLAQTLKKLNPERKMINDKHHFSLKE GSTRSTIDAVLAQTLKKLNPERKMINDKHHFSLKE FURMAIFDRRRIPDERVGHEASCSVLHSKPHAMADSRDPASDQMQ HMKEQRAAQKADVLTTGAGNPVGDKLNVITVGRGPLLVQDVVF TDEMAIFDRRRIPDERVGHAKGAGAPGYFEVTHDITKYSKAKVPE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIFFIRDPILFPSFILISQKRNPQTHLKDPDMVWDFWSLR PESLHQVSFLFSDRGIPDJHRHMNGVGSHTFKLVMANGBAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIDTHRKYPSW PVMYFAEVEQIAFDPSNMPPGIEAS PDKMLGGRLFAVPDTHRRR LGPNYLHIPVNCPYRRVANYQRDGPMCMQDNQGAPNYYPNSF GAPEQQPSALEHSIGYSGEVARFATANDDNVTQVRAPYVNVLNE EQRKRLCENIAGHLKDAGIFTQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPRNAIHTFVQSGSHLAAREKANL 6586 32 804 PLEEGPAESTSTMPVSGTPANKKKSSKLIMBLTGGGQESSGL NLGKKISVPRDVMLEELSLLTINGGSKMFKLRQMKVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGGYGSDQHHLGSGSGAGGTGGPAGQAGRGAAGTAGVGE TGSGDQAGGGKHTTVFKTYISPMERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNTAMPYGGYEKASKMTFQMPKV 6587 75 1117 RRVPSSLGKMPECWDGEHDIETPYGLLHVVIRGSFKGNRPAILTY HDVGLNHKLCFNTFFNFEDMGEITTHFVVCHVDAPGQVGASGF PQGYQFPSMEQLAMLPSVVQHFGFKYVIGIGVCAGAYULAKFA LIFPDLVEGLVLVNIDDMGKGWIDMAATKLSGTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFMNMYSRRDLD INRPGTVPNAKTLRCPVMLVVQDAPADGOVGCRSLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS	6584	189	1750	PLPMAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFAT
CPDGAPEAPPUNWWNFTPLARHRTLTAEBAEEEWERRNKVLNH FSIMQQRRLKDQDQDBEBEKEKGRAKASELRIHDLEDDLEMS SDASABSGEGGEVPKAKKAPLAKGGRKKKKKKGSDDEAPFEIS DDGDFEGGEVDWNSDGSSSQEPESKARAPQQEEGFKGVDEQS DSSESEBEKPPBEDKEEEEKKAPTPQEKKRKKDSDESBESDE ESDIDSEASSAFFMAKKKTPPKKERKPSGSSRGNSRPGTPSAE GGSTSSTLRAAASKLEGGKRVSBMPAAKKLRLDTGFQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRYLTKPMTTKDLLKKFQTKK TGLSSSQTVNVLAQLLKRLNPERKMINDKMHFSLKE GGSTSSTLRAAASKLEGGKRVSBMPAAKKLRLDTGFQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRYLTKPMTTKDLLKKFQTKK TGLSSSQTVNVLAQLLKRLNPERKMINDKMHFSLKE GFIRNSRIDDFVGGDPRAEASCSVLHSKPPAMADSSDPASDGMQ HWKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHFDRERIPERVVHAKGAGAFGYFSVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVBDRGFAVKFYTEDGNMDL VGNNTPIPFITDPILPSPIFINGVRNPPQTHLKDPDMVMDFWSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGBAVYCK FHYKTDGIKNLSVEDAARLSQEDPDYGRDLFNAIATGKYPSW TFYICOMTFNOABTFFNPPDTLKVWPHKDYPLIPVGKLVLNNN PVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRIR LGPNYLHIPVNCFYRARVANYQRDGPMCMQDAGGARNYYPNSF GAPEQQPSALEHSIQVSGEVRRFNTANDDNVTQVRAFYVNVLNE EQKRLCENIAGHLKDAQIFIQKKAVKNPTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL GSSAGQYGSDQCHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGGKHITVFKTYISPWERAMGVDPQOKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKMTFQMPKV 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRSSKIJMBLTGGGQESSGL MLGKKISVPRDWALBELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSMDHFQKFLPTVGGQLTGAGGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKMTFQMPKV 6587 75 1117 RRVPSIGKMPECMDGEHDIETPYGLLHVVIRGSPKONRPAILTY HDVGLMHKLCFNTFFMFEDMQEITKHFVVCHVDAPGQQVGASQP PQGYPPSMEQLAAMLPSVVQHFFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVUNIDPNGKGWIDMAATKLSGLTSTLPDTVUSH LFSQELVNNTELVQSYRQQIGNVVNQANLQLFWNNYNSRRDLD INRPGTVPNAKTLRCPVMLVUGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKUTEAFKYPLOGMYMPSASMTLARS				WNQARLERDLSNKKIYQEEEMPESGAGSEFNRKLREEARRKKYG
FSIMQQRRLKDQDQDEDEEKEKRGRRKASELRIHDLEDDLEMS SDASDASGEGGRVPKAKKAPLAKGGRKKKKKGSDDEAFEDS DDGDFKGQEVDMSDGSSSSEPESKAKAPQEEGFKGVDEGS DSSEESEEKPPEEDKEEEEKKAPTPQEKKRRKDSSEESDSSE ESDIDSEASSAFFMAKKKTPPKERKPSGGSSRGNSPGTTPSAE GGSTSTLRAAASKLEQGKVSEMPAAKKIRLDTGFQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TGLSSZQTVNVLAQILKRLNPERKMINDKMHFSLKE 6585 3 1678 GPIRNSRIDDFVGGDPRABASCSVLHSKPPIAMDSKDPASDOMQ HWKEQRAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHFDRERIPERVVHAKGAGAFGYFBVTHDITTYSKAKVFE HIGKKYPIAVRFSTVAGEGSADTVKDPRGFAVKFYTEOGNINDL VGNNTPIPFIRDPILPPSFIHSQKRNPQTHLKDPDMVMDFWSLR PESLHQVSTLFSDRGITPDGHRHMNGYGSHTFKLVNANGBAVYCK FHYKKTDGIKINLSVEDAARLSQBDPDYGIRDLFNATATKKYPSW TFYIQVMTFNQAETFPNPFDLTKVWPHKDYPLIPVGKLVLNRN PVMYFAEVECIAFDPSNMPPGIEASPDMMLGGRLFAYPDTHRRR LGPNYLHIPVNCYPRARVANYQRDGPMCMGDAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDVGSHIQALL DKYNAEKPNSAIHTFVQSGFMAMPGAGAFGYSKSNGGGSGSGAG GSGAGQYGSDQHHLGSGSGAGGTGGPAGQAGGGAAGTAGVGE TGSGDQAGGGKHITVFKYTISFWERAMGVPQCWELGIDLLA VGAKABLFYKKSFNTAMPTGGYEKASKRMFLGRWEKFIYENHP DVPSDSMMHFFGVFLFTVGGGVEKASKRMFTGMFKU 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGINHKLCFNTFFFFEMQGITKHFQWFKUFGGYGAGAYLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVQAALQLEWNNYNSRRDLD INRPGTVPNAKTLRCPVMLVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				IVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQ
SDASDASGEEGGRVPKAKKKAPLAKGGRKKKKKKGSDDEAFEDS DDGDFEGQEVDYMSDGSSSQEPESKARAPQQEEGPKGVDEQS DSSEESEEKPPEEDKEEEKKAPTQGEKKRKDSSESDSSE ESDIDSEASSAFFMAKKKTPPKRERKPSGGSSRGNSRPGTPSAE GGSTSSTLRAAASKLEGGKRVSEMPAKRLILDTOPQSLSGKST PQPPSGKTTPNSGDVQVTPDAVRRYLTRKPMTKDLLKKPQTKK TGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE GSBS 3 1678 GFIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDGMQ HMKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHPDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNNDL VGNNTPIFFIRDPILFPSFILAGKRNPQTHLKDPDMVNDFWSLR PESLHQVSFLFSDRGIPDGHRHMMGYGSHTFKLVMANGEAVYCK FHYKTDGGIKNLSVEDAARLSQEDPDYGTRDLFNALATGKYPSW TFYIQWMTRAQAETFPRNPFDLTKVWPHKDYPLIPVGKLVLNRN PVMYFAEVEGLAFPPSNMPPGIEASPDKMLGGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRFFATANDDNTYQVRAFYVNVLNE EQRKILCENTLAGHLKDAQIFICKKAVKMFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMFVSGTPAFNKKKSSKLIMELTGGGGESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLQMRVEKFIYENHP DVFSDSSMDHFQKKPLPTVGGQLGTAGGGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKABLPKYKSFNRTAMPYGGYEKASKRMTFQMFKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLMHKLCFNTFFNTEDDMGITKHFVVCHVDAPGQQASGF PQGYFPSMSGLAMMLPSVVQHFGFKYVIGIGVGGAGYVIAKFA LIFPDLVEGLVLVNIDPNGKGWIDMAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWMNYNSRRDLD INRPGTVPNAKTLRCPWALVVQANDALDLFWMNYNSRRDLD INRPGTVPNAKTLRCPWALVVQANDALDLFWMNYNSRRDLD INRPGTVPNAKTLRCPWALVVQANDALDLFWMNYNSRRDLD INRPGTYDVARATLRCPCWALVVQANDALDLFWMNYNSRRDLD INRPGTYDVARATLRCPCWALVVQANDALDLFWMNYNSRRDLD INRPGTYDVARATLRCPCWALVVQANDALDLFWMNYNSRRDLD INRPGTYDVARATLRCPCWALVVQANDALDLFWMNYNSRRDLD INRPGTYDVARATLRCPCWALVVQANDALDLFWMNYNSRRDLD INRPGTYDVARATLRCPCWALVVQANDALDLFWMNYNSRRDLD INRPGTYDNAKTLRCPCWALVVQANDALDLFWMYNSRRDLD			, .	CPDGAFEAFPVHNWYNFTPLARHRTLTAEEAEEEWERRNKVLNH
DDGDFEGQEVDYMSDGSSSQEEPESKAKAPQQEEGPKGVDEQS DSSEESEERKPPEEDKEEEKKAPTQEKKRRKDSSEESDSE ESDIDISEASSAFMAKKKTPYKREKPSGGSGRGNSFGTPSAE GGSTSSTLRAAASKLEQGKRVSEMPAAKRLRLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTKKPMTTKDLLKKFQTKK TGLSSEGTVMVLAQTLKKLNPERKMINDKMHFSLKE 6585 3 1678 GFIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HMKEQRAAQKADVLITTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHPDRRRIPBRVVHAKGAGAPGYPEVTHDITKYSKAKVPE HIGKKTPIAVRFSTVAGESGSADTVRDPRGPAVKFYTEDGNMDL VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVMDFWSLR PESLHQVSFIPSDRGIPDGHRMNGVGSHTFKLWNANGBAVTCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TYYIQWMTFRQAETFPRNPFDLTKWPHKDYFLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPDGIRASPDKMLQGRLFAYPDTHRHR LGFNYLHIPVNCCYRRAVANYQRDGMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFICKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKKSSKLIMBLTGGGGESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGGLGTAGQFFSYSKSMGRGGSQAGG SGSAGQYGSDQQHLLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDAGGEGKHITVFKTYISPWERAMGUPDQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLMHKLCFNTFFNFEDMGEITTHFVVCHVDAPGQQGASGF PQQYFFSMSGLAAMLPSVQHFGFKYVIGIGVGGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDMAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVQANLQLFMMYNSRRDLD INRPGTYPNAKTLRCPWALVVQANDANLQLFMMYNSRRDLD INRPGTYPNAKTLRCPWALVVQANDANLQLFMMYNSRRDLD INRPGTYPNAKTLRCPWALVVQANDANLQLFMMYNSRRDLD INRPGTYPNAKTLRCPWALVVQANDANLQLFMMYNSRRDLD INRPGTYPNAKTLRCPWALVVQANDANLDLFMMYNSRRDLD INRPGTYPNAKTLRCPWALVVQANDANLOLFMMYNSRRDLD INRPGTYPNAKTLRCPWALVVQANDANLOLFMMYNSRRDLD INRPGTYPNAKTLRCPWALVVQANDANLOLFMMYNSRRDLD INRPGTYPNAKTLRCPWALVVQANDANLOLFMMYNSRRDLD INRPGTYPNAKTLRCPWALVVQANDANLOLFMMYNSRRDLD				FSIMQQRRLKDQDQDEDEEEKEKRGRRKASELRIHDLEDDLEMS
DSSESSEKKPPEEDKEEEEKKAPTPQEKKRRKDSSEESDSSE ESDIDEASSAFMAKKTPPRKERKPSGSSRONSREPTBSAE GGSTSSTLRAASKLEQGKRVSEMPAAKRIRLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TGLSSEQTVNVLAQTLKKLNPERKMINDKHHFSLKE 6585 3 1678 GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQWQ HWKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHPDRRIPERVVHAKGAGAFGYFEVTHDITKYSKAKVPE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIPFIRDPILFPSFIHSQKRNPQTHLKDPDMVMDFWSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGBAVYCK FFYKTDQGIKNLSVFDAARLSGDPDPYGIRDLFKAIATGKYPSW TFYYLQVMTFNQAETFPFPDFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHR LGFNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGADNYYPNSF GAPEQQPSALBHSIQYSGEVRFNTANDDNVTQVRAFYVNVLNE ECKRILCENIAGHLKDAQIFICKKKKSSKLIMELTGGGQESSGL NLGKKISVFRDVMLEELSLLTNRGSKMFKLRQMKVEKFIYENHP DVFSDSSMDHFQKFLPTVGGGLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGTGGPAGQAGGAAGTAGVGE TGSGDQAGGEKHITVFTYYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPEKWDGEHDIETPYGLHVVLRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMGEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAVVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQERLVNNTELVQSYRQQIGGVVVQANLGFMYNKRRDLD INRPGTVPNATTLRCPVMLVVGDNAPAEDGGVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMYMPSASMTRLARS				SDASDASGEEGGRVPKAKKKAPLAKGGRKKKKKKGSDDEAFEDS
ESDIDSEASSAFFMAKKKTPPKRERKPSGGSSRGNSRPGTPSAE GGSTSSTLRAAASKLEQGKRVSEMPAAKRIRLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLKKFQTKK TGLSSEQTVNVLAQILKRLNPERKMINDKNHFSLKE 6585 3 1678 GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HMKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHFDRRIPEREVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIFFIRDPILFPSFIHSGKRNFQTHLKDPDMVNDFWSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGBAVYCK FHYKTDQGIKNLSVEDARALSGEDPDYGIRDLFMAIATGKYPSW TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSNNPPGILASPDKNLQGRLFAYPDTHHRH LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGADPNYYPNSF GAPEQQPSALEHSIQYSGEVRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGFLASPDKNLGGGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQGGGTAGGGGFSYSKSNGRGGSQAGG GSGAGQYGSDQHHGAGSGAGTGGPAGGAGTAGVGE TGSGDQAGGEKHTTVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMFKV 1017 RRVPSLGKMPEKDDGHDIETFYGLHVVIKGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVQHFGFKVVIGIGVGAGAVVLAKFA LIFPDLVGGLLVNIDPNGKGNIDMATKLSGLTSTLPDTVLSH LFPDLVGGLLVNIDPNGKGNIDMATKLSGLTSTLPDTVLSH LFPGLEVUNLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVVTQPGKLTEAFKYPLQGMGYMPSASMTRLARS				DDGDFEGQEVDYMSDGSSSSQEEPESKAKAPQQEEGPKGVDEQS
GGSTSSTLRAAASKLEQGKRVSEMPAAKRLRLDTGPQSLSGKST PQPPSGKTTPNSGDVQVTEDAVRYILTRKPMTTKDLLKKFQTKK TGLSSEQTVNVLAQILKRLMPERKMINDKMHFSLKE 6585 3 1678 GFIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HMKEQRAAQKADVLTTGAGMPVGDKINVITVGPRGPLLVQDVVF TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGEGGSADTVRDPRGFAVKFYTEDGNNDL VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR PESLHQVSFLFSDRGIPDGHRHMGYGSHTFKLWNANGEAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFMAIATGKYPSW TTYIQVMTFNQAETFFNPPDLTKVWPHKDYFLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPGIBAS PDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRFRTNANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGQGESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYEMPP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQCHHLGSGSGAGGTGGPAGQAGRGAAGTAGVGE TGSGDQAGGEKHITVFKTYISPMERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKKMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGRRPAILTY HDVGLNHKLCFNTFPNFDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKSWIDWAATKLSGLTSTLDDTVLSH LFSGELVNNTELVQSYRQQIGNVUNQANLQLFWMNNSRRDLD INRPGTVPNAKTLRCFVMLVVGDNAPAEDGCVVECNSKLDPTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				DSSEESEEKPPEEDKEEEEEKKAPTPQEKKRRKDSSEESDSSE
PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TGLSSEGTVNVLAQILKRINPERKMINDKMFSLKE 6585 3 1678 GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HMKEQRAAQKADVLTTGAGRPVGBKLNVITVGPRGPLLVQDVVF TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGRWDL VGNNTPIFFIRDPILFPSFIHSQKENPQTHLKDPDMVWDFWSLR PSSLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TTYIQVMTFNQAETFFFNPFDLTKVWPHHDYPLIPVGKLVLINRN PVMYFAEVEQ IAFDPSNMPPGIEAS PDKMLQGRLFAYPDTHHRR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALERSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYEMHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSQDQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGKABELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNRKLCFNTFFFFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLUVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMFSASMTRLARS		ļ		ESDIDSEASSAFFMAKKKTPPKRERKPSGGSSRGNSRPGTPSAE
TGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE 6585 3 1678 GFIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HKKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHFDRRRIPERVUHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR PESLHQVSFLFSDRGIPDGHRHMMGYGSHTFKLVNANGBAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDVGIRDLFNAIATGKYPSW TFYIQVMTFNQAETFPRNPFDLTKVWPHKDYPLIPVGKLVLNRN PVMYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHEHR LGPNYLHIPVNCPYRRAVANYQRDGPMCMQDNQGGAPNYYNDSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE ECRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDVGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGGGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDDRGKGNIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVQDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMFSASMTRLARS				GGSTSSTLRAAASKLEQGKRVSEMPAAKRLRLDTGPQSLSGKST
GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ HMKEQRAAQKADVLTTGAGNPVGDKLAVVITVGPRGPLLVQDVVF TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGMWDL VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR PESLHQVSFLFSDRGIPDGHRHMMGYGSHTFKLVNANGBAYYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TFYIQVMTFNQAETFPRNPFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQVSGEVRRFNTANDDNVTQVRAPYVNVLNE EQKKLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLTNRGSKHFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQBITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDDRGKGNIDMAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVQDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS		. , ,	'	
HMKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGIWDL VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR PESLHQVSFLFSDRGIPDGHRHMMGYGSHTFKLVMANGBAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLINRN PVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSKLIMBLTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGGKHITVFTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECVBGEHDIETPYGLLHVVLRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVBGLVLNNIDENGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEKLVNNTELVQSYRQQIGNVVNQANLQLFWMYNSRRDLD INRPGTVPNAKKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS			1:	
TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLWANAGBAYYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFMAIATGKYPSW TFYIQVMTFNQAETFPRNPFDLIKVWPHKDYPLIPVGKLVLNRN PVNYFASURQIAFDPSNMPPGIEAS PDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEBLSLLTNRGSKMFKLRQMRVEKFIVENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHTTVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYGFSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEKLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS	6585	3	1678	
HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR PESLHQVGFLFSDRGIPDGHRHMMGYGSHTFKLVNANGBAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAHTTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMFVSGTPAPNKKRKSSKLIMBLTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSMGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGTGGPAGQAGRGAAGTAGVGE TGSGDQAGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPXYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYYIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPMGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFNNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS			1	1
VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGBAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TFYIQVMTFNQAETFPRNPFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSKLIMBLTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMKVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWMMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				
PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPBQPAESTSTMPVSGTPAPNKKRKSSKLIMBLTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TCSGDQAGGECKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS			1:	
FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPGIEAS PDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNYQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMBLTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVGGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS			! :	
TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN PVNYFAEVEQIAFDPSNMPPGIEAS PDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLITNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLINHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				1
PVNYFAEVEQIAFDPSNMPPGIEAS PDKMLQGRLFAYPDTHRHR LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEKLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS		:		
LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMBLTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYOFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS		• :	: '	
GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMBLTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGGGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS			1	· · · · · · · · · · · · · · · · ·
EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGNIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				
DKYNAEKPKNAIHTFVQSGSHLAAREKANL 6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGNIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				
6586 32 804 PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TCSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				
NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				
DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEBLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS	6586	32	804] - · · · • · · · · · · · · · · · · · · ·
SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				i -
TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS		1		· · · · · · · · · · · · · · · · · · ·
YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV 6587 75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				
75 1117 RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				
HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				
PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS	6587	75	1117	
LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH LFSQEKLVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				1
LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA
INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH
FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS				LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD
		1		INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT
RTASLTSASSVDGSRPQACTHSESSEGLGQVNHTMEVSC				FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS
	L	<u></u>		RTASLTSASSVDGSRPQACTHSESSEGLGQVNHTMEVSC

Γ.	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
- 1		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
-		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	_	\=possible nucleotide insertion)
	6588	137	501	LGLQAQLLELRTNNYQLSDELRKNGVELTSLRQKVAYLDKEFSK
ı				AQKALSKSKKAQEVEVLLSENEMLQAKLHSQEEDFRLQNSTLMA
				BFSKLCSQMEQLEQENQQLKEGAAGAGVAQAGP
Г	6589	2	1405	RPWGSAMATFSRQEFFQQLLQGCLLPTAQQGLDQIWLLLAICLA
ı				CRLLWRLGLPSYLKHASTVAGGFFSLYHFFQLHMVWVVLLSLLC
-				YLVLFLCRHSSHRGVFLSVTILIYLLMGEMHMVDTVTWHKMRGA
1				QMIVAMKAVSLGFDLDRGEVGTVPSPVEFMGYLYFVGTIVFGPW
-				ISFHSYLQAVQGRPLSCRWLQKVARSLALALLCLVLSTCVGPYL
				FPYFIPLNGDRLLRNKKRKARGTMVRWLRAYESAVSFHFSNYFV
i				GFLSEATATLAGAGFTEEKDHLEWDLTVSKPLNVELPRSMVEVV
	}			TSWNLPMSYWLNNYVFKNALRLGTFSAVLVTYAASALLHGFSFH
				LAAVLLSLAFITYVEHVLRKRLARILSACVLSKRCPPDCSHQHR
	. 1			LGLGVRALNLLFGALAIFHLAYLGSLFDVDVDDTTBEQGYGMAY
\perp				TVHKWSELSWASHWVTFGCWIFYRLIG
	6590	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR
-				GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY
	•			GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY
	- 1			VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR
-				RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKNYEFLKSKREB
1				FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG
				KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL
1	l			SPTSENNKKLFNDLFKNNANRAENTERKQNQNYFMEVMTVEGVY
1	Ī			DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL
				EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM
	*			MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI VIQELFPELNKVQKEVTSVTSWM
-	6591	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR
1	1	21,1	838	GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTIMEGAMLPNY
				GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY
			•	VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR
1	;			RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKNYEFLKSKREE
1	.		•	FQBYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG
	ŀ	1	•	KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL
1	: [·		SPTSENNKKLPNDLFKNNANRAENTERKONONYFMEVMTVEGVY
	- 1			DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL
1	· I			EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM
;		ł		MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI
L				VIQBLFPELNKVQKEVTSVTSWM
	6592	3	1861	APEFLGSTISSGSMIDANLKLLQEAEQRLKAIVAEKFAIATKEG
				DLPQVERFFKIFPLLGLHEEGLRKFSEYLCKQVASKAEENLLMV
	1			LGTDMSDRRAAVIFADTLTLLFEGIARIVETHQPIVETYYGPGR
	I			LYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQFRHVQNNLMRNS
1	ŀ			TTEKIEPRELDPILTEVTLMNARSELYLRFLKKRISSDFEVGDS
				MASEEVKQEHQKCLDKLLNNCLLSCTMQELIGLYVTMEEYFMRE
	ŀ			TVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGRALSSSSIDCL
-	l			CAMINLATTELESDFRDVLCNKLRMGFPATTFQDIQRGVTSAVN
				IMHSSLQQGKFDTKGIESTDEAKMSFLVTLNNVEVCSENISTLK
	Í	1		KTLESDCTKLFSQGIGGEQAQAKFDSCLSDLAAVSNKFRDLLQE
		İ		GLTELNSTAIKPQVQPWINSFFSVSHNIEEEEFNDYEANDPWVQ
1		i		QFILNLEQQMAEFKASLSPVIYDSLTGLMTSLVAVELEKVVLKS
	- 1			TFNRLGGLQFDKELRSLIAYLTTVTTWTIRDKFARLSQMATILN
		İ		LERVTEILDYWGPNSGPLTWRLTPAEVRQVLALRIDFRSEDIKR
<u></u>		·		LRL
'	6593	3	1837	EAFSAGSRRRGLALQRGVLGGLGGYCPCCCRRRGRLLVLLLLVR
1		į		RGGEGGGRGRGDKRRRRQARRQRRRPEPAEARGGKMADVLSVL
L_		·		RQYNIQKKEIVVKGDEVIFGEFSWPKNVKTNYVVWGTGKEGQPR

0770	T 50 - 22		<u></u>
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
l NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
}	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł		residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			EYYTLDSILFLLNNVHLSHPVYVRRAATENIPVVRRPDRKDLLG
ĺ			YLNGEASTSASIDRSAPLEIGLQRSTQVKRAADEVLAEAKKPRI
			EDEECVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIAA
			IKAKIMAKKRSTIKTDLDDDITALKQRSFVDAEVDVTRDIVSRE
]	j		RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAPN
Į.			AAPVDPTLRTKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTYH
ĺ			GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRTP
ŀ			IIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENETL
			IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFVQ
			GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQKW
			DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF
6594	1	1096	EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWSA
			DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIBERYGKDLL
		J	NLSRKKPCGQSEINTLKRALEVFKQQVDNVAQCHIQLAQSLREE
			ARKMEEFREKQKLQRKKTELIMDAIHKQKSLQFKKTMDAKKNYE
			QKCRDKDEAEQAVSRSANLVNPKQQEKLFVKLATSKTAVEDSDK
ļ	,		AYMLHIGTLDKVREEWQSEHIKACEAFEAQECERINFFRNALWL
ŀ			HVNQLSQQCVTSDEMYEQVRKSLEMCSIQRDIEYFVNQRKTGQI
			PPAPIMYENFYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP
			NYSLVDDYSLLYQ
6595	57	781	PLGTMSDSDLGEDEGLLSLAGKRKRRGNLPKESVKILRDWLYLH
			RYNAYPSEQEKLSLSGQTNLSVLQICNWFINARRRLLPDMLRKD
}		- 9	GKDPNQFTISRRGGKASDVALPRGSSPSVLAVSVPAPTNVLSLS
		,	VCSMPLHSGQGEKPAAPFPRGELESPKPLVTPGSTLTLLTRAEA
		;	GSPTGGLFNTPPPTPPEQDKEDFSSFQLLVEVALQRAAEMELQK
			QQDPSLPLLHTPIPLVSENPQ
6596	2	1026	PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIBAMAAIY
,			GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP
		N. 1	PIYQLNAPWLKGQERADLSNSLBEIYIQNIGESILYLWVEKIRD
			VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD
			FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
	1		KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA
			AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN
CEAR			ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
6597	2	1026	PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY
•			GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP
			PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD
	1		VLIQKSQMTEPGPDVKKKTEEEDVBCEDDLILACQPESSVKALD
			FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
			KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA
			AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN
CE22	1000		ILVEKNYTNSPBESSKALGKNKKVRKDKKRNEH
6598	1099	419	PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL
	,		VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE
			LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV
			FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS
			DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD
			SKGLQS
	164	1593	KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR
6599		1	MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS
6599			
6599			DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST
6599			
6599			DPQKKTVC1YGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST
6599			DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMBESGSEGLDE
6599			DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE
6599			DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
	<u> </u>		VVGEQVTSYLTKKFAELRSPNEFKVYMGHGGKPWVSDFSHPHYL
			AGRRAMKTVFGVEPDLTREGGSIPVTLTFQEATGKNVMLLPVGS
1			ADDGAHSQNEKLNRYNYI EGTKMLAAYLYEVSQLKD
6600	2	934	PGRLFRVAAMESAGLEQLLRELLLPDTERIRRATEQLQIVLRAP
		•	AALSALCDLLASAADPQIRQFAAVLTRRRLNTRWRRLAAEQRES
			LKSLILTALQRETEHCVSLSLAQLSATIFRKEGLEAWPQLLQLL
			QHSTHSPHSPEREMGLLLLSVVVTSRPEAFQPHHRELLRLLNET
]			LGEVGSPGLLFYSLRTLTTMAPYLSTEDVPLARMLVPKLIMAMQ
			TLIPIDEAKACEALBALDELLESEVPVITPYLSEVLTFCLEVAR
	•		NVALGNAIRIRILCCLTFLVKVKSKALLKNRLLATLAAHPFPHC
1			GC .
6601	529	1420	PRAAARAPPPAVLRRDRRAATAPGAGEMTLHGPLAQRYFLNHIE
			KITTWQDPRKAMNQPLNHMNLHPAVSSTPVPQRSMAVSQPNLVM
			NHQHQQQMAPSTLSQQNHPTQNPPAGLMSMPNALTTQQQQQQKL
1			RLQRIQMERERIRMRQEELMRQBAALCRQLPMEAETLAPVQAAV
			NPPTMTPDMRSITNNSSDPFLNGGPYHSREQSTDSGLGLGCYSV
			PTTPEDFLSNVDEMDTGENAGQTPMNINPQQTRFPDFLDCLPGT
			NVDLGTLESEDLIPLFNDVESALNKSEPFLTWL
6602	127	617	LLDFPALPKFVLAQSPKAGKPSTMTSMTQSLREVIKAMTKARNF
i i			ERVLGKITLVSAAPGKVICEMKVBEEHTNAIGTLHGGLTATLVD
			NISTMALLCTERGAPGVSVDMNITYMSPAKLGEDIVITAHVLKQ
·			GKTLAFTSVDLTNKATGKLIAQGRHTKHLGN
6603	79	660	PVGPSSLAARTGLGHLPFLHRLASSRGLDMDLLQFLAFLFVLLL
•			SGMGATGTLRTSLDPSLEIYKKMFEVKRREQLLALKNLAQLNDI
	:		HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGPFPQDEKLKD
		•	AFSHVVENTAFFGDVVLRFPRIVHYYFDHNSNWNLLIRWGISFC
			NQTGVFNQGPHSPILSLM
6604	3	688	TSTAQRQGGERMSFRGGGRGGFNRGGGGGFNRGGSSNHFRGGG
		•	GGGGGGNFRGGGRGGFGRGGGRGGFNKGQDQGPPERVVLLGEFL
	: '		HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFGQLR
			DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQRFLPRPPGEK
			GPPRGGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
	<u>_</u>		GGFRGRGH
6605	/	848	SGSRRGAMRAAGVGLVDCHCHLSAPDFDRDLDDVLEKAKKANVV
· [,	ALVAVAEHSGEFEKIMQLSERYNGFVLPCLGVHPVQGLPPEDQR
1 : 1		•	SVTLKDLDVALPIIENYKDRLLAIGEVGLDFSPRFAGTGEQKEE
1 1			QRQVLIRQIQLAKRLNLPVNVHSRSAGRPTINLLQEQGAEKVLL
			HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGQQKLVKQLPLTSIC
			LETDSPALGPEKQVRNEPWNISISAEYIAQVKGISVEEVIEVTT
6606	2	1692	QNALKLFPKLRHLLQK
1 2008	2	1682	FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS
.			KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE
			KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR
			SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLEEYVHKRYPGL
]	1		VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP
	1		VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM
1	ļ		YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG
j í	l		MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI
1	ļ		GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER
Į l	l		RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC
			LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP
] [ł		DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG
6607	137	000	RCLEVBNRGLAGIDLILRSCTGQRWTIKNSIK
""	13/	986	VPACAGLKKEARSLIASPPRLINTKLQASCRALFSPPIQSRQTT
	ļ		GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD
L			KIEDELEMTMVCHRPEGLEQLEAQTNFTKRELQVLYRGFKNECP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	- '	\=possible nucleotide insertion)
			SGVVNEDTFKQIYAQFFPHGDASTYAHYLFNAFDTTQTGSVKFE
1			DFVTALSILLRGTVHEKLRWTFNLYDINKDGYINQEEMMDIVKA
			IYDMMGKYTYPVLKEDTPRQHVDVFFQKMDKNKDGIVTLDEFLE
İ			SCQEDDNIMRSLQLFQNVM
6608	224	1140	RPCFSSPTGLCPRLSYPMILLQHAVLPPPKQPSPSPPMSVATRS
		1	TGTLQLPPQKPFGQEASLPLAGEEELSKGGEQDCALEELCKPLY
			CKLCNVTLNSAQQAQAHYQGKNHGKKLRNYYAANSCPPPARMSN
			VVEPAATPVVPVPPQMGSFKPGGRVILATENDYCKLCDASFSSP
l			AVAQAHYQGKNHAKRLRLAEAQSNSFSESSELGQRRARKEGNEF
			KMMPNRRNMYTVQNNSGPYFNPRSRQRIPRDLAMCVTPSGQFYC
		1	SMCNVGAGEEMEFRQHLESKQHKSKVSEQRYRNEMENLGYV
6609	1	443	FRLRCRRFRVAGGRLAGAGLRESRVPAPEQRLSALTLLSWSAVT
			PAAEPGNFQLSPAEPRGPLASPVRAAPRAPCPAAEMSELNTKTS
		·	PATNQAAGQEEKGKAGNVKKAEEBEEIDIDLTAPETEKAALAIQ
			GKFRRFQKRKKDPSS
6610	319	881	GRKSLCNLHIFIRFPLTYPDMYMGMMCTAKKCGIRFQPPAIILI
			YESEIKGKIRQRIMPVRNFSKFSDCTRAAEQLKNNPRHKSYLEQ
			VSLRQLEKLFSFLRGYLSGQSLAETMEQIQRETTIDPEEDLNKL
		ļ	DDKELAKRKSIMDELFEKNQKKKDDPNFVYDIEVEFPQDDQLQS
			CGWDTESADEF
6611	978	212	PGCSGAGSRVWWLPALRHLAMGSTESSEGRRVSFGVDEEERVRV
Ĭ			LQGVRLSENVVNRMKEPSSPPPAPTSSTFGLQDGNLRAPHKEST
}			LPRSGSSGGQQPSGMKEGVKRYEQEHAAIQDKLFQVAKREREAA
			TKHSKASLPTGEGSISHBEQKSVRLARELESRBAELRRRDTFYK
ļ.			EQLBRIERKNAEMYKLSSEQFHEAASKMESTIKPRRVEPVCSGL
			QAQILHCYRDRPHEVLLCSDLVKAYQRCVSAAHKG
6612	1724	992	VSTHASALSRTQGQPQRQPRAAASGAGAGTAGGGGSGGAEGSKM
			STEAQRVDDSPSTSGGSSDGDQRESVQQEPERBQVQPKKKEGKI
1			SSKTAAKLSTSAKRIQKELAEITLDPPPNCSAGPKGDNIYEWRS
ľ			TILGPPGSVYEGGVFFLDITFSPDYPFKPPKVTFRTRIYHCNIN
	•	4 :	SQGVICLDILKDNWSPALTISKVLLSICSLLTDCNPADPLVGSI
		<u> </u>	ATQYMTNRAEHDRMARQWTKRYAT
6613	130	748	ELELSSNMPEQSNDYRVAVFGAGGVGKSSLVLRFVKGTFRESYI
Ī.			PTVEDTYRQVISCDKSICTLQITDTTGSHQFPAMQRLSISKGHA
			FILVYSITSRQSLEELKPIYEQICEIKGDVESIPIMLVGNKCDE
		· ·	SPSREVQSSEAKALARTWKCAFMETSAKLNHNVKELFQELLNLE
	<u> </u>		KRRTVSLQIDGKKSKQQKRKEKLKGKCVIM
6614	3	1191	SSAAEAMRVLVRRCWGPPLAHGARRGRPSPQWRALARLGWEDCR
[DSRVREKPPWRVLFFGTDQFAREALRALHAARENKEEELIDKLE
			VVTMPSPSPKGLPVKQYAVQSQLPVYEWPDVGSGEYDVGVVASF
1		1	GRLLNEALILKFPYGILNVHPSCLPRWRGPAPVIHTVLHGDTVT
1			GVTIMQIRPKRFDVGPILKQETVPVPPKSTAKELEAVLSRLGAN
]			MLISVLKNLPESLSNGRQQPMEGATYAPKISAGTSCIKWEEQTS
-			EQIFRLYRAIGNIIPLQTLWMANTIKLLDLVEVNSSVLADPKLT
Ì		i	GQALIPGSVIYHKQSQILLVYCKDGWIGVRSVMLKKSLTATDFY
	<u> </u>		NGYLHPWYQKNSQAQPSQCRFQTLRLPTKKKQKKTVAMQQCIE
6615	832	35	GRVGAGASAMSELPGDVRAFLREHPSLRLQTDARKVRCILTGHE
]			LPCRLPELQVYTRGKKYQRLVRASPAFDYAEFEPHIVPSTKNPH
1.			QLFCKLTLRHINKCPEHVLRHTQGRRYQRALCKYEECQKQGVEY
}	1		VPACLVHRRRREDOMDGDGPRPREAFWEPTSSDEGGAASDDSM
			TDLYPPELFTRKDLGSTEDGDGTDDFLTDKEDEKAKPPREKATD
			EGRRETTVYRGLVQKRGKKQLGSLKKKFKSHHRKPKSFSSCKQS
			G
6616	-347	1886	LLPPCQGARPLSSPPHASEDNLFLFWNCILCAFPHPSPQPLQYP
1		1	VWPLLLVITQIPAPRHLRNRPFSFSRGGLDSFSGSLSTPSICRS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
, ~ 1	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			PAWVKMAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSP
			PPQPHPCHTCRGLVDSFNKGLERTIRDNFGGGNTAWEEENLSKY
1			KDSETRLVEVLEGVCSKSDFECHRLLBLSEBLVESWWFHKQQEA PDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGOCEG
1		1 1	EGTRGGSGHCDCQAGYGGEACGQCGLGYFEAERNASHLVCSACF
1 1			GPCARCSGPEESNCLOCKKGWALHHLKCVDIDECGTEGANCGAD
	·		QFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKC
1 1			LDVDECETEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQ
1 1			IPESAGFFSEMTEDELVVLQQMFFGIIICALATLAAKGDLVFTA
			IFIGAVAAMTGYWLSERSDRVLEGFIKGR
6617	118	673	VWMAWQVSLLELEDRLQCPICLEVFKESLMLQCGHSYCKGCLVS
			LSYHLDTKVRCPMCWQAVDGSSSLPNVSLAWVIEALRLPGDPEP
	· ;		KVCVHHRNPLSLFCEKDQELICGLCGLLGSHQHHPVTPISTVCS
1 1			RMKEELAALFSELKQEQKKVDELIAKLVKNRTRIDGSAPSLCPC
		·	LGPATFTFL
6618	548	136	DGKVARRAPNSPAFQNDIYPLVSAPRATTAESPWSKVLQNTQCR NVPKMTSERSRIPCLSAAAAEGTGKKOOBGRAMATLDRKVPSPE
			AFLGKPWSSWIDAAKLHCSDNVDLEEAGKEGGKSREVMRLNKEA
1			WKYGT
6619	246	842	PASSEVLTAAVMFLLLNCIVAVSQNMGIGKNGDLPRPPLRNEFR
0015	210	0.12	YFORMTTTSSVEGKONLVIMGRKTWFSIPEKNRPLKDRINLVLS
	· ·	•	RELKEPPOGAHFLARSLDDALKLTERPELANKVDMIWIVGGSSV
			YKEAMNHLGHLKLFVTRIMQDFESDTFFSEIDLEKYKLLPEYPG
1			ILSDVQEGKHIKYKFEVCEKDD
6620	3	1879	NSRVDDFVARARMAAENEASQESALGAYSPVDYMSITSFPRLPE
		·	DEPAPAAPLRGRKDEDAFLGDPDTDPDSFLKSARLQRLPSSSSE
			MGSQDGSPLRETRKDPFSAAAAECSCRQDGLTVIVTACLTFATG
1			VTVALVMQIYFGDPQIFQQGAVVTDAARCTSLGIEVLSKQGSSV
	<i>.</i>	J	DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRNESHLIDFRES
1 1			APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS OVLAFAAAVAODGFNVTHDLARALAEQLPPNMSERFRETFLPSG
1			RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAO
1			HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI
1		,	SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD
	. :		STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT
		. •	AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS
1	;		WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA
1 . 1			LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV
			SIPHAANMG .
6621	1	662	VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP
			AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT
			SVKVIGAQRRRSPSALAIEVFBAHLGSHILQSLDGYVFALNQEG
			KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL
6622	2	319	GRASGAQEETEAGGPERARAMEANMPKRKEPGRSLRIKVISMGN
0024	2	213	AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN
1			IFDMAGHPFFYEVRKPF
6623	1886	189	KALFEKVKKFRLHVBEGDILYAMYVROTVLKVIKFLIIIAYNSA
			LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF
]			VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF
1 1			
; !			AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWIPDKL
			AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM
			RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM
			RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
	sequence		HLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSH
1			
l.			LFLCNKIRYLDLSYNDIRFIPPEIGVLQSLQYFSITCNKVESLP
			DELYFCKKLKTLKIGKNSLSVLSPKIGNLLFLSYLDGKGNHFEI
6624	0.7.0	1706	LPPELGDCRALKRAGLVVEDALFETLPSDVREQMKTE
0624	218	1786	GSRRGGGSRIPAVSTHVAPGRSVLRPFASGALRLRSLVKALGGC
		1	RGRPSGLAHLSQETSHWRAKRSGRACLGDFPGEILRSFIMKCTA
			REWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIA
Ì			KQRGKRAITDNDMQSILDLHNKLRSQVYPTASNMEYMTWDVELE
ļ			RSAESWAESCLWEHGPASLLPSIGQNLGAHWGRYRPPTFHVQSW
			YDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGC
	[AINLCHNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCS
			ACPPSFGGGCRENLCYKEGSDRYYPPRBEETNEIERQQSQVHDT
			HVRTRSDDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTCNRYEC
			PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITR
			QGRKHYFIKSNRNGIQTIGKYQSANSFTVSKVTVQAVTCETTVE
. 6625	1124		QLCPFHKPASHCPRVYCPRKLYASKSTLCSCNWNSSLF
6625	1124	543	PGPRGGGGSLLSTKALGRSRGLGMHPGPSSGGTEGGVPTALRPP
1			GPLVPSTSDDNLLKNIELFDKLALRFHGRLLFLKDVLGDEICCW
			SFYGQGRKIAEVCCTSIVYATEKKQTKVEFPEARIFEETLNILI
			YETPRGPDPALLEATGGAAGAGGGGGEDEENREHRVRRIHVRR
			HITHDERPHGQQIVFKD
6626	3	1498	SAVEFVYTDRFHLILGISVEFLCSLRSDATMESITACLHALQAL
	ŀ	1	LDVPWPRSKIGSDQDSGIELLNVLHRVILTRESPSIQLASLEVV
			RQIICAAQEHVKEKRRSAEVDDGAAEKETLPEFGEGKDTGGLVP
			GKSLVFATLELCVCILVRQLPELNPKLTGSPGVKATKPQILLED
	į		GSRLVSAALVILSELPAVCSPEGSISILPTILYLTIGVLRETAV
i			KLPGGQLSSTVAASLQALKGILSSPMARABKSRTAWTDLLRSAL
			TTILDCWDPVDETHQBLDEVSLLTAITVFILSTSPEVTTIPCLQ
			KRCIDKFKATLEIKDPVVQIKTYQLLHSIFQYPNPAVSYPYIYS
			LASCIMEKLQEIDKRKPENTAELEIFQEGIKVLETLVTVAEEHH
	* *		RAQLVACLLPILISFLLDENSLGSATSIMRNLHDFALQNLMQIG
			PQYSSVFKSLVASSPALKARLEAAIKGNQESVKVKIPTSKYTKS
		505	PGKNSSIQLKTSFL
6627	1	697	GIPHLSSRDMTGTPGAVATRDGEAPERSPPCSPSYDLTGKVMLL
			GDTGVGKTCFLIQFKDGAFLSGTFIATVGIDFRNKVVTVDGVRV
			KLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITNKSSFDNIRA
			WLTEIHEYAQRDVVIMLLGNKADMSSERVIRSEDGETLAREYGV
			PFLETSAKTGMNVELAFLAIAKELKYRAGHQADEPSFQIRDYVE
	<u> </u>		SQKKRSSCCSFM
6628	1	1861	QCAEFGGGGGGGGGGGGGGGGGGGENKENERPSAGSKAN
1			KEFGDSLSLEILQIIKESQQQHGLRHGDFQRYRGYCSRRQRRLR
1	1	·	KTLNFKMGNRHKFTGKKVTEELLTDNRYLLLVLMDAERAWSYAM
1			QLKQEANTEPRKRFHLLSRLRKAVKHAEELERLCESNRVDAKTK
			LEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTE
			EQAVLYNQRVEEISPNIRYCAYNIGDQSAINELMQMRLRSGGTE
l			GLLAEKLEALITQTRAKQAATMSEVEWRGRTVPVKIDKVRIFLL
			GLADNEAAIVQAESEETKERLFESMLSECRDAIQVVREELKPDQ
			KQRDYILEGEPGKVSNLQYLHSYLTYIKLSTAIKRNENMAKGLQ
l			RALLQQQPEDDSKRSPRPQDLIRLYDIILQNLVELLQLPGLEED
			KAFQKEIGLKTLVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLK
			YANEVNSDAGAFKNSLKDLPDVQELITQVRSEKCSLQAAAILDA
			NDAHQTETSSSQVKDNKPLVERFETFCLDPSLVTKQANLVHFPP
			GFQPIPCKPLFFDLALNHVAFPPLEDKLEQKTKSGLTGYIKGIF
			GFRS
6629	5653	4549	GATPLGSVGGRTGKMDAATLTYDTLRFAEFEDFPETSEPVWILG
L			RKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGC

Degianing No: location corresponding to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence P-Proline, Q-Glytamine, R-Arginine, S-Serien, T-Threenine, N-Baparagine, H-Histidine, N-Baparagine, L-Leucine, M-methionine, N-Baparagine, L-Leucine, M-methionine, N-Baparagine, L-Leucine, M-methionine, N-Baparagine, L-Leucine, M-methionine, N-Baparagine, L-Leucine, M-methionine, N-Baparagine, L-Leucine, M-methionine, N-Baparagine, L-Leucine, M-methionine, N-Baparagine, L-Leucine, M-methionine, N-Baparagine, M-Proline, Q-Glutamine, R-Arginine, S-Serien, T-Threenine, N-Valine, M-Tryptophan, Y-Tyrosine, X-Unknown,Stop Codon, /-possible nucleotide insertion)	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No:				
Costion Corresponding Cofirst			·	
corresponding to first amino acid residue of residue of residue of residue of amino acid residue of amino acid sequence solvent of the residue of amino acid sequence solvent of the residue of amino acid sequence solvent of the residue of amino acid sequence solvent of the residue of amino acid sequence solvent of the residue of amino acid sequence solvent of the residue of amino acid sequence solvent of the residue of amino acid sequence solvent of the residue of the	.]			
to first amino acid residue of amino acid residue of servine, T-Rineconine, V-Valine, amino acid amino acid and acid sequence seq	[]			
amino acid residue of amino acid sequence solvent straypeophan, Patyrosine, X-dunknown, *-Stop codon, /-possible nucleotide deletion,				
residue of amino acid sequence Codon, /-possible nucleotide deletoide KSIGOWYGPNYVAQVLKKIAN/PTORK) RENEGORIFACINE SALVENIMEN SALVENIME	1.			
amino acid sequence Codon, /-possible nucleotide deletion, /-possible nucleotide insertion) MERCOGNIFAGALVCENLGROMENTORKROPDSYFSVILNAFITE KUSYYSHOLADGAWCENKIGEROMENTORKROPDSYFSVILNAFITE KUSYYSHOLADGAWCENKIGEROMENTORKROPDSYFSVILNAFITE KUSYYSHOLADGAWCENKIGEROMENTORKROPDSYFSVILNAFITE KUSYYSHOLADGAWCENKIGEROMENTORKROPDSYFSVILNAFITE PERSPROMEN FOR STALLDESTAVVROGHLENCHENCH PROBESTHOLIPE PERSPROMENT STALLDESTAVVROGHLENCHENCH PROBESTHOLIPE PERSPROMENT STALLDESTAVVROGHLENCHENCH PROBESTHOLIPE PERSPROMENT STALLDESTAVVROGHLENCHENCH TRETTGETARFESMIG 6530 2 423 LWOCGGIFRESAMGAMPGRHUSRVERLYRKVLQLIMEVLEPPLKS LUDGYVEDERRHKTVGSDEAGRFLQEMEVYATALLQAMENRO NSTRKACGGTFLEPEKLINDFROEGIGGLGELMOGATKENROFSI SESMKFKF 6631 2 423 LVQCGGIFRESAMGAMPGRHUSRVERLYRKVLQLIMEVLEPPLKS LUDGYVEDERRHKTVGSDEAGRFLQEMEVATALLAGAMENRO NSTRKACGGTFLEPEKLINDFROEGIGGLGELMOGATKENROFSI SESMKFKF WENSERTGIGRAPHUSRALVRALVRAVLQLIMEVLEPPLKS SESMKFKF GICVLLGISLEDTQKELEHWYRKILINERVFEDESGKHMSKSVMD KOYEILCVSQFTLQCVLKGNKEPPHLAMFTEGAGGTYNSFLENG KOYEILCVSQFTLQCVLKGNKEPPHLAMFTEGAGGTYNSFLENG KOYEILCVSQFTLQCVLKGNKEPPHLAMFTEGAGGTYNSFLENG KOYEILCVSQFTLQCVLKGNKEPPHLAMFTEGAGGTYNSFLENG KOYEILCVSQFTLQCVLKGNKEPPHLAMFTEGAGGTYNSFLENG KOYEILCVSQFTLQCVLKGNKEPPHLAMFTEGAGGTYNSFLENG KOYEILCVSQFTLQCVLKGNKEPPHLAMFTEGAGGTYNSFLENG KOYEILCVSQFTLQCVLKGNKEPPHLAMFTEGAGGTYNSFLENG KOYEILCVSQFTLQCVLKGNKEPPHLAMFTEGAGGTYNSFLENG KOYEILCVSQFTLQCVLKGNKEPPHAMKENCLAPPTPVTYTEBHV GSGLECVCKDDVALGERVRQLFCHHLFHDGCIVPHLEQHISS GSGLECVCKDDVALGERVRQLFCHHLFHDGCIVPHLEQHISS GSGLECVCKDDVALGERVRQLFCHHLFHDGCIVPHLEQHISS GSGLECVCKDDVALGERVRQLFCHHLFHDGCIVPHLEQHISS GGGLECVCKDDVALGERVRQLFCHHLFHDGCIVPHLEQHISS GGGLECVCKDDVALGERVRQLFCHHLFHDGCIVPHLEQHISS GGGLECVCKDDVALGERVRQLFCHHLFHDGCIVPHLEQHISS GGGLECVCKDDVALGERVRQLFCHHLFHDGCIVPHLEQHISS GGGLECVCKDDVALGERVRQLFCHHLFHDGCIVPHLEQHISS GGGLECVCKDDVALGERVRQLFCHHLFHDGCIVPHLEQHISS GGGLECVCKDDVALGERVRQLFCHHLFHDGCIVPHLEQHISS GCGLECVCKDDVALGERVRQLFCHHLFHDGCIVPHLEQHISS GGGLECVCKDDVALGERVRQLFCHHLFHDGCIVPHLEGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1			
Sequence	1		1	
MILECOMITEROALVCENLIGEDMENTORKOPDSYFSVINATIDE KOSYYSHOLAGNOVGEKSIGOWGYONTYAQVIKALAPIDYSS SLAWITAMINTYVWEETERLCFTSVPCAGATAFPADSDEHOLALAPIDYSS SLAWITAMINTYVWEETERLCFTSVPCAGATAFPADSDEHOLALAPIDYS PAGABAYTINESPENEPLVLLIPLERLGLIOTINESPYCTIKACCHMPP PAGABAYTINESPENEPLVLIPLERLGLIOTINESPYCTIKACCHMPP QSLGVIGGKPRSAHYPIGTVGEELIYLDPHTTOPAVEPTOGCFI PDESFRIGGIPCRWSITAELDFSITAVVKSGHLSTQAPGAECCLAM TRKTTGFILEFFSHILG 6630 2 423 LVQCGGIRRESAMGAMPGRHVSRVRALYKRVLQLHRVLPPDELGA SESMKPKF 6631 2 423 LVQCGGIRRESAMGAMPGRHVSRVRALYKRVLQLHRVLPPDELGA LGDGYVKDEFRRHKTVGSDEAGRFLGWEVVATALLQQAMENNQ NSTGKACFGTFLPEEKLADFRDEGIGGLGEMQBATKNNRGFSI SSSMKPKF 6632 L1273 588 WINSGRTDGKAANHAWAVGRVTTASSVTTGGEDISAKT KONGCGTETLPEEKLADREDGIGGLGEMQBATKNNRGFSI SSSMKPKF GICVLLGISLEDOYKKLHRWANGTLINLRVERDESGHWSKSVAM KOYETLCVSGPTLACVLKGKKPDFFLLAMPTBGABGYMSPLEDL RKTYRPELLKDGKFGAYMWYHIQNDGPVTLELESPARGTATSDP KQLSKLEKQQGRESKTRAKKPGESSKSKRNTPRKEDGHATSDD KQLSKLEKQQGRESKTRAKKPGESSKSKRNTPRKEDGHATSDD KQLSKLEKQQGRESKTRAKKPGESSSKSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	1		Bedreinge .	
KOSYYSIHOIAOMSVEGEKSIGOWIGPNYTAQVIKKILAYPIDES SLAWYIAIMDIVWEEIRICLEYSPVCAGATAPPASISDEHCNOP PAGASYNIRPSPREPLULIPILEGILTUNDRAYVETIKHCPMMP QSIGVIIGQWRSAINYSIGVVEGELTYLDPHTOGPED PDESPHONIPPORNSIASIDPSIAVVROGHLSTQAPGAECCLOM TERTFEGTLARFPSNIG 6530 2 423 LVQCGGIRRESAMGAMPGRHVSRVERLYKRVLQHEWLDPDLSS LDDGYYVDGFRRHKTVGSDEAGRFJQEWEVTATALLQQARENG NSTKKACFOTTLEPEKLINDPTOGG IGGLEMMQGARKONKOFSI SSSMKPRF 6631 2 423 LVQCGGIRRESAMGAMPGRHVSRVERLYKRVLQLHRVLPDLSS LDDGYVDGFRRHKTVGSDEAGRFJQEWEVTATALLQQARENG NSTKACFOTTLEPEKLINDPTOGG IGGLEMMQGARKONKOFSI SSSMKPRF 6632 1273 588 MWSRGRTGGGAPLABAAMKAVVQRVTRASVTVGGEQISAIGR GICVILGISLEDTQKELEHMVRKILNIRVFEDESGKHNKSKVD KOYSTLLVSGFTLQCVLKGNKFDGIQGLEMMGARKONKOFSI SSSMKPRF 6632 1273 588 WNSRGRTGGGAPLABAAMKAVVQRVTRASVTVGGEQISAIGR GICVILGISLEDTQKELEHMVRKILNIRVFEDESGKHNKSKVD KOYSTLLVSGFTLQCVLKGNKFDPILAMPTERGAGFYNSFLEQI RRTYRPELIKOGKRGAYMQVHIQNG VYTELESPAPOTATSOP KOLEKLEKQOGNEKTRAKGPESS KERNTPRKEDSASSAGGAB DVSSSREP 6633 1145 617 ATGREGVYTLGGILGQUVNGIITPATTPSICKEDSASSAGBA DVSSSREP 6634 1 1134 CGGIRRGSGREFLEMBARLEDGLHHJFUGGVYDLGGBISCH GGGCKCVCKDIVAIGERVGLQLEHMIFUGGVYDPLEQHBOSCP VCRKSLTQQNTATINPPGUTGVFSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	<u> </u>	pequence	ļ <u> — — — — — — — — — — — — — — — — — — — </u>	
SLAVHIAMDNTVVMEBIRILCHTSVPCAGATAPPADSDRINGNE PAGARVTNRSPWRPLULIPRICGITDINARYVPTLIKICHMIN QSIGVIGGKPNSAHYPIGVVGEBLIVLDPHTYQPAVEPTDOCTE PDESPHOCHEP PCMSTABLDPSIAVVRGHILSTQAFGAECCIGM TRKTFGFLRFFSMLG TRKTFGFLRFRHTVGSDEAQRFLQEMEVYATALLQQAMENG NSTGKACFGFFLPEEKINDFRDEQIGGLGELMGEATKENRGFSI SSSMKPKF TLGQTVLTGERFRHTVGSDEAQRFLQEMEVYATALLQQAMENG NSTGKACFGFFLPEEKINDFRDEQIGGLGELMGEATKENRGFSI SSSMKPKF GICVLLGISLEDTOKELEHMEKILLIKFFEDESGKHRSKSVMG NSTGKACFGFFLPEEKINDFRDEQIGGLGELMGEATKENRGFSI SSSMKPKF GICVLLGISLEDTOKELEHMEKILLIKFFEDESGKHRSKSVMG KYPELLCVSGPFLGCULKGNKEDFHLAMFTSDAGGFYNSFLEGL RRTYPEPLILKDGKFGAMYGULADGGPVISTEDSGKHRSKSVMG KYPELLCVSGPFLGCULKGNKEDFHLAMFTSDAGGFYNSFLEGL RRTYPEPLILKDGKFGAMYGULADGGPVISTEDSGKHRSKSVMG KOMSELEVCUCONTATTEPDELTGGVSFSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS				_ = = = ===============================
PAGABVTNRPSDWRPLULLI PLRIGITDINDATVPETLERICPMP QSIGVIGGRNSAHYPIGVORBELI YLDPHOPMOPTODCTOP PDESPHOCHPP CRMSTAELDPS LAVVRGGHLSTQAFGAECCIGM TRKTFOFFARFFSMLG 1 LVQCGGTRRSAMGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS LGDQYVKDEFRRHITVGSDEAGRE LGEMEVYATALLQAMENGQ NSTGKACFGTFIPEEKLINDFSDEGIGGLELMGATKRNNRQFSI SSSMRPIF 6631 2 423 LVQCGGTRRSAMGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS LGDQYVKDEFRRHITVGSDEAGRE LGEMEVYATALLQAMENGQ NSTGKACFGTFIPEEKLINDFSDEGIGGLELMGATKPNNRQFSI SSSMRPIF 6632 1273 588 MINSGRTJGRADAPLAPAAMKAVVQRVTTASVTVGGEDISALGE SSSMRPIF 6632 GICVLLGISLEDTOKELEHMVRKI LINLRVFEDESGKHNSKSVMD KQYSEILCVSQFTLQCVLKGNNFPDFHLAMFTSQAEGFYNSKSVMD KQYSEILCVSQFTLQCVLKGNNFPDFHLAMFTSQAEGFYNSKSVMD KQYSEILCVSQFTLQCVLKGNNFPDFHLAMFTSQAEGFYNSKSVMD KQYSEILCVSQFTLQCVLKGNNFPDFHLAMFTSQAEGFYNSKSVMD KQYSEILCVSQFTLQCVLKGNNFPDFHLAMFTSQAEGFYNSKSVMD KQYSEILCVSQFTLQCVLKGNNFPDFHLAMFTSQAEGFYNSKSVMD KQYSEILCVSQFTLQCVLKGNNFPDFHLAMFTSQAEGFYNSKSVMD KQYSEILCVSQFTLQCVLKGNNFPDFHLAMFTSQAEGFYNSKSVMD KQYSEILCVSQFTLQCVLKGNNFPDFHLAMFTSQAEGFYNSKSVMD KQYSEILCVSQFTLQCVLKGNNFPDFHLAMFTSQAEGFYNSKSVMD KQYSEILCVSQFTLQCVLKGNNFPDFHLAMFTSQAEGFYNSKSVMD KQYSEILCVSQFTLQCVLKGNNFPDFHLAMFTSQAEGFYNSKSVMD KQYSEILCVSQFTLQCVLKGNNFPDFHLAMFTSQAEGFYNSKSVMD KQYSEILCVSQFTLQCVLKGNNFPDFHLAMFTSQAEGFYNSKSVMD KQYSEILCVSQFTLGGTGAPHTFRASKTTRACHASKSVMD KQYSEILCVSQFTLGGTGAPHTTSSAEGRAFTSLEGG RGCAGFFERLENGTSFSSSSSSSSPSNSNATSNS KQLISHMSVGTSSSSSSSSSSSSSSSSSSSSSSSSSSAEG VCKRSLTCGNATATATATTTSLLESSFAFTSLTSKTL GSGLKFYCKDDYALGEFYNSKNTLGCLTTDLKDLIDLSGAY SKCVLIGHUNGGTFTSPTAFTSLTSKTLDGAEAGTYSTSTAKK LEHPAQLLKSSYTYFFQ1BWFPEFMSSINDFKVLKKLIFTSHSTG IGKKQCLTTBLDEATYTVFQCRGALGGFTNIFSCLDJKK HATTVAAMFANTLADELPSSRAKKLADEQLSSV1QDMAVRQHL LTINLVEVUDGRFVWRNALDATTSPTSMSWILLFGSKSTTFNSIAK HATTVAAMFANTLADELPSSRAKKLADEQLSSV1QDMAVRQHL LTINLVEVUDGRFVWRNALDATGHLDKILAFGSKTTFNSIAK HATTVAAMFANTLADELPSSRAKKLADEQLSSV1QDMAVRQHL LTINLVEVUDGRFVWRNALDATGHLDKILAFGSCLTSFSSSSG HATTVAAMFANTLADLEPSSRAKKLADEQLSSV1QDKARGKSTT LGGGGAGFFFELPSSRAKLADEQLSSV1GDELINGHAKTOT VUSFFCKNSTVLSONSKRTCQQNSERSKKQDLITGACEBKISD LVRRRVLPMVQNSEFTLHQLINTAGARSKYTCAGRASKKI VUSFFCKN				
QSIGYIGGKPNSAHYPIGYVGRELIYLDPHTTOPAVEPTOCCE PDESPHOUPP COMSTABLDPS LAVVRGGHLSTQAFGAECCLGM TRKTFGFLRFFSMLG 6530 2 423 LVQCGGIRRESAWGAWFGRHVSRVARLYKRVLQLHRVLPPDLKS LUQCGGIRRESAWGAWFGRHVSRVARLYKRVLQLHRVLPPDLKS LUQCGGIRRESAWGAWFGRHVSRVARLYKRVLQLHRVLPPDLKS SESMKPKF 6531 2 423 LVQCGGIRRESAWGAWFGRHVSRVARLYKRVLQLHRVLPPDLKS SESMKPKF 6531 2 423 LVQCGGIRRESAWGAWFGRHVSRVARLYKRVLQLHRVLPPDLKS LUQCYGGIRRESAWGAWFGRHVSRVARLYKRVLQLHRVLPPDLKS SESMKPKF 6532 1273 588 WNSRGRTQRGAPLAPAAMKAVVQRVTRASVTVGGEQISAIGR KOYELLCVSGFTLQCVLKGNKPPDHLAWFTENSVAND KQYELLCVSGFTLQCVLKGNKPPHLAWFTENSSKSVAND KQYELLCVSGFTLQCVLKGNKPPHLAWFTENSSKSVAND KQYELLCVSGFTLQCVLKGNKPPHLAWFTENSSKSVAND KQUELCVSGGVRKEKTRAGPSESSKENSTRYSDASGAGG KRYTKPPLLKGGKFGAYMQVHIQNDGPVTIELSSAPSATSGAG DVSSERBP 6633 1145 617 ATGRHEGVPTLEGIIQLVNGIITPATTESLGPWGVLHSNPMDY AMGANGLDAIITOLLNOFENTGPPPADKEKIQALPTVPTEEHV GSGLECPVCKDDYALGERVRQLPCNHLPHDCITVPHEQHDSCY CVCKSLTQQNTATNPPGLTGVSFSSSSSSSSSSSSSSNENATSNS GGLECPVCKDDYALGERVRQLPCNHLPHDCITVPHEQHDSCY VCRKSLTQQNTATNPPGLTGVSFSSSSSSSSSSSSSSSNENATSNS CGLCSFHILVALWSLGKGFGAPTFAPARHPACLSDPSIGTTG VVRIKDSGLRFHYVAAGREGKPLMLLHGSFPEFWSNRYQLKGF KSSERVVALDLARGFGTTAPTARPACLSPDSIGTTG VVRIKDSGLRFHYVAAGREGKPLMLLHGFPEFWSNRYVNYFLTLISEASH WLQQDQPDIVNKLIWTFLKEETRKKD 6635 1420 470 EBRAGQQLASMIRNTEARWLDRESGLEPHBPSFRAVVNYFRLTLISEASH WLQQDQPDIVNKLIWTFLKEETRKKD 6636 1514 1801 SPCWFSHKQDSHFQNAPAVPRYVNYNYFLTLISEASH WLQQDQPDIVNKLIWTFLKEETRKKD 1LAQQTGRRVLTVDARNHGDSPHSPMSYEMSQLOQLIPQLG LLPVCVVGHSWAGKTAMLLAQPELVERLHGGSKTNFNSIAK LLAQQTGRRVLTVDARNHGDSPHSPMSYEMSQLOQLIPQLG LLPVCVVGHSWAGKTAMLLAQPELVERLHGGSKTNFNSIAK 1LAQQTGRRVLTVDARNHGDSPHSPMSYEMSQLOGDLPQLG LLTNLWEDGGRVWRVLDALALQPELVERLHGGSKTTFNSIAK 1LAQQTGRRVLTVDARNHGDSPHSPMSYEMSQLOGSVLGFTLG LLGGNSGVVHPSHERPERMRLPRESGLIGFBHFGFSHDGDCCRVD DGGGOVP ALRGERY PLVCGGALVNGGSFTHALQPGLVARATRTTSGVHGEHKARA 6637 2 1501 KSSSSCPHDGTTVLDKASSYKCALGATGRTGNKNGGRAPS CTPICGKINTTAPKTGGLRWPAGGALTGRTGSTORSHKKRL PLAGGALVNGASSYKCALGATRTTGSTORGSHKKAD PLVCGGALVNGASSTYLGGRUFTVAGARTATRTTSGVHGSLHKGAN PLVCGGALVNGASSTYLGGRUFTVAGARTATRTTSGVHGSLH	 .	ĺ	ĺ	
PDESPHOCHEPCRMSTABLDPSIAVVRGGHLSTQAPGABCCLGM TRKTTGFLAFFSMLG LVQCGGIRRSAWGAMFGRHVSRVBALYKRVLQLHRVLPPDLKS LDGQYVRDEFRRHKTVGSDBAQRFLQBMGVATRALLQAGARENQ NSTGKACGGTFLPEEKLINDFENGGIQQLEJMGATKRNNXQFSI SSSMCPUF 6631 2 423 LVQCGGIRRSAWGAMFGRHVSRVBALYKRVLQLHRVLPPDLKS LGDQYVRDEFRRHKTVGSDBAQRFLQBMGVATRALLQAGARENQ NSTGKACGGTFLPEEKLINDFENGGIQQLEJMGATKRNNXQFSI LCDQVVRDEFRRHKTVGSDBAQRFLQBMGVATRALQAGARENQ NSTGKACGGTFLPEEKLINDFENGGIQGLEJMGATKRNNXGFSI SSSMCPUF SSSMCPUF 6632 1273 588 WNSGGRTQGRADLAPAAMKAVVQRVTAGSVTYGGEGISATGR GICVLLGISLBDTQKBLEHMVRKILALRVFBDESGKHNSKSVAD KQYEILCVSQFTLACVLKGNKDPHLAMPTSGAFKNNXGFSI SSSMCPUF RKTYRPELIKDGKFGAYMQVHIQNDGPVTIELESPAPGTATSDP KQLSKLEKQQGRBKKTRAKGFSESSKENNTFRKEDRSSSGARG DVSSSRBP 6633 1145 617 ATGREGVFTLEGIIQUNNGIITFPATIFSLGFWGVLHSNPMDY AMGANGLDAITQLLANGFSTSSSSSSSSSSSSSSPSNENNATSNS AMGANGLDAITQLLANGFSTSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS				
TRKTTGFLRFFSMLG				· ·
LUQCGGIRRISANGAMPGRIVERVERLYKEVUQLIRRULPPILKS LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANERON NSTGKACFGTFLPEEKINDFRDEQIGQUQELMQEATKPNRQFSI SSBMKPKF				
LGDQVYKDETRERKTVGSDEAQETJQERGYATALLQQAMENNO NSTGKACFGTFLPEEKINDFRDEQIGQLQELMQRATKPNRQFSI SESMKPKF 6631 2 423 LVQCCGTRRSAWGAMBGRINVSRVRALYKRVLQLHRVLPPDLKS LDQQVYKDEFRERKTVGSDEAQFFLQEWEVYATALLQQAMENNO NSTGKACFGTFLPEEKINDFRDEQIGQLQELMQEATKPNRQFSI SESMKPKF 6632 1273 588 WINSGRTQGGAAJLAPAAAMKAVVQRVTRASVTVGGEBISAIGR GICVLLGISLBEDTQKEELEHMVRKILINLAVFEDESGKHRSKSVMD KQYEILCVSQPTLQCVLKGNKPDFHLAMPTEQAEGFYNSFLEQI RKTTRPELINDGKFGAYMQVHIQNDGFVTIELESPAPGTATSDP KQISKLEKQOQKKEKTRAKGPESSKERNTPKKEDRSASSGAEG DVSSSREP 6633 1145 617 ATGRIEGGYPTLEGIIQQLVNGIITPATTIPSLGPWGVLHSNPMDY AMGANGLDAIITQLLMQFENTGPPADKEKIQALPTVPVTEBIV GGSLEKCVCKDDYALGGENVQLCPCHLEHDGCIVFMLEQHDSCD VCRKSLTQQNTATNPPGLTGVSFSSSSSSSSSSSSSSSNSNATSNS 6634 1 1134 CGGIPRKGSGPRRELEMARLEDCLPFLMLTLRSLLFWSLVYCYC GGIPRKGSGPRRELEMARLEDCLPFLMLTLRSLLFWSLVYCYC GCASIHLKKLIMSLGKGPAQTFRRPAREPPACLSDPSIGTHC YVRIKDSGLRFHYVAACERGKPLMLLHGGFPEFWXRYQLERF KSETRVVADLLKGYGETDAPFIRMATLLJCLTIDIKDILDSLGY SKCVLIGHDWGGMIAWLIAICYCPPWWMKLLVINFPNDVTFESI LGKKGQLTTBDLBAYIYVSQDGALSGPINHYRHIPSCLPLKH HHVTTPTLLIMGENDAFMEVEMAEVTRFYLNFYFLITLSEASH WLQQOQPDIVNKLINTELKEETKKD 6635 1420 470 EMRAGQQLASMIRWITARKRIPREGIGPHGPSPARVPVAPSSSG GRGGABPRIPLSTRLLDGEAALPAVYFLHGLFGSKTNYNSIAK LIAQQTGRRVLTVDARHGDSPHSSDMSYSINSQOLLPCJUG LUPCVVGHSMMGKTAMLLALQRPBLUERDJUNDSVCHSTSTGV HPATTVAAMRAINIADELPRSARRIADDZLSSVIGMAVGRUL LUTNLEVUGHFWGWILLALQRPBLUERDJUNDAWORGH LUTNLEVUGHFWGWILLALQRPBLUERDJUNDAWORGH LUTNLEVUGHFWGWTHALLALQRPBLUERDJUNDAWORGH LUTNLEVUGHFWGWTHALLALQRPBLUERDJUNDAWORGH LUTNLEVUGHFWGWTHALLALQRPBLUERDJUNDAWORGH LUTNLEVUGHFWGWTHALLALQRPBLUERDJUNDAWORGH LUTNLEVUGHFWGWTHALLALQRPBLUERDGGNAWAGHAL LUTNLEVUGHFFWGWTHALLALQRPBLUERDGGNAWAGHAL LUTNLEVUGHFFWGWTHALLALQRPBLUERDGGNAWAGHAL LUTNLEVUGHFFWGWTHALLALQRPBLUERDGGNAWAGHAL LUTNLEVUGHFFWGWTHALLALQRPBLUERDGGNAWAGHAL LUTNLEVUGHFFWGGATAMLALALQRPBLUERDGGNAWAGHAL LUTNLEVUGHGFFWGWTHALLALQRPBLUERDGGNAWAGHAL LUTNLEVUGHGFFWGWTHALLALQRPBLUERDGGNAWAGHALTULLGGGNAKAG CIPTCGCLBRPLCGVLGFPQQQCDFPSLGFVLSPHENGCRV VSFFCNNSYLSGMERTCQQAGBWSGKGPLCHAGGKSCHAAB CUPTCGCLBRPLCGGUSHFFTHALLARGFT DDDRAGGETTGG	6630		422	
NSTGKACFGTFLJEEKLNDFRDEQIGQLQEIMQEATKPNRQFSI SRSMKPKF 6631 2 423 LVQCGGIRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS LDGQVYKDEFREHKTVGSDEAGR FLQEBWEYYATALQQAKENRQ NSTGKACFGFTJEPEKLNDFRDEQIGQCJQEIMQEATKPNRQFSI SSSMKPKF 6632 1273 588 WNSRGRTQRGAAPLAPAAAMKAVVQRVTRASVTVGGEGISAIGR GICVULGISLEDTQKELEHMVRKILNLAVERDESGKHWSKSVVM KQYEILCVSQFTLQCVLKGNKPDFHLAMPTEQAEGFYNSPLEQI RRTTRPELIKDGKFQAYMQVHQNDGFVTILLESSPAPGTATSDP KQLSKLEKQQQKKEKTRAKGPEGSSKERNTPRKEDRSASGAEG UVSSRSEN UVSSRSEN UVSSRSEN 46633 1145 617 ATGRHEGVPPLEGI IQQLVNGIITPATTPSLGPWGVLHSNPMDY GGGLECPVCKDDYALGERVRQLDCHHLPHDGCIVPWLEGHDSCP VCKKSLTQNTATNPPQLTGVSFSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSPENENATSRS GGGAECPVCKDDYALGERVRQLDCHHLPHDGCIVPWLEGHDSCP VCKSLTGNTATNPPQLTGVSFSSSSSSSSSSSSSPENENATSRS SKCVLIGHDAI 11Q1LNGFENTGPPARKERIOLDFTUNTYEEH GGGLECPVCKDDYALGERVRQLDCHHLPHDGCIVPWLEGHDSCP VCKSLTGNTATNPPQLTGVSFSSSSSSSSSSSPPSNENATSNS KCVLIGHDAI 11Q1LNGFENTGPPARKERIOLDFTUNTYEEH GGGLECPVCKDDYALGERVRQLDCHHLPHDGCIVPWLEGHDSCP VCKSLTGNTATNPPQLTGVSFSSSSSSSSSSSSPPSNENATSNS KCVLIGHDAI 11Q1LNGFENTGPPARKERIOLDFTUNTYEEH GGGLECPVCKDDYALGERVRQLDCHHLPHDGCIVPWLEGHDSCP VCKSLTGNTATNPQLTCXVSTPSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSPPSNENATSNS KCVLIGHDAIG TYPUTATHEN TO THE TOTAL TO T	1 0030	4	423	
SSBMKPKF LVQCGGIRRSANGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS LDQVVKDEFRRIKTVGSDEAQRFLQEMEVYATALLQQANENRQ NSTGKACFGTILPEEKLNDFADEQIGGLQELMQEATKPNRQFSI SSBMKPKF 6632 1273 588 MNSRGRTQRGABLAPAAMKAVVQRVTRASVTVGGEQISATGR GICVLLGISLEDTQKELEHMURKLINLRVPEDESGKIHSATGR KQYEILCVSQFTLQCVLKGNKPDFHLAMPTEQARGFYNSFLEQL RKTYRPELIKDGKFGAYMQVHIQNDGFVTILELSPAPGTATSDP KQLSKLERQQQRKEKTRAKGFSESSKERNTPREDRSASSABG DVSSSREP 6633 1145 617 ATGRIEGOPTLEGITQQLVNGIITPATIPSIGFWGVLHSNPMDY AWGANGLDAIITQLLNQFENTGPPPADKEKIQALPTVPVTEEHV GSGLECVVCKOLDVALGERVRQLPCNHLFFEDGCTYPMLEGHBGSV VCRKSLTGQNTATNPPDFTGVSFSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS				
LVQCGGIRRRSAWGAMPGRHVSRVPALYKRVLQLHRVLPPDLKS	1			
LGDQYVKDEPRRHKTVGSDEAQRPIQEMEVYATALLQQANENNQ NSTGRACFGTIPEEKLNDFRDEQIGGLQELMQEATKPNRQPSI SSSMKYF 6632 1273 588 MNSRGRTQRGAAPLAPAAAMKAVVQRVTRASVTVGGEQISACISACISSISSMKYF GICVLLGISLEDTQKELEHMYRKILIRUFEBESGKHWSKSVMD KQYEILCVSQPTLQCVLKGNKPDFHLAMPTBGABGFYNSFLEDL RKTYRPELIKDGKPGAYMQVHIQNDGPVTILELSPAPGTATSDP KQLSKLEKQQQRKEKTRAKGPSESSKERNTPRKEDRSASSGAEG DVSSRRBP 6633 1145 617 ATGRIEGGPTILGGILVNGIITPATTIPSIGFWGVLHSNPMDY AMGANGGLDAIITQLLNQFENTGPPPADKEKIQALPTVPVTEHNV GSGLECPVCKDDVALGERVRQD-PCNHLFHDGCIVPWLEQHDSCP VCRKSLTQQNTATNPPGLTGVSFSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	6621		400	
NSTGKACTGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI SESMKPKF	1 0031	2	423	
SESMKPKF		•	ļ: ·	
1273 588 WINSERTQRGAPLAPAAAMKAVVQRVTRASVTVGGEQISAIGR GICVLLGISLEDTQKELEHMVRKILINLEVFDEGSKHWSKSVMD KQYEILCVSQFTLQCVLKGNYEPDEGSKHWSKSVMD KQYEILCVSQFTLQCVLKGNYEPDEGSKHWSKSVMD KQYEILCVSQFTLQCVLKGNYEPDEGSKHWSKSVMD KQYEILCVSQFTLQCVLKGNYEPDEGSKHWSKSVMD KQYELLCVSQFTLQCVLKGNYEPDEGSKHWSKSVMD KQLSKLEKQQQRKEKTRAKGPGSSKERTPRKEDRSASSGAGG DVSSEREP AGRREGVPTLEGIIQQLVNGIITPATIPSLGPWGVLHSNPMDY AGGANGLDAIITQLLNGFENTGPPADKEKIQALPTVPVTEEHV GSGLECPVCKDDVALGERVRQLDCCHLHFHDGCIVPWLEQHDSCD VCRKSLTQONTATHPPQLTGVSFSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS				
GICVLGISLEDTQKELEHMVRKILNIRVFEDESGKHWSKSVMD KQYEILCVSQFTLQCVLKGNKPDPHLAMPTEQAEGFYNSFLEQL RKTYRPELIKDSKFQAYMQVIQNDGPVTIELESPAPGTATSDP KQLSKLEKQQQRKEKTRAKGPSESSKERNTPRKEDRSASSGAEG DVSSEREP 6633 1145 617 ATGRIEGVPTLEGIIQQLVNGIITPATIPSIGPWGVLHSNPMDY AMGANGLDAITTQLLNQFENTGPPPADKERIQALPTVVPTERHV GSGLKCPVCKDVALIGERVRQLPCNHLFHDGCIVPHLEQHDSCP VCRKSLTGQNTATNPPGLTGVSFSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	F 6633	1272	F.5.2	
KQYEILCUSQFTLQCULKGNKPDFHLAMPTEQAEGFYNSFLEQL RRTYRPELIKDGKFGAYMQVHIQNDGPVTIELESPAPGTATSDP KQLSKLEKQQRKEKTRAKGPSESSKERNTPRKEDRSASGAEG DVSSRREP 6633 1145 617 ATGRIEGVPTLEGIIQQLVNGIITPATIPSIGPWGVLHSNPMDY AMGANGLDAIITQLLNGFENTGPPPADKEKIQALPTVPVTEEHV GSGLKCPVCKDDYALGERVRQLPCNHLPHGCIVPHLEGHDSCP VCRKSLTQCMTATNPPGLTGVFSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	0032	12/3	288	,
RKTYRPELIKDGKFGAYMQVHIQNDGPVTIELESPAPGTATSDP KQLSKLEKQQQRKEKTRAKGPSESSKERNTFRKERPSASSGAEG DVSSREP 6633 1145 617 ATGRIEGUFTLEGIIQQLVNGIITPATIPSLGPWGVLHSNPMDY AWGANGLDAIITQLLNGFENTGPPADKEKIQALPTUPVTEEHV GSGLRCPVCKDDYALGERVRQLPCHHLFHDGCIVPWLEQHDSCP VCRKSLTGQNTATNPPGLTGVSFSSSSSSSSSSSSSSSSNRTATSNS 6634 1 1134 CGGIPRKGSGPRRTEDMALRDCLPFRLMTLESLLFWGLVYCYC GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTHC YVRIKDSGLRFHYVAAGERGREPMLLHGFPFFWSWRYQLREF KSERVVALDLBGYGGTDAP HRQNYKLDCLITDIKDLIDSLGY SKCVLIGHDWGGMIAWLIAICVPEMWWKLIVINPPHPNVFTEYI LRHPAQLLKSSYYYFFQIPWFPEFFWFSINDFKVLKHLFTSHSTG IGRKGCQLTTEDLEAYIYVFSQPGALSGPINNYRNIFSCLPLKH HMVTTPTLLLWGENDAFMEVEMAEVVTFYVKNYFPLLTILSEASH WLQQDQPDLVNKLIWFFLKEFTRKD 6635 1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAFSSSG GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTMFNSIAK LILAQOTGRRVLTVDARNHGDSPHSPEMSYLDMAVRGHL LINLVEVDGRFWWNLLALDLATQHLDKILAFPCRGESYLIGMAVRGHL LINLVEVDGRFWWNLLALALQHPSLVERLIAVDISPVESTGVS HPATTVAAMRAINIADELPRSRARKLADEQLSSVIQMAVRGHL LINLVEVDGRFWWNLLALALTQHLDKILAFPCRGESYLIGMAVRGHL LINLVEVDGRFWWNLLALALTQHLDKILAFPCRGESYLIGMAVRGHL LINLVEVDGRFWWNLALALTQHLDKILAFPCRGESYLIGMAVRGHL LINLVEVDGRFWWNLALALTQHLDKILAFPCRGESYLIGMAVRGHL LINLVEVDGRFWWNLALALTQHLDKILAFPCRGESYLIGMAVRGHL LANGGFLYVYLVSGRFWRTCQNGBWSKQFQCRPTLFACREPHISD AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGFBYQQQLPPSLGPVLSPHSDPGWCRVD DGGGGYF CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGMEKRTCQQNGBWSKQFCICIKACREPHISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYGHLHTQLQTECISPFYRRIGSSRRTCLRTGKWSGRAPS CIPPIGKLENTIAPRTGGLERSSRRTCLRTGKWSGRAPS CIPPIGKLENTIAPRTGGLERSFSRRTCLRTGKWSGRAPS CIPPIGKLENTIAPRTGGLERFSKRTULDADIAILKLLDKARIS TRVQSICLARSRDLSTSFQESHIIVAGMWVLADVRSFGFKNDTL		•		_
KQLSKLEKQQQRKEKTRAKGPSESSKERNTPRKEDRSASSGAEG DVSSEREP 6633 1145 617 ATGRIEGVPTLEGIIQQLVNGIITPATIPSLGPWGVLHSNPMDY AMGANGLDAIITQLLMQFENTGPPPADKEKIQALPTVPVTERHV GSGLBCPVCKDDYALGERVRQLPCNHIFHDGCIVPWLEQHDSCP VCRKSLTQNTATNPPGLTGVSFSSSSSSSSSSSNENATSNS 6634 1 1134 CGGIPRKGSGPRRTLDMARLRDCLPRLMLTLESLLFWSLVYCYC GLCASIHLLKLLWSLGKGPAQTFRRPARREHPPACLSDPSLGTHC YVRIKDSGLRFHYVAAGERGKPLMLLHGFPEFWYSMYQLREF KSBYRVVALDLKGYGGTDAPIHRQNYKLDCLITDLKDLLDSLGY SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINPPHPNVFTEYI LRHPAQLLKSSYYYFFQIPWFPEFWFSINDFKVLKHLFISHSTG IGRKGCQLTTBDLEAYIVYFSQPGALSGPINNYRNIFSCLPLKH HHVTTPTLLLMGENDAFMEVEMAEVYRFYVKNYFRLTILSEASH WLQQDQPDIVNKLIWTFLKEETRKD 6635 1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSG GRGAPPREPLBYSKLLDGLBPHGPSFARVPVAPSSSG GRGAPPREPLBYSKLLDGLBPHGPFSFARVPVAPSSSG GRGAPPREPLBYSKLLDGLBPHGPSFARVPVAPSSSG GRGAPPREPLBYSKLLDGLBPHGPSFARVPVAPSSSG GRGAPPREPLBYSKLLDGLSGPHGPSFARVPVAPSSSG GRGAPPREPLBYSKLLDGLSGPHGPSFARVPVAPSSSG GRGAPPREPLBYSKLLDGLSGPHGPSFARVPVAPSSSG GRGAPPREPLBYSKLLDGLSGPHGPSFARVPVAPSSSG GRGAPPREPLBYSKLLDGLSGPHGPSFARVPVAPSSSG GRGAPPREPLBYSKLLDGLSGPHGPSFARVPVAPSSSG GRGAPPREPLBYSKLLDGLSGPHGPSFARVPAPSSSG GRGAPPREPLBYSKLLDGSPHSTVENGDSVCGNARVRHL LINLVEVDGRFVWVNLDALTQHLDKILAFPQRGSYLGPTLFL LGGNSQFVHPSHPEIMRLFPRAGMCTVPNAGHWHADRPQDFI AAIRGFLV DGGGVF 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQQRLKHPAE QPIVRGCLQRPPLCGVLGBVQQQDPPSLGPVLSPHSDPGWCRVD DGGGVF 6637 2 1501 CSSSPGFHGCTCVLDKAGSYKCACLAGYTGCRCBNLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGMEKRTCQQNGEWSKQPICIKACEPRISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKRPALPFG DLPMGYQHLHTQLQYECISPFYRRLIGSSRRTCLRTGKWSGRAPS CTPIGGKLENTTAPKTQGLRAPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRBKTIQSQISSHILIPANVDPILLDADIAILKLLDKARIS TRVQSICLAASRDLSTSFQESHITVAGMVVLADVRSPGFKNDTL	1			
DVSSEREP		,		
6633 1145 617 ATGRHEGVPTLEGIIQQLVNGIITPATIPSLGPWGVLHSNPMDY AWGANGLDAIITQLLNGFENTGPP PADKEKIQALPTUPVTEHV GSGLRCPVCKDVALGERVRQLPCNHLPHDGCIVPWLEOHDSCYP VCRKSLTGQNTATNPPGLTGVSFSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS			,	
AWGANGLDAIITQLLNGFENTGPPPADKEKIQALPTVPVTEEHV GSGLRCPVCKDDYALGERVRQLPCNHLFHDGCIVFWLEQHDSCP VCRKSLTGQKTAINPPGLTGVSFSSSSSSSSSSSSNENATSNS 6634 1 1134 CGGIPRKGSGPRRLFMARLRDCLPRLMLTLRSLLFWSLVYCYC GLCASIHLLKLLWSLGKGPAQTFERPAREHPPACLSDPSLGTHC YVRIKDSGLRFHYVAAAGRGKQFLMLLLHGFPEFWYSWRYQLREF KSEYRVVALDLRGYGETDAPIHRONYKLDCLITDIKDILDSLGY SKCVLIGHDWGGMIAWLIAICYPEMWMKLIVINPPHPMVFTEYI LRHPAQLLKSSYYYFFQIPWFPEMWFSINDFKVLKHLFTSHSTG IGRKGCQLTTBDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH HNVTTPTLLLWGENDAFMBVEMABUTRFYVKNYFRLTILSEASH WLQQDQPDIVNKLIWTFLKEETRKD 6635 1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGABPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTMFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HRATYVAAWRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEUDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSGFVHPSHHPEIMRLPPRAQMQTVPNAGHWHADRPQDFT AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKRLRRAPWRAFAQPQRLKHPAE QPIVRGCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNSYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKTCQQNGEWSGKQPICIKACREPKISD LVRRKVLPMQVQSRETPLHQLVSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISFFYRRLGSSRRPCLRTKRSGRAPS CIPICGKENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQFICLAASRDLSTSFQSSHTTVAGWNVLADVRSPGFKNDTL	6633	3345		
GSGLECPVCKDDYALGERVRQLPCNHLFHDGCIVPWLEQHDSCD VCRKSLTGQNTATNPPCLTGVSFSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	0033	1142	617	
VCRKSLTGQNTATNPPGLTGVSFSSSSSSSSSSSNENATSNS				1
CGGIPRKGSGPRRLPMARLRDCLPRLMLTLRSLLFWSLVYCYC GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTHC YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYSWRYQLREF KSEYRVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLGY SKCVLIGHDWGGMIAWLIAICYPEMVMKLJVINPPHPNVFTEYI LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG IGRKGCQLTTEDLEAYIYVFSQPGALSGPINFYRNIFSCLPLKH HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEASH WLQQDQPDIVMKLIWTFLKEETRKKD GRGABEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HPATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCBNLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYLJSGNEKTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYCISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVWERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARIS TRVQFICLAASRDLSTSFQBSHITVAGWNVLADVRSPGFKNDTL				1
GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTHC YVRIKDSGLRFHYVAAGBRGKPLMILLHGFBFFWYSKRYQLREF KSEYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLGY SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINPPHPNVFTEYI LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEASH WLQQDQPDIVNKLIWTFLKEETRKKD 6635 1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGABPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPCRQESYLGFTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRCCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGFGLINGHAKIGT VVSFFCNNSYVLSGNEKRTCQNGEWSGKQPICIKACREFKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLGYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSLHKGAW FLVCSGALVWERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQBSHITVAGWNVLADVRSPGFKNDTL	-6634		7,72	
YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYSWRYQLREF KSEYRVVALDLRGYGETDAP HRQNYXLDCLITDIKDILDSLGY SKCVLIGHDWGGMIAWLIAI CYPEMVMKLIVINPPHPNVFTEYI LRHPAQLLKSSYYYFFQIPWPPEFMFSINDFKVLKHLFTSHSTG IGRKGQLTTBDLEAYYYVFSQPGALSGPINHYRNIFSCLPLKH HMVTTPTLLLWGENDAFMEVEMAEVYRFYVKNYFRLTILEEASH WLQQDQPDIVNKLIWTFLKEETRKKD 6635 1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPPLG LVPCVVVGHSMGGKTAMILALQRPELVERLTAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTMLVEVDGRFVWRVALDALTQHLDKILAFPQRQESYLGFTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGMEKRTCQQNGEWSGKQPICIKACREPKISD LVRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYCHLHTQLQYECISFFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	0034		1134	
KSEYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLGY SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINPPHPNVPTEYI LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG IGRKGCQLTTBEDLEAYIVVFSQPGALSGPINHYRNIFSCLPLKH HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEASH WLQQDQPDIVNKLIWTFLKEETRKKD 6635 1420 470 EMRAGQQLASMLFMETAWRLPREGLGPHGPSFARVPVAFSSSG GRGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMILALQRPBLVERLIAVDISPVESTGVS HPATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFWWRNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVMGYQKITGGPGLINGRIAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTGGLRWPMQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVLUKKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	1. 1			
SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINPPHPNVFTEYI LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG IGRKGCQLTTBDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH HMVTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEASH WLQQDQPDIVNKLIWTFLKEETRKKD 6635 1420 470 EMRAGQQLASMLRWTRAWRLPREGIGPHGPSFARVPVAPSSSSG GRGABPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNRNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPBLVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTMLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNERRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIVRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLIGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLDKKARIS TRVQPICLAASRDLSTSFQBSHITVAGWNVLADVRSPGFKNDTL	1		• • •	<u></u>
LRHPAQLLKSSYYYFFQI PWFPEFMFSINDFKVLKHLFTSHSTG IGRKGCQLTTBDLERYIYVFSQPGALSGPINHYRNIFSCLPLKH HMVTTPTLLLWGENDAFMBVEMAEVTRFYVKNYFRLTILSEASH WLQQDQPDIVNKLLWTFLKEETRKKD 6635 .1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQOTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGRTMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMMAINTADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGGRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTUVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL]	* :		
IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH HMVTTPTLLLWGENDAFMBVEMAEVTRFYVKNYFRLTILSEASH WLQQDQPDIVNKLIWTFLKEETRKKD 6635 1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGAEPRIPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPBLVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE OPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQBSHITVAGWNVLADVRSPGFKNDTL			l. t.	
HMVTTPTLLLWGENDAFMBVEMAEVTRFYVKNYFRLTILSEASH WLQQDQPDIVNKLIWTFLKEETRKKD 6635 1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMILLALQRPBLVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	1 · ·			
WLQQDQPDIVNKLIWTFLKEETRKKD 6635 1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	[· .]			1
6635 1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPBLVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVWERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFFR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL		'		· ·
GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTNIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	6635	1420	430	
ILAQQTGRRVLTVDARNHGDS PHS PDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	0,033	1420	4.70	
LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL				
HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL		ļ	•	"" " " " " " " " " " " " " " " " " "
LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTTFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	}	•		· · · · · · · · · · · · · · · · · · ·
LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	[
AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL				15
6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL				
QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	6635		1001	
DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	1 3030	7374	TOAT	
6637 2 1501 CSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL				
KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	F-633		3.50.	
VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	003/	2	1501	-
LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	1			
DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	1			19.15
CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL				
FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL	1 1			
DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL				
TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL]			
DASSESSED DASS				-
	} {	ľ		RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC
TAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAF	L			TAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAF

Predicted Predicted Predicted Predicted Predicted No: Incleotide In		•		
Note location corresponding to first mino acid residue of	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Note location corresponding to first mino acid residue of	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid amino acid amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence security company	NO:		location	
L=Leucine, M=Methionine, N=Asparagine, amino acid residue of residue of amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, mino acid sequence V=Tytopian, V=	1			
to first amino acid residue of amino acid residue of amino acid amino acid amino acid sequence 8-Sestine, T-Threonine, V-W-Yliosie, W-Tryptophan, Y-Tyrosine, X-Unknown, *-stop Codon, *-possible nucleotide deletion, '-possible nucleotide deletion, '-possible nucleotide deletion, '-possible nucleotide deletion, '-possible nucleotide insertion) 15/LPF/KOMTERNEN 6638 1391 224 6619 6619 204 6619 204 6629 2046 1268 6639 2046 1268 6639 2046 1268 6639 2046 1268 6639 2046 1268 6639 2046 1268 6640 117 1043 1269 1268 6640 117 1043 1269 1268 6640 117 1043 1269 1269 1268 6640 117 1043 1269 1269 1269 1260 1270 128	1		-	
amino acid residue of amino acid sequence				
meino acid sequence s				· · · · · · · · · · · · · · · · · · ·
amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion) TKYLPFKONTERNEK 31391 224 GGTQGGGGGKARAPWERALCECERREKGFSTSAVLGERTPPLGFM PNSDIDLSHLEFLEKYTGSPREYBERAGCGAGAPHWERTYLEYEG EXTDYEKIDLGINELEKYTGSPREYBERAGCGAGAPHWERTYLEYEG EXTDYEKIDLGINELEKYTGSPREYBERAGCGAGAPHWERTYLEYEG EXTDYEKIDLGINELEKYTGSPREYBERAGCGAGAPHWERTYLEYEG EXTDYEKIDLGINELEKYTGSPREYBERAGCGAGAPHWERTYLEYEG EXTDYEKIDLGINELEKYTGSPREYBERAGCGAGAPHWERTYLEYEG EXTDYEKIDLGINELEKYTGSPREYBERAGCGAGAPHWERTYLEYEG EXTOYEKING THE PLANT TO THE TENDER OF THE TOTAL TO THE TENDER OF THE TENDER OF THE TOTAL TO THE TENDER OF THE TOTAL TO THE TENDER OF THE TENDER OF THE TOTAL TO TENDER OF THE TE				
Sequence		residue of	amino acid	
6638 1391 224 GGIPOGGGKMANJCECRRWKGPSISAVIGRETTPELGPM PNSDIDLSNLEELEKYRSTPEYRRAEQEAQAPHWRITYBEYDE BKIDDVEKIDIGLEKYRSTPEYRRAEQEAQAPHWRITYBEYDE BKIDDVEKIDIGLEKYRSTPEYRRAEQEAQAPHWRITYBEYDE BKIDDVEKIDIGLEKYRSTPEYRRAEQEAQAPHWRITYBERAA BLETASVELDAVRAERBERTCGPYHKGRLAEYYGLYRDLFERGAT VERVPLHVANVARGEDLMPYVCOKUPTPERAQAPETYTEABEG SLWTLLITSIDGHLLEPDAEVIHKULTRITPORKVAEGOVTCPYL PPFPARGSGIRLAFILKYCOOPIDFSEDARPSCYCLAQRITR TEPPFYKROGITTPAGAISFFCOKUNDSVTITHIQLLDMKEFVIFE FVERPPFYRRYPHYROKREPHROQLEXYLDKYRDSEPEKYRKPE DPBECPERVYDRRSLYBRIQECKDRKQGSVERGFFKONWYRGE BURTHFLEVENSGOGLIEKGRREERLEKELKEYNHALKKYGIGGE NKKEVEKKLTYKPIETNINFSQAKLLAGAVKHKSBEGNIVKRPE DPBECPERVYDRRSLYBRIQECKDRKQGSVERGFFKONWYRGE KREVEKKLTYKPIETNINFSQAKLLAGAVKHKSBEGNIVKRPE BURTHFLEVENSGOGLIEKGRREERLEKELKEYNHALKKYGIGGE NKKEVEKKLTYKPIETNINFSQAKLLAGAVKHKSBEGNIVKRPE KAPPPDDKRAGPSSKCSIGNISTSGOFBIKTRSAARVIGGILBGI GAVSGSSDSSSSSSSSGGTINATGKUNSSISTPINTFLEAP RIAAQAVTKNCCKASRENGGRULLVVDIPGIFFTKSSLDTTKA- KREVEKKLTYKLEITNINFSQAKLLAGAVKHKSBEGNIVKLTAK- FRIENDAMPONINFALVILLIGATHVALLIGATHVALGASFSKKSTAKLIKAVFTKSSAK- NKKTSKAREKSOVGELVELIEKNIVKOSGNINFIKTIGBEITDS NKKTSKAREKSOVGELVELIEKNIVKOSGNINFIKTIGKETPS NKKTSKAREKSOVGELVELIEKNIVKOSGNINFIKTIKAVFTKSSAK KHWILIFTKREBLEGGSFFRIFTAADAVGLKSIVKECONRCCKSKS NKKTSKAREKSOVGELVELIEKNIVKONGSHINFIKKKCKFYSS NKKTSKAREKSOVGELVELIEKNIVKONGSHINFIKKKCKFYSS NKKTSKAREKSOVGELVELIEKNIVKUNGSBURHEFIKKCKFYSS NKKTSKAREKSOVGELVELIEKNIVKONGSAKSTAKKKINKLIK VERKINKREBARNIFIKTOVRINFIKENSETRIKKKEKIKIKLIK VERKINKREBARNIFIKTOVRINFIKENSETRIKKATAK KAPPPKPRGLSROMGULLUNDTPGTFTKSLAGTRAGA NKOREFURNITATIONATIONATIONATIONATIONATIONATIONAT	İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
6638 1391 224 GGIPOGGGKMANJCECRRWKGPSISAVIGRETTPELGPM PNSDIDLSNLEELEKYRSTPEYRRAEQEAQAPHWRITYBEYDE BKIDDVEKIDIGLEKYRSTPEYRRAEQEAQAPHWRITYBEYDE BKIDDVEKIDIGLEKYRSTPEYRRAEQEAQAPHWRITYBEYDE BKIDDVEKIDIGLEKYRSTPEYRRAEQEAQAPHWRITYBERAA BLETASVELDAVRAERBERTCGPYHKGRLAEYYGLYRDLFERGAT VERVPLHVANVARGEDLMPYVCOKUPTPERAQAPETYTEABEG SLWTLLITSIDGHLLEPDAEVIHKULTRITPORKVAEGOVTCPYL PPFPARGSGIRLAFILKYCOOPIDFSEDARPSCYCLAQRITR TEPPFYKROGITTPAGAISFFCOKUNDSVTITHIQLLDMKEFVIFE FVERPPFYRRYPHYROKREPHROQLEXYLDKYRDSEPEKYRKPE DPBECPERVYDRRSLYBRIQECKDRKQGSVERGFFKONWYRGE BURTHFLEVENSGOGLIEKGRREERLEKELKEYNHALKKYGIGGE NKKEVEKKLTYKPIETNINFSQAKLLAGAVKHKSBEGNIVKRPE DPBECPERVYDRRSLYBRIQECKDRKQGSVERGFFKONWYRGE KREVEKKLTYKPIETNINFSQAKLLAGAVKHKSBEGNIVKRPE BURTHFLEVENSGOGLIEKGRREERLEKELKEYNHALKKYGIGGE NKKEVEKKLTYKPIETNINFSQAKLLAGAVKHKSBEGNIVKRPE KAPPPDDKRAGPSSKCSIGNISTSGOFBIKTRSAARVIGGILBGI GAVSGSSDSSSSSSSSGGTINATGKUNSSISTPINTFLEAP RIAAQAVTKNCCKASRENGGRULLVVDIPGIFFTKSSLDTTKA- KREVEKKLTYKLEITNINFSQAKLLAGAVKHKSBEGNIVKLTAK- FRIENDAMPONINFALVILLIGATHVALLIGATHVALGASFSKKSTAKLIKAVFTKSSAK- NKKTSKAREKSOVGELVELIEKNIVKOSGNINFIKTIGBEITDS NKKTSKAREKSOVGELVELIEKNIVKOSGNINFIKTIGKETPS NKKTSKAREKSOVGELVELIEKNIVKOSGNINFIKTIKAVFTKSSAK KHWILIFTKREBLEGGSFFRIFTAADAVGLKSIVKECONRCCKSKS NKKTSKAREKSOVGELVELIEKNIVKONGSHINFIKKKCKFYSS NKKTSKAREKSOVGELVELIEKNIVKONGSHINFIKKKCKFYSS NKKTSKAREKSOVGELVELIEKNIVKUNGSBURHEFIKKCKFYSS NKKTSKAREKSOVGELVELIEKNIVKONGSAKSTAKKKINKLIK VERKINKREBARNIFIKTOVRINFIKENSETRIKKKEKIKIKLIK VERKINKREBARNIFIKTOVRINFIKENSETRIKKATAK KAPPPKPRGLSROMGULLUNDTPGTFTKSLAGTRAGA NKOREFURNITATIONATIONATIONATIONATIONATIONATIONAT	ľ	sequence		\=possible nucleotide insertion)
GGIPOLGGERMALPHERADEGRAPHHERATECTER BINDLICHINELLE KEYPSIDE YERRADEGRAPHHER TYPE YER EKTDPLEEN LIGHPPEVER ROCKLERKOJOELDANVEEREN EKTDPLEEN LIGHPPEVER ROCKLERKOJOELDANVEEREN EKTDPLEEN LIGHPPEVER ROCKLERKOJOELDANVEEREN VERVILIVA YANGEDDIMP VICONEVIT PERAGA PEVIT PERAGE SLATILLIIS LIGHLIE POR BETLIHHLITHI FERRIVAREGYUT CEPT PPPPARGGERI HARPLIFKOOPE IDTS SIBMER PE CYCLIAGRIFF PPPPARGGERI HARPLIFKOOPE IDTS SIBMER PE CYCLIAGRIFF PPPPARGGERI HARPLIFKOOPE IDTS SIBMER PE CYCLIAGRIFF PVERPPYHP KORKETHING DE KYLIAGRIKHER PUTE PE PERPPYHP KORKETHING DE KYLIAGRIKHER PUTE PE PERPPYHP KORKETHING DE KYLIAGRIKHER PUT SILME FURDPEP HYBROGERI KERNEGERE KERKERGE EMERIKE SEGNING NICKEVER KERNEGER KYRIALKOVI SILMEN ENTIFICIE SEGNING SEGNI				
PNSDITLSHLEKYRSTBYRRAEQEAQAPHWRTYTSFERA EKTDYEKE IDIGLERWAJGELERWAJGELARVICEBRAA EKTDSEK DIA DER SANGERER EKTDYEKE IDIGLERWAJGELARVICEBRAA EKTDSEK DIA DER SANGERER EKTDE SENTELLER EKTDE SENTELLETSBEDELBEVYCOREVITYERAGA PEVTYABEBE SLATILLITSIDGHLIBEDAELIHLITSITERREVABGQVICEYL PPFPARGGIRKLAFLLERGOOFIDES BEDARFS PC-TQLAARTET TEPFYKKRIGTTHEPGGISF PCCKHODSVITTIFELGLIAMREVYFE FVERPPYHRRAEGISF PCCKHODSVITTIFELGLIAMREVYFE FVERPPYHRRAEGISF PCCKHODSVITTIFELGLIAMREVYFE FVERPPYHRRAEGISF PCCKHODSVITTIFELGLIAMREVYFE FVERPPYHRRAEGISF PCCKHODSVITTIFELGLIAMREVYFE DPBECPERVYDPRSLYBRIJGEKORKOGSVEGCFFFRNWYGLISG BEDETHELDEVSROGGLIEKGREFERALDEKKKREVSHAKKVGISGE NKKEVEKKLTYKSIETKINFSOAKLLAGAVKHKSSESGINSVKTORE LEDETHFLDEVSROGGLIEKGREFERALKIKKVGISGE NKKEVEKKLTYKSIETKINFSOAKLLAGAVKHKSSESGINSVKTILGEBEIFDS RIAAGAVTRKCOKASRENGGROLLVOTPGLEPTIKSELDTTCKE ISRCIISSCGEPHATULVILLIGRYTSBERKTVALLKAVPKSSA KHAVILTFIREBLESGSFFDITLAADVELKSIVKECUNGCASF NSKKTSKABKESGVOELVELLEKMVOCHGGAFFSDDITKINGER KHAVILTFIREBLESGSFFDITLADAVGLISGINGENGCASF NSKKTSKABKESGVOELVELLEKMVOCHGGAFFSDDITKINGER LKOREGULRIKTUDIAMEIKUNGVEGGFFTANTILGEBEIFDS RIAAGAVTRKOCKASRENGGROULVOTPGLEPTIKSELDTTCKE ISRCIISSCGPHATULVILLIGRYTSBERKTVALLKAVPKSAS HANGEVLRIKTUDIAMEIKUNGVEGGFFTANTILGEBEIFDS RIAAGAVTRKOCKASRENGGROULVOTPGLEPTIKSELDTTCKE ISRCIISSCGPHATULVILLIGRYTSBERKVALLKAVPKSAS LKOREGULRIKTUDIAMEIKUNGVEGGFFTANTILGEBEIFDS RIAAGAVTRKOCKASRENGGFFTANTILGEREIFDS NSKKTSKABKESGVOELVELLERKNICKSCHEKEITKALLKAVPKSAS LKOREGULRIKTUDIAMEIKUL LKOREGULRIKTUNGVEGAFFFTANTILGEREIFDS RAAPPROFSATISCTVEGAFFFTANTILGEREIFDSTANTILGEREIFDS RAAPPROFSATISCTVEGAFFFTANTILGEREIFDSTARGLGSSAS TLRRIDSTYBASSLYGISAMDOVEPTILHRREGKKSCSPLAFSAF GDLTIKSGABFFTANTILGEREIFDSTARGLGSSAS TLRRIDSTYBASSLYGISAMDOVEPTILHRREGKKSCSPLAFSAF GDLTIKSGABFFTANTILGEREIFDSTARGLGSSAS TLRRIDSTYBASSLYGISAMDOVEPTILHRREGKKSCSPLAFSAF GDLTIKSGABFTANTILGEREIFDSTARGLGSSAS TLRRIDSTYBASSLYGISAMDOVEPTILHRREGKKSCSPLAFSAF GDLTIKSGABFTANTILGEREIFDSTANTILGEREIFDS ROADPOVERSTANTILGEREIFDSTANTILGEREIFDSTANTILGEREIFDS ROADPOVERSTANTILGEREIFDSTANTILGEREIFDSTANTILGEREIFD	6670	1201	224	
EKTDPKENIDIG,DPPKVSKTQQLIERKQALGERRAN BLETASVELDAVBARMETCGEPHKQALGENGVALGYBLAYBLAGE BLETASVELDAVBARMETCGEPHKQALGENGVALGYBLAYBLAGE SLATLLITSLOGHLIEPDASVIHRULTNITEGRIFAQAPETVETABEG SLATLLITSLOGHLIEPDASVIHRULTNITEGRIFAQAPETVETABEG SLATLLITSLOGHLIEPDASVIHRULTNITEGRIFAQAPETVETABEG SLATLLITSLOGHLIEPDASVIHRULTNITEGRIFAQAPETVETABEG SLATLLITSLOGHRILEPDASVIHRULTNITEGRIFAGAPETVETABEG SLATLLITSLOGHRILEPDASVIHRULTNITEGRIFAGAPETVITY FVPPPPHPKRKQETMIPAGISFFQCRUDDSVTYITHQLLIMMEVPFE FVPPPPHPKRKQETMIPAGISFFQCRUDDSVTYITHQLLIMMEVPFE FVPPPPHPKRKQETMIPAGISFFQCRUDDSVTYITHQLIMMEVPFE FVPPPPHPKRKQETMIPAGISFFQCKINKQEVERGEPTKRNAVRGLO BETTIPLDEVSRQQELIEKQREBELKELKEVRINLIKKVISGE NKKEVSKLITVKSITEKTRSCAKLLIGAVIKKSSEGRINVKRIL EDETTIPLDEVSRQQELIEKQREBELKELKEVRINLIKKVISGE NKKEVSKLITVKSITEKTRSCAKLLIGAVIKKSSEGRINVKRIL KPPPEPDDKNQEPSSCKSLANTISLIGSPIHCPSANVCIGILPGI GAYSGSBISSESSDSGEVITANTIKUSSEGRINVETTEGAP 1043 VLEPPDVSNAGSSDBSSIDSKILVLOVENGASKATANTILGEEIPDS RIKATSKASSSDSGEVITANTIKUSSEGRINVETHEAP RAAQAVTKNOKASREBORGALLVOVPTGELPTKEELPTTCKE ISRCIISSCPOPHATVULLLGRYTEEROKTVALIKAVPGKSAM HHWILIPTREBLEGGSHPUTADADVIKISTKORGNCAFSA NSKITSKABKSSOVBLUELIERMYOCNEGATPSDDIYVAKTEA LKQREVURATYTYOOLNEELKULDEDKISSEKKKKITULLIKK VIDEKIKNITEBARNIFROVPNRIHKMLSEIHMEFLSKCKFYSS NSKITSKABKESOVBLUELIERMYOCNEGATPSDDIYVALTEE LKQREVURATYTYOOLNEELKULDEDKISSEKKKKENTULLIKAT KLEPLANTOTAVDVALGGISLDAASCP SKIGGLLERTASGSASA TLARNDSIYLBASILCTIKADAGPFKITANGSASASATULLAKSSASA TLARNDSIYLBASSLICTIKADAGPFKITANGSASASATULCKKRICV KLEPLANTOTAVDVALGGISLDAASCP SKIGGLLERTASGSASA TLARNDSIYLBASSLICTISADADGPFTLIHTPETSLOCKTYV HOPPYTRIVLENSSEBKHELOPPSKIAGASSPDSMAPGSGTE KRAMITKOYKMIGFTNIHIPAMDFTOPPGHIALDMILYLAKV HOPPYTRIVLENSSEBKHELOPPSKIAGASTBLIRLGOSSE MSQDDTOSPPIVELREKTOPPLIKTETSLOCKTYV ADIKATVTCHINFTSLOPPKINGDENSKIAGRESPTHILGENDYTHS MSQDDTOSPPIVELREKTOPPLIKTETSLOCKTYV ADIKATVTCHINFTSLOOPPKINGENSTALLEGONYHERMILL LEDRINGTNEDPPINGENSTALLEGONYHERMILL DATTVIECHTFCSCLIVKLEDDNOTHSLOGHLYTIDOR CHARLOGHLYNDENDINGSTANDSNICHTERNICTHOPPMULL LUTTRILDTITGCSCLIVKLETDIDONSKALKRICHTERNICHTERNICHTERNOTHURDHUNGENITHERNICHT	6636	1391	224	_
BLRTASVELDAVBARRETTGEPYHRQLARYGLYRDLFHIGATF VPRYPHANAVAGEDIMPYOCONEVPTEADES SIMTLLITSLDGHILBPDAEYLHHLLTNIFGMRVABEGOVTCPYL PPPFRARGGIHRIAFILBFRODGIPTGESDARPS PGYCHLAGTTR TEPPYKRHQETURPAGISF PGYMDDSVYTIFHQLIADMREBVOTE 6639 2046 1268 IGGFIMGGGDGHALITKERVEGAERLDERREKRGERBEKVRKPE DPECCEBVYDPRSLYRRLGEGKDEKOGEYEEQFKFRONVARLD EDERTNIFLGEVSGAELIEKREKGERBEKVRKRPE DPECCEBVYDPRSLYRRLGEGKDEKOGEYEEQFKFRONVARLD EDERTNIFLGEVSGAELIEKREKGERBEKVRKRPE DPECCEBVYDPRSLYRRLGEGKDEKOGEYEEQFKFRONVARLD EDERTNIFLGEVSGAELIEKREKGERBEKKEKREKGERBEKVRKPE DPECCEBVYDPRSLYRRLGEGKDEKOGEYEEQFKFRONVARLD EDERTNIFLGEVSSAELIEKREKGERBEKVRKRPE DPECCEBVYDPRSLYRRLGEGKDEKOGEYEEQFKFRONVARLD KKEVEKKLTYKSIETIKKFSGAKLLAGAKKKSSEBGKVKRL KPDPEDDKKNGESSKSKLSGAELIEKREGERBEKVRKRPE BORGHVEKLTYRSIETIKKFSGAKLLAGAKKKSSEBGKVKRL KPDPEDDKKNGESSKSKLSGAELIEKREGERSAELIELEE INGATSGSBGRSSGBSGBSGTINATIKLVSSIFRTNIFLERD GAYSGSSBGRSSGBSGTINATIKLSSIFRTNIFLERD RIAGAVTKNCQKASREWGGRDLLVVDTPGLEFDTCKE ISRCIISSCPOPHALVAULLGRYTEBEGKTVALIKAVFGKSMA KHWTLFFTKEBLEGGSTEHPIADADVGLKSIVKSGAMKCAFKS RIAGAVTKNCQKASREWGGRDLLVVDTPGLEFDTCKE ISRCIISSCPOPHALVAULLGKTSTTEBERGKTVALIKAVFGKSMA KHWTLFTKREBLEGGSTEHPIADADVGLKSIVKSGAMKCARKS KKTSKKTKAEKESGVGBLVELLERMVQCNBGATFSDLYKTGEM KKREVLKRIVTDOLMERIKUEDHCHSEKKKKEK RILLELK YDGKIKNIREBARNI FEDVFRILIKMESIHHRFLSKCKFYSS ASAPPRGFSAISCTVEGAPASGKSFRAKMPDVFORFALGLAMSS KKTSKKTKAEKESGVGBLVELLEFSVCOMBOKASVSKKKRKKV KLIPLAATDTAVFDVALGGKTKTVBGYFLRIGDMGGFAIWKKAK APRPVBKRGGSRDMGGLSDAASGKSFRAKMDPVFORFARGLGSASS TLRRNDSIYBRSSILMGGSBDAAGASGKSFRAKMFARGLGSASS TLRRNDSIYBRSSILMGGSBDAAGSGRSFRAKGASGSFRAGGGAFTLAGATAVE GDLTIKSSLAGLAGENAWILGESFVCOMBOKASAVSKKKRKKK KLIPLAATDTAVFDVALGGKTKTVBGYFLRIGDMGGFAIWKKAK APRPVBKRGGSDMGGLSDAASGFRAKMDPVFORFARGLGSASSGSTAGG GDLTIKSLAGLAGENAWILGESFVCOMBOKASAVSKKKRKKK REPROVERBERGEMENDITAFSBDAAGLAGSFRAGGSSPALGAGATSGRAGGSTAGGATTALLTAMMTLTAKL GGGATATALASKAMATATATATATATATATATATATATATATATATATATA	l	1		1
SLINTLINISLOGHLEPPASYLHMILTUNIPGRIVAGEOVICPYL PPPPARGGIHRLAFILFKODOPIDFSDARPSPCYCLAGRIFR TFDFYKRKQETMYPAGLSFPCCKHDSVTYIFHCLINKEVPFF FVRPPYHRRYGKREHROPKIDERKRERGESBERKYRFE FVRPPYHRRYGKFPHROPKIDERKRERGESBERKYRFE DPBECCEWVPDPSLYBRLQGEDERKKRGESBERKYRFE DPBECCEWVPDPSLYBRLQGEDERKKRGESBERKYRFE DPBECCEWVPDPSLYBRLQGEDERKKRGESBERKYRFE DPBECCEWVPDPSLYBRLQGEDERKKRGESBERKYRFE DPBEDDKNQBPSSCKSLGNTSLGGPSIPKTROMAGNAL BETTIPLDEVSRQOELIFKGREBELKELKEVRINLIKKYSISG NKKEVKKLYVKIT EITMKYSQAKLLAGAVKHSSBGGNVKRL KPDPEPDDKNQBPSSCKSLGNTSLGSPSHCPSAAVCIGILFGL GANGGSSDSSPSSDEGCTIRAKKISSSGKATANTILGEBIFDS RIAAQAVTKNCQNASRBQGRILLIVVDTRGLFDTKRSLIDTTCKE ISKCIISSCOPPHALVIVLLLGRYTBEBGKYTALIKAPGKSAM KHWILIPTRKBELBGGSFHDFTADADVGLKSIVKGCONNCCAFS NSKKTSKARKESVOELVELIKMYGCNGBAYFSDDIYKDTERF LKQREVLRKIYTDQLINEIKLVEDDKHKSEBKKEKSILKLKLK YDKKINTRREBERGYPSHLAVIVLLGRYTBEBGKYTALIKACKTYSS NSKKTSKARKESVOELVELIKMYQCNGBAYFSDDIYKDTERF LKQREVLRKIYTDQLINEIKLVEDDKHKSEBKKEKSILKLKLK YDKKINTRREBERGIFSTUPKINIKMLISSIHKKKCKTYSS NSKKTSKARKESVOELVELIKMYQCNGBAYFSDDIYKDTERF LKQREVLRKIYTDQLABEIKLVEDDKHKSEBKKEKSILKLKLK YDKRINTRREBERGIFTSTOHADASPGKSFARKSCHLSKCKTYSS NSKRTSKARKSSOVELVELIKMYQCNGBAYFSDLYKTGTSMGGTA AFRYVEKRGLASTGTUPCHADASPGKSFARKSCAPLASKCKTON KLIPLIAATUTAVEDVRLSGKTKTVFGVILRIGHMGGTALSKGKAK AFRYVEKRGLASKOVGLUELIBERTASRLGSRAS TLRRINSIYERSSLKVILSAMDGVFTLHFREFGKSCSPLAFSAF GDLTIKSLADIEBERNYGVFVVEKTAARALPED-TLLSSLIGLBER NGDDTGSFTLTVILLEBENNYGVVEKTAARALPED-TLLSSLIGLBER NGCDTGSFTVTAVEDVRLSGKTKTVFGVILRIGHMGGTALDBMIYLLAKV HQDTYTRIVLENSSREDKHECPFGSSATELTKMLCELLGVGELP NEGGROVITHERFTHORAPETLFOICLGLIKMEMATAADF KVMQVVRGQITRALPSKNISLOPKSKLRSLSYSSILRLLGGSER NGCDDTGSFTLVGTGGSATLKTKUCCHLAKMENTALDER NGCRFWYCRLAKMIKTHALDDFTSKYRBALDTLLSBERNINGSE NGCDDTGSFTLOGGSALLKKHKYGGDLATLLKKHKAADDTTLLSBERNINGSF NGCRFWYCRLAKMIKTRICAGATVLLHKKELDADTTLGEGSSFRKIG NRRGGRFWYCRLAKMIKTRICAGATVLHLKKELDADTTLGEGSSFRKIG NRRGGRFWYCRLAKMIKTRICAGATVLHLKKELDADTTLGEGSFFRLG NRRGGRFWYCRLAKMIKTRICAGATVLHLKKELDADTTLGLGSBERNE LDENIGTDFT GRANGKATKALLSFTREDDUTTLOG LENDALSCHARTERTITTOREERGANLTHFOILDGE LENDALTHEN NACHORDSTRICTTOREE				
SLMTLLITSLOGHLERPARYLHMILITNIFGRRVABEGOVTCYTL PPPPARGSGITHELATLIKERODO I 19 FSEDAR FYCHALARITH PREPARGSGITHERATLIKERODO I 19 FSEDAR FYCHALARITH FOR THE THE THE THE THE THE THE THE THE THE	1			1
PPPPARGG IHRLAFILIPKODOPIDFSEDARPSPCTQLAQRIFR TEPPYKKNGETWPAGLSF POCKMODSVTJ LOLLDMREDVYE FVRPPYHRYPAGLSF POCKMODSVTJ LOLLDMREDVYE FVRPPPYHRYPAGLSF POCKMODSVTJ LOLLDMREDVYE FVRPPPYHRYPAGLSF POCKMODSVTJ LOLLDRREVYES 1 GGFIMOGODGMLITKKREVSERAELDERKREGESBEKVRPE DPBECPERVYDPSLYBRLQEKDERKGETSGEFKFKNWRGLSG BKKEVEKLITVKEJ IETKRESCAKLLGAVEKKGESERKVRSIGE BETTIPLDEVSRQGELIEKGREBELKELKEVRNINIKKVISGE KKKEVEKLITVKS IETKRESCAKLLGAVEKKGSEGSSNSVERI KPDEEPDDKNQEPSSCKSLGNTSLGGPSHCFSARVCIGIPGI GAYSGSISISSS SDGSGTINAKTKI VSSIFFRTYFLERAP 6640 117 1043 VLEPPDVSKASSEDRSJLVUVDVEGGKSATAWTIGEBIPGS RIAAQAVTKNCQKASREWGGRDLIVVDTPDELDTTKSELDTTCKE ISRCIISSC POPHALVLVLLGRYTEBEQKTVALI RAVFGKSAM KHWYLLFTRKEBLEGGSFHDFIADADVGLKSTEKKETSLALLKLK VDKKTISKAEKSOVGELVELI KHMYQCNEBAST FSDD YKUTEER LKQRESVLRKIYTDQLMEEIKLVEEDGKTVALI RAVFGKSAM KHWYLLFTRKEBLEGGSFHDFIADADVGLKSTEKKETKSLKLKLK VDKKTISKAEKSOVGELVELI KHMYQCNEBAST FSDD YKUTEER LKQRESVLRKIYTDGLMEEIKLVEEDGKTKVALI RAVFGKSAM KHWYLLFTRKEBLEGGSFHDFIADADVGLKSTEKKETKSKATKSS NSKKTISKAEKSOVGELVELI KHMYQCNEBAST FSDD YKUTEER LKQRESVLRKIYTDGLMEEIKLVEEDGKTKAVAT FSDD YKUTEER LKQRESVLRKIYTDGLMEEIKLVEEDGKTKSTAKSEKKETKALLKLK VDRKINNIRGEARRI FKDVPRINKIMIGSTEKKEKTYSS ASAPPROFRSISCTURGLAGSFGK FARGKSFAKSKEKKENG KLEPLGATTAVTPOVALSGKTKTVPG YLRIGDMGGFAIWCKKAK APRPVFKRGLISCDMGGISLDARGCP SKOGLLERTAGRIGSASA TLRRINDSIYEASSLKGISADGOFFILEFREFGKSC SPLAFSAF GDLTIKSLADI EERNINGTVEKTAARLDEFSVS 6642 22 1296 PLEERMIKMDPDDGAGGDI FELER LAFDARSDDSTAR RANGENGEN FYLLEGESSFRICH ROMODFILEFRIKTOPELITERENGESSFRICH ROMODFILEFRIKTOPELITERENGESSFRICH ROMODFILEFRIKTOPELITERENGESSFRICH ROMODFILEFRIKTOPELITERENGESSFRICH ROMODFILEFRIKTOPELITERENGESSFRICH ROMODFILEFRIKTOPELITERENGESSFRICH ROMODFILEFRIKTOPELITERENGESSFRICH LDLENGILTPELITERENGESSFRICH LDLENGILTPELITERENGESSFRICH LDLENGILTPELITERENGESFRICH FLIEGGSFRICH LDLENGILTPELITERENGESFRICHTERENDITTERENDITTERENGENGENTERPHOLDTILTERENDITTER LDLENGILTPELITERENGESFRICHTERENDITTERENDITTERENDITTERENDITTERENGESFRICHTERENDITTERENDITTERENDITTERENDITTERENDITTERENDITTERENDITTERENDITTERENDITTERENDITTERENDITTER		1		VPRVPLHVAYAVGEDDLMPVYCGNEVTPTEAAQAPEVTYEAEEG
TFDFYKKIQETMYPAGLISFGCKMDDSVTY1FHGLIDMREPYTE FVRPPYPHEROKKRPRINGDLEYLDRYNDSHEPTIGIY 6639 2046 1268 IGCFIMOGDDGNLIIKKRFVSEAELDERRKGROEBIEKVRKPE DFBECPESVYDPKSLIVERLOGGOKORKQEYEEGFKFKNWRGLI EDETMYLDEVSRQQELIEKQRREELKEKLKSYRNNLKKYGISQE NKKEVSKKLITYKSIETKKFSQAKLLAGAVKHKSSESGRSVKRK. KPDPEPDOKNQEPSSCKSLGSTELSGSPFSANCTGLIEGE GANSGSIDSBSSIDSBGTINATGKLIVGSIFFTNTYFLEAP 1043 VLEPPPVSHASSEGRSIRIVLVULGTGTGSGKSATANTIGEEIDS RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKSSLDTTCKE ISRCIISSC PGPHAIVLVLLUGRYTSERGKTVALIKGVGTGSGKA KHWILFTKEELEGGSFTHPTIADADVGKSIVKEGONRCCAFS NSKKTSKAEKESQOVGLVELLEKWOQCNSGAYFSDDIYKDTEER LKQRESVLRKIYTDGINEE IKLVEEDKHSKEKKEKSIKLLKLK YDRKIKNIREBARRIFKUVENHRESAEMSPOPTOTSAPLAGLAMSS ASAPPRGFSAISCTVEGAPASFGKSFAKKKTYCY KLKDFLOATTAVFDVLRISSKTYTPGYLREKSKKEKSIKLLKLK YDRKIKNIREBARRIFKUVENHRESAEMSPOPTOTSAPLAGLAMSS ASAPPRGFSAISCTVEGAPASFGKSFAKKKTYCY KLKDFLOATTAVFDVLRISSKTKTYPGYLREKSLEKKEKSIKLLKK YDRKIKNIREBARRIFKUVENHRESAEMSPOPTOTSAPLAGLAMSS ASAPPRGFSAISCTVEGAPASFGKSFAKKKTYCY KLKDFLOATTAVFDVLRISSKTKTYPGYLREIDDMGGFAIKKKAA APRPVFKPRGLSRAMGUSIDAASGPSKGGLBERTARGSARAS GDLTIKSLADIESTNYGFVVEKKAAARLPPSVS GDLTIKSLADIESTNYGFVVEKKAAARLPPSVS GDLTIKSLADIESTNYGFVVEKKAAARLPPSVS FERENMYTHERPSTIDARFELFFGGICTQLIKTWKERRATABDFN KVMQVVRGGITRALPSKYNSLOGKSKKKINGVEYTLERRGSSFSFSGG MSQDBTGSFFVCIBKRINGDEVFSKALLERUNGSESFKIG NRRGGRFFYCRLALHRKVLHYGDLDNPOGEVFFSSLOGKIFV ADIALATVTROCHMEKSSALKONKEVLEILKTRUCESSFFRIG NRRGGRFFYCRLALHRKVLHYGDLDNPOGEVFFSSLOGKIFV ADIALATVTROCHCHMEKSALKONKEVLEILKTRUCESSFFRIG NRRGGRFFYCRLALHRKVLHYGDLDNPOGEVFFSSLOGKIFV ADIALATVTROCHCHMEKSALKONKEVLEILKTRUCESSFFRIG NRRGGRFFYCRLALHRKVLHYGDLDNPOGEVFFSSLOGKIFV ADIALATVTROCHCHMEKSALKONKEVLEINTELEGESFFRIG NRRGRFFYCRLALHRKVLHYGDLDNROGEVFFSSLOGKIFV ADIALATVTROCHCHMEKSALKONKEVLENGESSFRIG NRRGBRFFYCRLALHRKVLHYGDLDNROGEVFFSSLOGKIFT LADNITYRIVILDFGCRACHKKORFFYRIKGEBEVFSEDONYTH LADNITYRIVILDFGCRACHKKORFFYRIKGEBEVFSEDONYTH LADNITYRIVILDFGCRACHKKORFFYRIKGEBEVFSEDONYTH LADNITYRIVILDFGCRACHKKORFFYRIKGEBEVFSEDONYTH LADNITYRIVILDFGCRACHKORFFYRIKGBEVFSEDONYTH LADNITYRIVILDFGCRACHKORFFYRIKGEBEVSEDONY	1	1		SLWTLLLTSLDGHLLEPDAEYLHWLLTNIPGNRVAEGQVTCPYL
TFDFYKKIQETMYPAGLISFGCKMDDSVTY1FHGLIDMREPYTE FVRPPYPHEROKKRPRINGDLEYLDRYNDSHEPTIGIY 6639 2046 1268 IGCFIMOGDDGNLIIKKRFVSEAELDERRKGROEBIEKVRKPE DFBECPESVYDPKSLIVERLOGGOKORKQEYEEGFKFKNWRGLI EDETMYLDEVSRQQELIEKQRREELKEKLKSYRNNLKKYGISQE NKKEVSKKLITYKSIETKKFSQAKLLAGAVKHKSSESGRSVKRK. KPDPEPDOKNQEPSSCKSLGSTELSGSPFSANCTGLIEGE GANSGSIDSBSSIDSBGTINATGKLIVGSIFFTNTYFLEAP 1043 VLEPPPVSHASSEGRSIRIVLVULGTGTGSGKSATANTIGEEIDS RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKSSLDTTCKE ISRCIISSC PGPHAIVLVLLUGRYTSERGKTVALIKGVGTGSGKA KHWILFTKEELEGGSFTHPTIADADVGKSIVKEGONRCCAFS NSKKTSKAEKESQOVGLVELLEKWOQCNSGAYFSDDIYKDTEER LKQRESVLRKIYTDGINEE IKLVEEDKHSKEKKEKSIKLLKLK YDRKIKNIREBARRIFKUVENHRESAEMSPOPTOTSAPLAGLAMSS ASAPPRGFSAISCTVEGAPASFGKSFAKKKTYCY KLKDFLOATTAVFDVLRISSKTYTPGYLREKSKKEKSIKLLKLK YDRKIKNIREBARRIFKUVENHRESAEMSPOPTOTSAPLAGLAMSS ASAPPRGFSAISCTVEGAPASFGKSFAKKKTYCY KLKDFLOATTAVFDVLRISSKTKTYPGYLREKSLEKKEKSIKLLKK YDRKIKNIREBARRIFKUVENHRESAEMSPOPTOTSAPLAGLAMSS ASAPPRGFSAISCTVEGAPASFGKSFAKKKTYCY KLKDFLOATTAVFDVLRISSKTKTYPGYLREIDDMGGFAIKKKAA APRPVFKPRGLSRAMGUSIDAASGPSKGGLBERTARGSARAS GDLTIKSLADIESTNYGFVVEKKAAARLPPSVS GDLTIKSLADIESTNYGFVVEKKAAARLPPSVS GDLTIKSLADIESTNYGFVVEKKAAARLPPSVS FERENMYTHERPSTIDARFELFFGGICTQLIKTWKERRATABDFN KVMQVVRGGITRALPSKYNSLOGKSKKKINGVEYTLERRGSSFSFSGG MSQDBTGSFFVCIBKRINGDEVFSKALLERUNGSESFKIG NRRGGRFFYCRLALHRKVLHYGDLDNPOGEVFFSSLOGKIFV ADIALATVTROCHMEKSSALKONKEVLEILKTRUCESSFFRIG NRRGGRFFYCRLALHRKVLHYGDLDNPOGEVFFSSLOGKIFV ADIALATVTROCHCHMEKSALKONKEVLEILKTRUCESSFFRIG NRRGGRFFYCRLALHRKVLHYGDLDNPOGEVFFSSLOGKIFV ADIALATVTROCHCHMEKSALKONKEVLEILKTRUCESSFFRIG NRRGGRFFYCRLALHRKVLHYGDLDNPOGEVFFSSLOGKIFV ADIALATVTROCHCHMEKSALKONKEVLEINTELEGESFFRIG NRRGRFFYCRLALHRKVLHYGDLDNROGEVFFSSLOGKIFV ADIALATVTROCHCHMEKSALKONKEVLENGESSFRIG NRRGBRFFYCRLALHRKVLHYGDLDNROGEVFFSSLOGKIFT LADNITYRIVILDFGCRACHKKORFFYRIKGEBEVFSEDONYTH LADNITYRIVILDFGCRACHKKORFFYRIKGEBEVFSEDONYTH LADNITYRIVILDFGCRACHKKORFFYRIKGEBEVFSEDONYTH LADNITYRIVILDFGCRACHKKORFFYRIKGEBEVFSEDONYTH LADNITYRIVILDFGCRACHKORFFYRIKGBEVFSEDONYTH LADNITYRIVILDFGCRACHKORFFYRIKGEBEVSEDONY	j	1	j	PPFPARGSGIHRLAFLLFKODOPIDFSEDARPSPCYOLAORTFR
FVRPPPYHROKERPEROLEYLDRYRDSHEYTGTY G639 2046 1268 1268 1268 126FIMOGDDGNLIIKKRYVSEAELDERKRRGEENEKVRYEE DPBECPERVYPRESLYBELDERKRRGEENEKVRYEE DPBECPERVYPRESLYBELDERKRRGEENEKVRYEE NKKEVEKKITVKVEITETKKFSQAKLLAGGVERGEKSEKVRIKVGISUE KKEVEKKITVKVEITETKKFSQAKLLAGGVERKSESSGNSVKRI KPDPEPDDKNOEPSSCKSLGNTSISGPSIHCPSAAVCIGILLGIL GANGSISDSSSSSDSGTINATKKIVSJFFNTNFILEAP 6640 117 1043 VLEPPDVSMAESEDRSLRIVLVGKTGSGKSATANTILGEEIFDS RIAAQAVTKNCQKASREWGGRDLLVVDTGIFDTKSELDTTCKE ISRCIISSFOPHAITUVLLLGRYTEEEGKTVALIKAVFGKSAM KHWILLFTRKEELEGGSFHDFIADADVGLKSIVKEONRCCAFS NSKRTSKARKESQVGSLUEVDFRIVELKENVQCORGAYFSDDIYKDTEER LKGREEVLRIYTDOLNEEIKLWEDKHRSEEKKEKILLLKA VDEKINNIBERBERNIYEVDFRIVELKENVGCORGAYFSDDIYKDTEER LKGREEVLRIYTTOLNEEIKLOWDFRIVELMEHFISKCKFYSS 6641 1 894 SAAVGRRSEVRGCAPRFELRRSARNDDVPGTDSAPLAGLAWSS ASAPPPROFSAISCTVEGAPASFGKSFAAKSGYFLCLSIGSLE NPOENVADIJUVUNSKSJELJEGSFYCOMBSKASVSKKKRNCV KLUPLGATDTAVFDVVLISGKTKTVPGYLSIGDMGGFAINCKAK APRPVFKRFGISRMGGLSDLAGAGPSKGLLERTARICKSSAS TLRNDSIYEASSLYGISAMGOVPFTLHPRFEGKSCSPLAFSAF GDLTIKSLADIEBEYNNGFVVEKTAARLPPSVS 6642 22 1296 PLEERMWTKMPBNDQAGRDIIFELRRIAPAESDPSNAPGSGTE KRKAMTKOYMKLGFTNHINPAMDFTQTPPOMLALDMMYLAKV HOPTYRTULENSREDEKHECPGRSASILGHEATARICKSSAS TLRNDSIYEASSLYGISAMGOVPFTLHRREGRSCSPLAFSAF GDLTIKSLADIEBEYNNGFVVEKTAARLPPSVS MGGNDYHEMFTDRAFEELFGICIQLLNKTWERMATAEDFN KVMQVVRBGJTRADPSKINSLDOPKS KLEHSJSSBILRIRGGSER MSQDDFQSPPIVELREKIQPEILELIKQGRINKLCELLCYGEL NRRGGRFWYCRLALMHKVLHYGDLDDNPGGEVTFSELGKIFFV ADIALVTSKCPCHMEKSSALKONKEVLEHASSLLAYBSELGKIFFV ADIALVTSKCPCHMEKSSALKONKEVLEHASSLLAYBSELGKIFFV ADIALVTSKCPCHMEKSSALKONKEVLEHASSLLAYBSELGKIFFV ADIALVTSKCPCHMEKSSALKONKEVLEHASSLLAYBSELGKIFFV ADIALVTSKCPCHMEKSSALKONKEVLEHASSLLAYBSELGKIFFV ADIALVTSCCHMENSSTANDARKONKEVLEHASSLLAYBSELGKIFFV ADIALVTSCCHMENSSTANDARKONKEVLEHASSLLAYBSELGKIFFV LUENNGLINGETKAADDSSNKERABEKPEEDONIATH LARNGSDFTRGTTKADDSSNKERABEKPEEDONIATH LARNGSDFTRGTTKADDSSNKERABEKPEEDONIATH LARNGSDFTRGTTKADDSSNKERABEKPEEDONIATH LARNGSDFTRGTTLAKFVORTORYTHUGGSKYLTHOORMYTHDOR LARNGSLENGETKANDSSNK	1	į.		
1268 IGCPINDGODGNLIIKKRYUSERLDERRRRQEENERVIKPR DPBECPEVYDPRSLYBRLQENDRRQQYEGYFKYNWYRGLD EDBTTNFLDEVSRQQELIKQRYBELLGEKYRNNILKKVG1SQE NKKEVEKKLTYKPIETKKKFQAKLLAGAVKHKSSSEGKSVERL KPPPEPDDKNQEPSKCKSLGHTSLG9FSLHCPSAAVCIGILDEG GAYGGSDSEGSSDSGTINATGKIVSJEFKTNTFLEAP 1043	Į.	1		
DPBECGBEVYDPRSLYRRIQGECKDRKQQEYEEQFKFKINNVRGIJQ EDBTNFLDEVSRQQELIEKQRRBEEKELKEYRNNIKKVGISQE NKKEVSKKLTVKPIETTMIRSCAKLLAGAVKHRSSESGRSVVRI KPDPEPDDKNQEPSSCKSIGNTSLSGPSIHCPSAAVCIGILEGE GAYGGSSDSESSSESTINATGKIVSSIFRTATFILEDP GAYGGSSDTINATGKIVSSIFRTATFILEDP EASTGTINATGKIVSSIFRTATFILEDP FIRE STANDAVTHOCKASREWGGRLLLAVSSIFRTATFILEDP ISRCIISSCPGPHAIVIVLLLGRYTEEQKTVALIKAVFGKSAM KHMVILFTRKEELESGSFHDFIADADVGLKSIVKEGGRCCAFS NSKKTSKARKESQVQULVELIREMVGGATSDLTVKEGGNRCCAFS NSKKTSKARKESQVGULVELIREMVGGATSDLTVKEGGNRCCAFS NSKKTSKARKESQVGULVELIREMVGGATSDLTVKEGGNRCCAFS NSKKTSKARKESQVGULVELIREMVGGATSDLTVKAUFGKSAM KHMVILFTRKEELESGSFHDFIADADVGLKSIVKEGGNRCCAFS NSKKTSKARKESQVGULVELIREMVGGATSDLTVKAUFGKSAM KHMVILFTRKEELESGSFHDFIADADVGLKSIVKEKEIKLLKLK VDRKIKNIREBERNIRIKDVFNIRMLSSIWHRFISKCKFYSS NSKKTSKARKESQVGULVELIREMVGGATSVDTIVKAUFGKSAM KHMVILFTRKEELESGSFHULFSAREMDDVOOTDSADLAGLANSS ASAPPPREPRGSISTMOGLSLDAASGSYSPLCISSLGSLA NPGENVVADIQIVVDKSPLPLGFSIVCDPMDSKASVSKKKKMCV KLLDLGATDTAVFDVRLSGKTKTVDGVJRIGMGGATIVCKKAK APPRVPKPRGISRDMGGLSLDAASGS SKGGLBERTASRIGGRAS TLRRNDSIYEASSLYGISAMDGVPTTLIPRFECKSCSPLAFSAF GDLIIKSLADIESENTAUFGVVEKTAALDPSVA GDLIIKSLADIESENTAUFGVVEKTAALDPSVA GDLIIKSLADIESENTAUFGVVEKTAALDPSVA GDLIIKSLADIESENTAUFFTURFSCKSCSPLAFSAF GDLIIKSLADIESENTAUFFTURFSCKSCSPLAFSAF GDLIIKSLADIESENTAUFTURFSCKSCSPLAFSAF KRKMTTKOYKMLGFTHHINPAMDFTOTPFOMLALDNMLYLLAKV HOTTYLTILENSSREDKHECPGFGS ALELTKMLCEILGVGELP NEGRNDYHMFFTHDRAFEELFGICIQLLAKTWKLERAPATAEDFN KYMGVVRGUTREGITAALDSKHECPGFGSAFELTKMLCEILGVGELP NEGRNDYHMFTTHDRAFEELFGICIQLAKTWKLERAPATAEDFN KYMGVVRGITAALDSKHECPGFGSSFRLIG NRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQKEIP ADIKALVTSKOCPHMRKSSALKONEVLELAFSILVDPETINF IANNKYEYCIMTDGLSALLGKOMSSELTKSDLDTLLSMMMKRL CLEUNSKLESSTSTLLTRUDGLSALLGKOMSSELTKSDLDTLLSMMMKRL APRIVERGERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQKEIP ADITALVTSCLOPERSSYDCYTHYGG GG43 3049 2265 SLHAPAGGTRGRAERFRMLTRKIKLMDINAHITCRLCSGYLI HDRTMQDIVYKLVPGLQBAEMRKGREFYHKLGMEVPGDIKGETC SAKQHLDSHNINGETKADDSSMKRABEERFEBDLDYILGDETC SAKQHLDSHNINGETCHOSSTMANTERDELPKYDLL LUTTMHLDVSTMANTESDLOVSU CLEUNSKLERGERFRMLTRKTK		2015		
EDETNILDEVSRQGELIEKQREBELKELKEYENNILKKYGISQE NKKEVEKKLTVKPIETKNKFSQAKLLAGAVKKSSEGNSVRCI KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPSAAVCIGILDEGL GAYSGSDSESSSDSETINATGKIVSSIFRITHFLEAP **VLEPPDEVBNASEBEDSEIVIVUKYKGSGKSATANTILGEEIFDS** RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKRSLDTTCKE** ISRCIISSCPGPHAIVIVLLLGRYTEEGKYTALIKAVFGKSAM KHMYLLPTRKEELESGSFHDFIADADVGLKSIVKEGGNRCCAFS** NSKKTSKABKESQVQELVELIEKMVQCMEGAYFSDDIYKDTEER** LKQRESVLRKIYTDOLMEEIKLVEEKKSEEKKEREIKLLKLK YDBKIKNIERBARENIFKDYFNRIKKMLSEIMTRFLSKCKYYSS** **ASAPPREGESAISCTVEGAPASFGKSFAQKSGYFLCLSSLGSLE** NPOGNVVADIQIVVDKSPLPLOGFSPVCDPHDSKASVKKKRNCV** **LLFLGANTTAYFDVRLSGKTKTVPGYTKRIGMGGFAINCKKAK** APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS** TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF* GDLTIKSLADIEBENNGFVVEKTAAARLEPSVS** **GENTYLPASSLYGISAMDGVPFTLHRFEGKSCSPLAFSAF* GDLTIKSLADIEBENNGFVVEKTAAARLEPSVS** **HORDYTRIVLENSSREDKHECPPGRSAIELTKMLCEILQVGELP** NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTMKMKEMRATAEDFN** KVMQVVRRQITRALPSKPNSLOCPTS, SLREILKMLCEILQVGELP** NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTMKMKEMRATAEDFN** KVMQVVRRQITRALPSKPNSLOCPTS, SLREILKRNLCESLSFKEK** MSQDDFQSPPIVELRERIQPEILEILKQQRLNTHLCRGSSFFRKI** NRRGGRFFYCCLLAINKVLHYMGLDDAPQGEVTFFSLGKIFV** ADIKATVTGKDCPHMKRKSALKONKEVLELAFSILDDPLEMENLRL** LDLENIQIPERPPPIFKEPSSYDFVYHYG** 6643** 3049** 2265** SLHAPAGGRTRGRLAEKFRMLTRKIKLMDINAHITCRLCSGYLI** HDRTMODIVYKLYPGLQBABMRQREFYHLGMSPEDQVSI** CLECNSSKLRGLKRKWIRCSAAFEKPEDDDYSTLSDDGVSI** CLECNSSKLRGLKRKWIRCSAAFEKPEDDDYSTLSDDGVSI** CLECNSSKLRGLKRKWIRCSAAFEKPEDDDYSTLSDDGVSI** CLECNSSKLRGLKRKWIRCSAAFEKPEDDDYSTLSDGWST** SAKQHLDSHRNGETKADDSSNKEAAEEKPEDDDYSTLSDGWST** LLATHILDTIKSFIRDSFTILOQVDETTRUTETRYBDGVSI** LLATHILDTIKSFIRDSFTILOQVDETTRUTETRYBDGVSI** LLATHILDTIKSFIRDSFTILOQVDETTRUTETRYBCHVDLLCPPRKOVL** LLYTFNHLDTIKSFIRDSFTILOQVDETTRUTETRYGLSAKALR** TVYERLAHASIMKLNQASMOKLYDLMTMAPKYQVLLCPPRKOVL** LLATHMYSVAQDVETHVSGSSKNLASWTQSSIAPNLAREELIF* EVPGLIRMFNINGGESVKI IFFKRIGGNTYQULCPPRKOVL** LLATHMYSVAQDVETHVSGSSKNLASWTQSSIAPNLAREELIF* LARLMGMBIKKPSGGPEPGFRLNLFTTDEEEGQAALTRDEBELSY* EVPGLIRMFNINGGESVKRI IF	0039	2046	1798	I
NKKEVERKLTVEP TETRINFSGAKLLAGAWKHKSSESGRSVKRI. KPDPEPDRINGEPSSCKSLGNTSLSGPSIHCPSAAVCIGILPGL GANGSSDBESSSBSGTTINATGKLVSSIPRTNTTLEAP 6640 117 1043 VLEPPDVSNAESEDRSLTVLVGKTGSGKSGTANTILGEEIFDS RAAQAVTINCKASREWGGRCLLVVDTPGLFDTKSSLDTTCKE ISRCIISSCPGPHAIVLVLLLGRYTEEBOKTVALIKAVPGKSAM KHNVLLFTKEBLEGQSFHDFIADAVUGLKSIVEGGNGCCAFS NSKKTSKAEKESQVGBLVELIEKMVQCNEGAYPSDDIYKDTEER LKOREEVURKIYTDOLNEEIKLVEEDKHKSEEKKEIKLLKLK VDEKIKNIBEAERNIEKDVFNIEKMUSSIMHEFISKCKYFS 6641 1 894 SAAVGRSEVRGCAPEPRURRSAREMDEVPOTDSAPLAGLAMSS VASAPPPREPSSAISCTVSAAPSGFGSFAQKSGYFLCLSSLGSLE NPQENVVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKKRNCV KLLPLGATDTAVFDVRLSGKTKTVFGYLRIGDMGGFAIMCKKAK APREVERPGISRDMGGLSLDAASGP SKGGLEERTASRLGSBAS TLRNDSIYEASSLYGISAMDGVPFTLHPRFECKSCSPLAFSAF GDLTIKKLADIESENKOFVVEKTAABLEPSVS 6642 22 1296 PLEERMYKMDDNDQAGRDIIFELRFIAPAGESDSNAPAGSGTE KRAMYTKOYKMUGFTNHINDAMDFTQTPDGMLALDMMLYLAKV HQDTYIRIVLENSSREDKHECPFGRS ALELIKMLCESILQVGELD NEGRNDYHBMFFTHDRAFEELEGICIQLLKTWKEMRATABDFN KVMGVVVEGITRALDSKFNSLOPFRS ALELIKMLCESILQVGELD NEGRNDYHBMFFTHDRAFEELEGICIQLLKTWKEMRATABDFN KVMGVVFGITRALDSKFNSLOPFRS KEISTSSELLRIRGSER MSQDDFOSP PIVELREKIQPE LIELI KQQILNKINLEGSSFRRIG NRROGEFFYCRLAINKVLHYGULDDAPQGEVTFFSLJCEKIPV ADIKALVTGKOCPHMKEKSALKQNKEVLELAFSILYDDDETLNF IADNKYSYCIMUDGLSALIGKDMSSELTKSDLDTLLSMEMKLRI 6643 3049 2265 SLHAPAGGRTGRIABERFRILITRKIKLMDINLITCRLCSGYLI IANTVESCHHTERSSNOCHYHUG ADITALTURELPHPIPKERSNCOPTYHUG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVFGDIKGETC SAKQHLDSHRINGETKADDS SNICAABERFERDLTKJDGLIKGTKC SAKQHLDSHRINGETKADDS SNICAABERFERDLTKJDGLIKGTKTDAF CLEENSSKLINGLKKRWIRCSAQATVLHIKKITLAKLIGLINGGER CLEENSKLINGLKSKWIRCSAGAERFPERDATHRIDLINGGEN CLEENSKLINGLKSKWIRCSAGAERFPERDATHRIDLINGGEN LUTTNHLIDTIKGFTROSFTILQVUETERFKULLDFINGGLSAGAFQ LIRQTLLIFFGGSDFVOLGSTBSVTLIPLININGGENVILDOR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPOLLYBKPULL VYTTRILAHDIIKFRYNDESTRANDGSTHARDBSTURLDFTLIGGLSGAGFQ LIRQTLLIFFGGSDFVOLGSTBSVTLIGHTLINGGENVILDOR LUTTNHUDTIKFTROSFTILGVUETERFKOULLCTPRKOUL LUTTNHUDTIKFTROSFTILGVUETERFKOULLCTPRKOUL LUTTNHUDTIKFTROSFTILGVUETERFKOULLCHEVFGODEUL KLGTMYSVOQOV	1	1		
KPPDEPDDKNØRESSCKSLGNTELSGRSHCTSANCTGILPGI GAYGGSDSRSSDSEGTINATGKIVSSIFRTNTFLEAP 1043 VLEPPDVSNAESEDRSLRIVLVGKTGGKSATANTILGEETFOS RIAAQAVTKNCQKASREWQGRDLLVVDTPGLEDTKESLDTTCKE ISRCIISSCGPIRATUVLULLGGYLEDGKTVALKAVFGKSAN KHWYLLFTREELEGGSPHDFLADADVGLKSIVKEGGNECAFS NSKKTSKARKSOVQBLVELIEKMVQCNEGAYPSDDIYKDTEER LKQREEVLRKIYTDQLNEEIKLIVEDKHKSEEKKEKEIKLLKLK YDBRIKNIRBEAERNIFKDVENRIWKMLSEIWHRFLSKCKFYSS 6641 1 894 SAAVGRSEVGGGADFPLRESAENDFVGTDSAFLAGLAWS 5AAVGRSEVGGAPPELRESAENDFVGTDSAFLAGLAWS KLIPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK APREVPKPRGSAISCTVEGAPASFCKSFAQKSGYFLCLSSLGSLE NPGGNVADJUVVKSPLPLIGFSPVCDFWDRSKAVSKKKRMCV KLIPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK APREVPKPRGSLSDMGGISLDAASQPSKGGLLERTASKLGSRAS TLERNDSIYEASSLVGISAMGGUFTHFFFEGKSCSPLAFSAF GDLTIKSLADIEEEVNYGFVVEKTAAARLEPSVS 6642 22 1296 PLEERMMTKNDPNDQAGRDIIFELRRIAFDAESDPSNAPGSGTE KRKMMTKNYKNYKMLGFTNNINPAMPTQTPFGMLALDMNLYLAKV HQDTYIRIVLENSSEDKHECPFGRSAIELITMLCEILQVGELP NGGNNYDHMFFTHDAFEELFGICIQLLNKTWKEMRATABEFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPFIVELREKIQPFILELIKQCRIRLCEGSSFFRIG NRRQGRFMYCCLALANIKVLHYGDLDDNPCGBVTPESLGELIPV ADIKATUTGKDCPHKKEKSALKOMKEVLELAFSILYDDDETINF LAPINKYSQTWINGISAALLGKOMSELITKSDLDTLLSKGMEKLRL LDLENIQIPPAPPPIPKEPSSYDEVYHYG 6643 3049 2265 SLHAPAGGRTGKLAEKFRINTRIILKUNDINAHITCRLCSGYLI HDRTMQDIYYKLVPGLQBAEMRKORFFYHKIBLGWFFGIKGFTC SAKGHLDSHNIGGTKADDSSNKEARE EKKPEDNDYHRSDGVSI CLECNSKLRGLKRWIRCSAQATVLHLKKFIAKKLNLSFNEL DILCNEEILGKDHTLKFVVVTRNEFKKAPELLHYRPKDDLU LRANIPGDLKARKVLNDIISTMFRNEFKEEPKPQDLYSKRLE TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQDLYGFRYDGUT LLRANIPGDLKARKVLNDIISTMFRNEFKEEPKPQDLYSKRLE TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQULYGPRDVU KLATNMYSVAQPYETHVSGSSKNLASWTQBISTAPHPLAKEEINF LARIMGMBIKKRSGPEGPGGPRLNLPTTOBEEBQAALTREELSY EVPOLITRMFNKSESVKRIEFKHGGNVYADPEGSFFFYGDRU KLATHMYSVAQPYETHVSGSSKNLASWTQBISTAPHPLAKEEINF LARIMGMBIKKRSPGPEGPGFRLNLPTTDEEBEQAALTREELSY EVPOLITRMFNKGESEKKREFFENDOTVAPAPKEGSFFFYGDRU KLATHMYSVAQPYETHVSGSSKNLASWTQBISTAPHPLAKEEINF LARIMGMBIKKRSPGPEGPFRLNLPTTOBEEBGAALTREELSY	1		1	1
GAYSGSDESGSSDEGTINATGKIYSSIPRITTELEAP 6640 117 1043 VLEPPDVSMAESEDRSLRIVLVGKTGSGKSATANTILGEEIPDS RIAAQAVTKNCQKASREWQGRDLLVVDTRGLPDTKESLDTTCKE ISRCIISSCPGHATVLVLLLGRYTEEBCKTVALIKAVFGKSAM KHWYLLFTRKEBLEGOSHDFILADVGKSIVKEGNRCCAFS NSKKTSKABKESQVQBLVELIEKMVQCNEGAYFSDDIYKDTEER LKQREEVLBKIYTDQLNEE IKLVBEDKHKSEBKEKEKIKLLKLK YDBKIKNIREABRINIFKDVENNI KMLSEIMHRFISKCKFYSS 6641 1 894 SAAVGRRSEVGCAPEPBLRSAARMDPVGTDSAPLAGLAMSS ASAPPPRGPSAISCTVEGAPASFGKSFAQKSGYFLCLSSLGSLE NPQENVVADIQIVVDKSPLPLIGFSPVCDPMDSKASVSKKRKKCK KLLDLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAJWCKKAK APRPVPRKGLSRDMGGISLDDASQPSKGGLLERTASRLIGSRAS TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF GDLTIKSLADIBEENINGFVVEKTAAARLPFSVS 6642 22 1296 PLEERMYKMDPNDQAQRDIIFFELR RIAFDAESDPSNAPGSGTE KRKMMYTKDYKMLGFTNNINPAMDFTCTPFGMIALDNNLYLAKV HQDYYIRIVLENSSREDKHCCPFGCARLEITMKLGELIQVGELP NEGRNDYHMFFTHDRAFBELFGICIQLLNKTWKEMRATAEDFN KVMQVVEGQITRALESKPNSLDQFKSKLBLYSBLILALRQSER MSQDDFOSPPIVELBEKTQPEILELI KQQRINNLCEGSSFRKIG NRRRQGRFFWCRLALNHKVLHYGDLDDNPGGSVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAPSILYDDDETLINF LARNKYSYCIWIDGLSALLGKDMSSELTKSDLDTLLSNEMKLIL LDLENIQIPBAPPPIPKBPSSYDFVYHYG 6643 3049 2265 SLHAPAGGFTFWCRLALNHKVLHYGDLDNPGGSVTFESLQEKIPV ADIKAIVTSKCCPHKKEKSALKQNKEVLELAPSILYDDDETLINF LARNKYSYCIWIDGLSALLGKDMSSELTKSDLDTLLSNEMKLET, LDLENIQIPBAPPIPKBPSSYDFVYHYG 6644 1489 290 SHAPAGGFTFWCRLALNHKVLHYGDLDNPGGFVFFKNDLL CLCCNSSKLRGLKRKWIRCSAQATVLHLKKFTAKKINLSSFNEL DILCNEELIGKDHTLKFVVVTRWFKKAPALLHLYHRDBGCVSI CLCCNSSKLRGLKRKWIRCSAQATVLHLKKFTAKKINLSSFNEL DILCNEELIGKDHTLKFVVVTRWFKKAPALPLLHYRRDBGCVSI CLCCNSSKLRGLKRKWIRCSAQATVLHLKKFTAKKLNLSSFNEL DILCNEELIGKDHTLKFVVVTRWFKKAPALPLLHYRRDBGCVSI CLCCNSSKLRGLKRKWIRCSAQATVLHLKKFTAKKLNLSSFNEL DILCNEELIGKDHTLKFVVVTRWFKKAPALPLLHYRRDBGCVSI CLCCNSSKLRGLKRKWIRCSAQATVLHLKKFTAKKLNLSSFNEL LVTFNHLDTIKGFIRDSSVKSTMSVTRUFLGGEMSTVLDQR LRAQNIFGDLKRARVLNDIISTMFNKFMCELFKPQGLYSKKALR TVYKRLAHASIMKLNAGSMDKLIVOLTMARFKYQULCPRKDVUL LVTFNHLDTIKGFIRDSHTLEGGVFADFSKYLEFRPODLYKGF EVPGLIRMFNKGESVEKRIEFKKGGTVPADFRESSFEFYGDRVL KLGTNMYSVNQPVETTUSGSSKNLASVTQESTAPNPLAK	Ι΄	· ·		NKKEVEKKLTVKPIETKNKFSQAKLLAGAVKHKSSESGNSVKRL
117 1043 VLEPPDVSMAESEDRSLRIVLVGKTGSGKSATANTILGELIPDS RIAAQAVTKNCQKASREWQGRDLLVVDTRGLDTKESLDTTCKE ISRCIISSCOPHATVUVLLLGYTEEDGKTVALKAVFGKSAM KHMYLLFTKRELEGQSFHDFIADADVGLKSIVKEGGNRCCAFS NSKKTSKAEKESQVQELVELLEKMYQCNEGAYFSDDIYKDTEER LKQREEVLRKITTDQLNEEIKLVEEDKHKSEEKKEKEIKLLKLK YDBRIKNIRBEAERNIFKDVENNIKMLESHURFISKCKFYSS SAAVGRSEVGGADFPELRRSAERMDPVGTDSAPLAGLAWS ASAPPPRGFSAISCTVEGAPASFGKSFAQKSGYFLCLSSLGSLE NPQBNVVADIQIVVDKSPLPLGFSPVCDPWDBJAGLAWS ASAPPPRGFSAISCTVEGAPASFGKSFAQKSGYFLCLSSLGSLE NPQBNVVADIQIVVDKSPLPLGFSPVCDPWDBKASVSKKKRMCV KLDELGATTAAVFDVALGSKKKTVFGYLRIGDMGGFAIWCKRAK APRPVPKPRGLSRDMGLISLDAASQPSKGGLLERTASRLGSRAS TLRRNDSITIKASSLYGISAMDGVPFTLAARRLPFSVS GDLTIKSLADIEBEENYGFVVETAAARLPFSVS GDLTIKSLADIEBEENYGFVVETAAARLPFSVS GDLTIKSLADIEBEENYGFVVETAAARLPFSVS GDLTIKSLADIEBEENYGFVVETAAARLPFSVS PLEERMMTKMDPNDQAQRDIIFELRAFABSDPSNAPGSGTE KRKAMYTKDYKMLGFTNININPAMPTGPPGMLALDNMLYLAKV HQDTYTRIVLENSSRENKHCPPGRSAIBLIKMLCEILQVGELP NEGRNDYHPMFFTHDRAPBELFGICQLQUKKWKEMRATABDFN KVMQVVREQITRALPSKPNSLODPKSKLESLSYSBEILKIRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRINFLCEGSSFRKIG NRRRQBEFFYCRLALINHKVHYGDLDDNCQSTVTESLGGEKIPV ADIKALTVTGKCPHWKEKSALKONKEVLELAFSILYDDDETINF IAPNKYSYCIWLDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDPVYHYG GATTVTECLHTTGRSCLVKTLEEMTIKKIKUMDINAHITCRLCSGYLI DATTVTECLHTTGRSCLVKTLEEMTIKKIKUMDINAHITCRLCSGYLI DATTVTECLHTTGRSCLVKTLEEMTIKKIKUMDINAHITCRLCSGYLI DATTVTECLHTTGRSCLVKTLEEMTKRIKUMDINAHTGRLCSGYLI DATTVTECLHTTGRSCLVKTLEEMTVTKIKAALLALLALLALLALLALLALLALLALLALLALLALLAL	1			KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPSAAVCIGILPGL
RIAAQAYTKNCQKASREWGGRDLLVVDTPGIFDTKESLDTTCKE ISRCIISSCPGPHATVLVLLLGRYTEBQKTVALIKAVFGKSAM KHWYILFTKREBLEGGSFHDFTADADVGLKSIVKECUNRCCAFS NSKKTSKABKESQVQBLVBLIEKMYQCWBGYFSDTYKDTEBR LKQREVLRRIYTDQLMEBIKLVBEDKHKSBEKKEBIKLLKLK YDBKIKNIRBEAERNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS 6641 1 894 SAAVGRRSEVGCAPRPBLRRSARRMDPVFTDSAPLAGLAWSS ASAPPRGFSAISTTVBCAPASFGKSFAQKSGYPFLCLSSLGSLE NPQENVVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKRMCV KLLPLGATDTAVPDVRLSGKTKTVPGYPASFGKSFAQKSGYPFLCLSSLGSLE APREVPKPRGLSSADMGGSLDAASQPSKGGLLERTASRLGSRAS TLRRNDSIYBASSLYGISAMDGVPFTLHFREGKSCSFLAFSAF GDLTIKSLADIBERYNYGFVVEKTAAARLPPSVS 6642 22 1296 PLEERMMTKMDPNDQAGRDIIFELRIAFDAESDPSNAPGSGTE KRKAMYTKOYKMLGFTNHINPAMDETQTPPGMLALDKMLYLAKV HQDTYIRIVLENSREDKHECPGRSAIELKTMLCEHLQVGELP NEGRNDYHPMFFTHDRAPELFGICIQLINKTWKEMRATARDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSBILRIRQSER MSQDDFGSPPIVSLRSKLOPBLIELIKQQRLNRLCEGSSFRKIG NRRQGRFWYCRLALMHKVLHYGDLDDDFGGEVTFESLQEKIPV ADIKAIVTGKCHAMKENSALKGVEVLELAPSILVDDEETINF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPBAPPPIPKBRSSYDFVYHKS 6643 3049 2265 SLHAPAGGRTGGLABKFKMLTKRIKLMDINAHTTCRLCSGYLI DATTVTECLHTFCRSCLVKYLBENNTCPPCRIVIHOSHPLQYIG HDRTMODIVYKLVPGLQBAEMRKGREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGSTKADDSSNKEABEEREEBENDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVILHKKFIAKKLNISSFNEL FUENICHTEBILGKUBTLKFVVYTRRFKKAPLLLHYPFWDLL LTVERKLAHASIMKINQASMBKLYDLMTWAFKYQVILCPRFKVUL LVTFNHLDTIKGFIRDSPTILQQVDETLRGUTEIYGGLSAGEFQ LIRQTLLIFFQDLHREVSSLKYDLTMTMFKKYQVLLCPRFKVUL LVTFNHLDTIKGFIRDSPTILQQVDETLRGUTEIYGGLSAGEFQ LIRQTLLIFFQDLHREVSSLKYDLSTAMPSKKGSLGAFGPUPVEG LIRQTLLIFFQDLHREVSSKNLASWTQSIADNPLAKEEINF EVEGLILMFNNKGESVKITEFKKGONYVDAKEGSFEFYGDRVL KLGTNMYSVRQPVETHVSGSSKNLASWTQSIADNPLAKEEINF EVEGLILMFNNKGESVKITEFKKGONYVDAKEGSFEFYGDRVL KLGTNMYSVRQPVETHVSGSSKNLASWTQSTADNPLAKEEINF EVEGLIRMFNKGEBEVKRTEFKKGONYVDAKEGSFEFYGDRVL KLGTNMYSVRQPVETHVSGSSKNLASWTQSTADNPLAKEEINF EVYGLIRMFNKGEBEVKRTEFKKGONYVDAKEGSFEFYGDRVL KLGTNMYSVRQPVETHVSGSSKNLASWTQSTADNPLAKEEINF EVYGLIRMFNKGEBEVKRTEFKKGONYVDAKEGSFEFYGDRVL KLGTNMYSVRQPVETHVSGSSKNLASWTQSTADNPLAKEEINF	i	1	ĺ	GAYSGSSDSESSSDSEGTINATGKIVSSIFRTNTFLEAP
RIAAQAYTKNCQKASREWGGRDLLVVDTPGIFDTKESLDTTCKE ISRCIISSCPGPHATVLVLLLGRYTEBQKTVALIKAVFGKSAM KHWYILFTKREBLEGGSFHDFTADADVGLKSIVKECUNRCCAFS NSKKTSKABKESQVQBLVBLIEKMYQCWBGYFSDTYKDTEBR LKQREVLRRIYTDQLMEBIKLVBEDKHKSBEKKEBIKLLKLK YDBKIKNIRBEAERNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS 6641 1 894 SAAVGRRSEVGCAPRPBLRRSARRMDPVFTDSAPLAGLAWSS ASAPPRGFSAISTTVBCAPASFGKSFAQKSGYPFLCLSSLGSLE NPQENVVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKRMCV KLLPLGATDTAVPDVRLSGKTKTVPGYPASFGKSFAQKSGYPFLCLSSLGSLE APREVPKPRGLSSADMGGSLDAASQPSKGGLLERTASRLGSRAS TLRRNDSIYBASSLYGISAMDGVPFTLHFREGKSCSFLAFSAF GDLTIKSLADIBERYNYGFVVEKTAAARLPPSVS 6642 22 1296 PLEERMMTKMDPNDQAGRDIIFELRIAFDAESDPSNAPGSGTE KRKAMYTKOYKMLGFTNHINPAMDETQTPPGMLALDKMLYLAKV HQDTYIRIVLENSREDKHECPGRSAIELKTMLCEHLQVGELP NEGRNDYHPMFFTHDRAPELFGICIQLINKTWKEMRATARDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSBILRIRQSER MSQDDFGSPPIVSLRSKLOPBLIELIKQQRLNRLCEGSSFRKIG NRRQGRFWYCRLALMHKVLHYGDLDDDFGGEVTFESLQEKIPV ADIKAIVTGKCHAMKENSALKGVEVLELAPSILVDDEETINF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPBAPPPIPKBRSSYDFVYHKS 6643 3049 2265 SLHAPAGGRTGGLABKFKMLTKRIKLMDINAHTTCRLCSGYLI DATTVTECLHTFCRSCLVKYLBENNTCPPCRIVIHOSHPLQYIG HDRTMODIVYKLVPGLQBAEMRKGREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGSTKADDSSNKEABEEREEBENDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVILHKKFIAKKLNISSFNEL FUENICHTEBILGKUBTLKFVVYTRRFKKAPLLLHYPFWDLL LTVERKLAHASIMKINQASMBKLYDLMTWAFKYQVILCPRFKVUL LVTFNHLDTIKGFIRDSPTILQQVDETLRGUTEIYGGLSAGEFQ LIRQTLLIFFQDLHREVSSLKYDLTMTMFKKYQVLLCPRFKVUL LVTFNHLDTIKGFIRDSPTILQQVDETLRGUTEIYGGLSAGEFQ LIRQTLLIFFQDLHREVSSLKYDLSTAMPSKKGSLGAFGPUPVEG LIRQTLLIFFQDLHREVSSKNLASWTQSIADNPLAKEEINF EVEGLILMFNNKGESVKITEFKKGONYVDAKEGSFEFYGDRVL KLGTNMYSVRQPVETHVSGSSKNLASWTQSIADNPLAKEEINF EVEGLILMFNNKGESVKITEFKKGONYVDAKEGSFEFYGDRVL KLGTNMYSVRQPVETHVSGSSKNLASWTQSTADNPLAKEEINF EVEGLIRMFNKGEBEVKRTEFKKGONYVDAKEGSFEFYGDRVL KLGTNMYSVRQPVETHVSGSSKNLASWTQSTADNPLAKEEINF EVYGLIRMFNKGEBEVKRTEFKKGONYVDAKEGSFEFYGDRVL KLGTNMYSVRQPVETHVSGSSKNLASWTQSTADNPLAKEEINF EVYGLIRMFNKGEBEVKRTEFKKGONYVDAKEGSFEFYGDRVL KLGTNMYSVRQPVETHVSGSSKNLASWTQSTADNPLAKEEINF	6640	117	1043	VIEPPDVSMAESEDRSIRIVLVGKTGSGKSATANTILGEEIFDS
ISRCIISSCGPHAIULULLGRYTEEBCKTVALIKAVPGKSAM KHMVILFTRKEELEGQSFHDFIADADVGLKSIVKECGNRCAFS NSKKTSKARKESQVGELVELIEKMVQCMEGAYFSDDIYKDTEER LKQREEVLRKIYTDOLINEEKKUVGCMEGAYFSDDIYKDTEER LKQREEVLRKIYTDOLINEEKKUVECDKHKSEKKEKEKKEKKEKKEK YDBKIKNIREAERNIFKDVFNRIKMKLSEIMRFLSKCKFYSS 6641 1 894 SAAVGRRSEVGGCAPFPELRRSÄRRMDEVPCTDSAPLAGLAWSS ASAPPRGGSATSCTVEGAPASFGKSFAJKGSVFYKLTSLGSLGSLE NPQENVVADIQIVUDKSP.DLPGASGYFYKLTSLSLGSLE NPQENVVADIQIVUDKSP.DLPGASGYFYKLTSLSCSLE APREVPKPRGLSRDMGGISLDAASQPSKGMENTGKAKK APPRVFKPRGLSRDMGGISLDAASQPSKGLEETASRIGSRAS TLRRNDSIYRASSLYGISAMDGAYPFILHFRFEGKSCSPLAFSAF GDLTIKSLADIEESYNYGPVVEKTAAARLPPSVS GDLTIKSLADIEESYNYGPVVEKTAAARLPPSVS FLEERMMTKNDPMDDQAGNDIFELREITAFDAESDPSNAPGSGTE KRKAMYTKDYKMGFTHNINPAMDFTQTPPGMLALDMMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLINKTWKEMRATAEDFN KVMQVVREQITRALPSKYNSLOPFKSKLRSLSYSSILRILRGSER MSQDDFGSPIVSLREKIQPEILELIKQORINRLCEGSSFRKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPGGEVTFESLQEKIPK NRRRQERFWYCRLALNHKVLHYGDLDDNPGGEVTFESLQEKIPK NRRRQERFWYCRLALNHKVLHYGDLDDNPGGEVTFESLQEKIPK TAPNKYSYCIWIGGLSALLGKOMSSELTKSDLDTLLSMEMKIRL LDLEINIQIPBAPPIPKEPSSVDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKFKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLWYLEENNTCPTCRIVIHQSHPLQYIG HDRTMGDIVYKLWPGLQRAEMRKQREFYHKIGMRVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHKKHIAKKLNLSSPNEL DILCNESILKGBUTLKFVVVTRNFKKAPLLHTYPRMDLL 6644 1489 290 FRPLATEPGGSPVQUVSSTMSVRTLPLLFUNGGEMLYILDOR LRAQNIFGROSPTILQVYDGTKRKFMELFKPQELYSKKALR TVYERLAHASIMKNOASMBLYDLMTMPKYQVLLCPRPKPUL LVTRNHLDTIKGFIRDSPTILQVDETLAGGEMLYILDOR LRAQNIFGROSPTILGVVGSNNLASWFVGSIASPGFQTVMC KLGTNMYSVQPVETHVSGSSKNLASWTYGSIANDFSCOPPOGT LIRQTLIFFPQLHIRVSGSKNLASWTYGSIANDFSCOPPOGT LARLMGGMEIKKPSGPEPOFRLNFTTDEEESGAPEPGGRUL KLGTNMYSVQPVETHVSGSSKNLASWTYGSIANDFSLELSF	3323	1	1 2010	
KHMVILPTRKEELEGQSFHDFIADADVGLKSIVKECGNRCCAFS NSKKTSKARKESQVGBLUELIEKMYQCMEGAY F3DDIYKDTEER LKQREEVLRKIYTDQLMEEI KLWEDKHKSEEKKEKSIKLLKLK YDBKIKNIREAERNIPKDVFNRIKKMLSEUMHRFLSKCKFYSS 6641 1 894 SAAVGRESEVRGCAPEPELRRSARRMDEVETDSAPLAGLAWSS ASAPPRGFSAISTTUGGAPASFGKSFAQKSGYFLCLSSLOSLE NPQENVVADIQIVVDKSPLPLGFSVCDPMDSKASVSKKKRMCV KLLPLGATDTAVFDVRUSGKTKTVPGYLRIDMGGFAIWCKKAK APREVPKPRGLSSADMGGLSLDAASQP SKGGLLERTAGRLAGSRAS TLRRNDSIYEASSLYGISAMDGVPFTLHFREGKSCSPLAFSAF GDLTIKSLADIEEEYNYGFVVEKTAAARLPPSVS 6642 22 1296 PLEERMMTKNDPDDQAQRDIFELRR IAFDAESDPSNAPGSGTE KRKAMYTKDYKMLGFTINHINPAMDFTQTPPGMLALDMNLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELGGICJQLINKTWKEMRATABDFN KVMQVVREQITRALPSKYNSLOOFKSKLKSISYSBILRLRQSER MSQDDFQSPPIVELREKIQPEILEILKQQCLUFTESLQEKIPV ADIKAIVTGKOCPHMEKSALKQNKEVLELAFSILYDPDETINF IAPNKYBYCIWIDGLSALLGKDMSSELTKSDLDTLISMMEMKLRL DLENIQIPEAPPPIRKBSSUDFVHYG 6643 3049 2265 SLHAPASGRTRGKLAEKFMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENDTYCPTGIVINGSHPLQYIG HDRTMODIVYKLVPGLQRAEMRKQREFFHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKFEDNDYHRSDEQVSI CLECNSKLIGGLKRKWIRCSAQATVLHLKKPILAKKLALSSFNEL DILCNEEILGKDHTLKFVVVTRWFKKAPLLLHYPKMDLL LRAQNIPGGRBEKFWLTRKIKLRUDGGEMYJILDQR LRAQNIPGGRBEKFWLTRKIKLRUDGGEMYJILDQR CLECNSKLIGGLKRKWIRCSAQATVLHLKKPILAKKLALSSFNEL TVYERLAHASIMKLNQASNDKLYDLLTRUGGEMYJILDQR LRAQNIPGRKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASNDKLYDLLTRUGGEMYJILDQR LRAQNIPGRKARVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASNDKLYDLDNTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETTLOGLTEITGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQVNNNGRPVQDLVSGAPVPGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFFYGDRVL KLGTNMYSVRQPVETHVSGSSKNLASWTGSIANPLAKEELINF LARMGMBELKEGSPEFOFRUNFTTDEEEEGAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	1	1		
NSKKTSKARKESQVQBLVELIEKMVQCNEGAYPSDDIYKDTEER LKQREEVLRKI YTDQLNEEI KLVEEDKHKSEEKKEKEI KLLKLK YDBKI KNIRBEARENI PKUVPNRI WKMLSSIMHRFLSKCKFYSS 6641 1 894 SAAVGRRSEVEGCAPRFLRRSAARMDEVPOTDSAPLAGLAWSS ASAPPRGFSAISCTVEGAPASFGKS FAQKSGYFLCLSSLGSLE NPQENVVAD TQIVVDKSPLPLGFSPVCDPMDSKASVSKKKRMCV KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF GDLTIKSLADIEESYNGFVVEKTAAARLPPSVS 6642 22 1296 PLEERMMTKMDPNDQAQRDII FELRR IAFDAESDPSNAPGSGTE KRKAMYTKOYKMLGFTNHINPAMDFYQTPFGMLALDNMLYLAKV HQDTYIRIVLENSSREBKHECPFGRSAIELTKMLCETLQVGELP NEGRNDYHPMFFTIDRAFEBLFGICIQLLKKTWKEMRATABDFN KVMQVVRQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFGSPPIVELRERIQPEILELIRQQSLINRLGEGSSFTKLG NRRQERFWYCRLALNIKKUMPLDDNDPQGSVTFESLGERIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYSYCIWIDGLSALLGKDMSSELTKSDLDTLISMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVVHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKFKMLTRKIKLMDINNHTTCRLCSGYLI HDRTMQDIVYKLVBGLQBEAMRKQREFYHKLGMEVPGDI KGETC SAKGHLDSHRNGETKADDSSNKEABERFPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEELLGKDHTLKFVVVTRNFFKRAPLLHKTPIRMDLL 6644 1489 290 FRPLATEFRGSSPVOLVSSTMSVRTLPLLFINLGGEMIYILDQ LRAQNI PGDKARKVLNDI ISTMFNRK FMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMNKLYDLMTMAFKYQVLLCPRFKDVL LVTFNHLDT IKGFIRDSFTILQQVDETRQLITETYGGLSAGEFQ LIRQTLLIFPQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGESVKRIFFKKGGNVVAPAKEGSFEFYGDRVL KLGTNMYSVNQPUSTHVSGSSKALASKTQBSIAPNPLAKEELNF LARLMGGMEIKKRSGEGSKALASKTQBSIAPNPLAKEELNF LARLMGGMEIKKRSGEGSKALASKTQBSIAPNPLAKEELNF LARLMGGMEIKKRSGEGSKALASKTQBSIAPNPLAKEELLNF LARLMGGMEIKKRSGEGSKALASKTQBSIAPNPLAKEELLNF LARLMGGMEIKKRSGEGSKALASKTQBSIAPNPLAKEELLNF LARLMGGMEIKKRSGEGSKALASKTQBSIAPNPLAKEELLNF LARLMGGMEIKKRSGEGERARIMGEFEICAALTRPEELSY EVINIQATQDQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM		İ .		
LKQREEVLRKIYTDQLNEEIKLVEEDKHKSEEKKEKEIKLLKLK YDBKIKNIREBAERNIFKDVFNRIWKLSISIMRFISKCKFYSS 6641 1 894 SAAVGRSEVGCAPPFPLRRSARRMDPVPOTDSAPLAGLAWSS ASAPPPRGSAISCTVEGAPASFGKSFAQKSGYFLCLSSLGSLE NPQENVVADIQIVVDKSPLPLGFSPVCDPNDSKRASVSKKKMCV KLLPLGATDTAVFDVRLSGKTKTVPGVLRIODMGGFAIWCKKAK APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS TLRRNDSIYEASSLYGISANDGVPFTLHPRFEGKSCSPLAFSAF GDLTIKSLADIEEEYNNGFVVEKTAAARLPPSVS 6642 22 1296 PLEERMMTKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTE KRKAMYTKDYKMLGFTTHINPANDFTPFDFMLALDMINLTLAKV HQDYTRIRVLENSSRENKEEPGGSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKIRSLSYSEILRLRQSER MQODFGSPPIVELRERIQPEILLIKQQRINRLCEGSSFKKIG NRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKRKSALKQNKEVLELAFSILVDPDETLNF IAPNKYSYCHUTOGLSALLGKDMSSEITKSDLDTILLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDEVYHYG 6643 3049 2265 SLHAPABGRTTGGLAEKFKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHFTCRSCLVKYLEENNTCPTCRIVHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGBTC SAKQHLDSHRNGETKADDSSNKEAAEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKKWHTGSAQATVLHLKKFIAKKLMISSFNEL DILCNEEILGKDHTLKFVVVTRWFFKKAPLLLHYRPKMDLL 6644 1489 290 FRPLATEBRGSSPVQLVSSTMSVETLELFENLGGEMLYILDQR CLECNSSKLRGLKKWHTGSAQATVLHLKKFIAKKLMISSFNEL LIRQNIPGDKARKVINDII ISTMFNRKFMEELFKPOELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSFTLLQQVDETLRQLITEIYGGLSAGEFQ LIRQNIPGDKARKVINDII ISTMFNRKFMEELFKPOELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSFTLLQQVDETLRQLITEIYGGLSAGEFQ LIRQTLLIFFGDJHHRVSMFRIKDKVQNNNGRFVLPVSGSPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVGSSSKULASTQBSIAPNPLAKEELINF LARRMGMETKKRSGPEPEFRINLFTTDEEEGQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	1 .	1	ļ	1 ·· · · · · · · · · · · · · · · ·
YDEKIKNIREEAERNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS 6641 1 894 SAAVGRRSEVEGCAPRELRESARMDPVPGTDSAPLAGLAWSS ASAPPROFSAISCTVEGAPASFGKSFAQKSGYPLCLSJGSLE NPQENVVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKKMCV KLLPLGATDTAVFDVRLSGKTTTVPGYLRIGDMGGFAIWCKKAK APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS TLRRNDSIYEASSLYGISAMGVPFTLHPRFEGKSCSPLAFSAF GDLTIKSLADIEEENYGFVVEKTAAARLPPSVS 6642 22 1296 PLEERMMTKMDPNDQAQRDIIFELRIAPDAESDPSNAPGSGTE KRKAMYTKDYKMLGFTNNINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRTVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTTHDRAPEELFGICIQLINKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCESSSFRKIG NRRRQERFWYCRLALMHKVLHYGDLDDNPGGVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILVDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKERSSYDFYHYG DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQEAEMKRQREFYHKLGMEVFGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEKFEEDNDYHRSDEQVSI CLECNSSKLRGLKKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEETLGKDHTLKFVVVTRWFFKKAPLLLHYRPKMDLL LRAQNIFGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRFKOVL LVTFNHLDTIKGFIRDSFTILQQVDETLRGLTEIYGGLSAGEFQ LIRQTLLIFFGQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT LVTFNHLDTIKGFIRDSFTILQQVDETLRGLTEIYGGLSAGEFQ LIRQTLLIFFGDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFFFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTGESIAPNPLAKEELNF LARLMGGMEIKKPSGGPEFOFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM				
SAAVGRRSEVRGCAPRFRLRRSARRMDPVPGTDSAPLAGLAWSS ASAPPPRGFSAISCTVEGAPASFGKSFAQKSGYFLCLSSLGSLE NPQENVVAD JQIVVDKSEJPLGFSPVCDPMBKASVSKKRKCKV KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS TLRRNDSIYEASSLYGISAMDGUPFTLHPRFEGKSCSPLAFSAF GDLTIKSLADIEEEYNYGFVVEKTAAARLPPSVS 6642 22 1296 PLEERMTKMDPNDDQQRDIIFELRRIAFDAESDFSNAPGSGTE KRKAMYTKDYMLGFFINIPAMDEPTQTPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAPFEGLGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDOFKSKLRSLSYSEILRLRQSER MSQDDFOSPPIVELREKIQPEILEILKQQRLNRLCEGSSFRKIG NRRQGRRWYCRLALNHKVLHYGDLDDNPGGEVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYSECIMIDGLSALLGKDMSSELTKSDLDTLLSMENKKRL LDLENIQIPEAPPPIPKEPSSYDTYHYG 6643 3049 2265 SLHAPAEGRTRGRLÄREKPKMLTTKKLKDDINAHITCRLCSGYLI DATTVTECLHTFCRSCLWKYLEENNTCPTCRIVIHQSHPLQYIG HDRIMQDIVYKLVPGLQRREMKKQREFYHKLGMEVPGDIKGSTC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNESILGKDHTLKFVVVTRNPRKKAPLLLHYRPKMDLL LRAONIPGDKARKVLNDIJISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSFTILQCUPETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHTRUSMFLKDKVQNNNSRFVLPVSGPVPWGT LLRQTLLIFFQDLHTRUSMFLKDKVQNNNSRFVLPVSGPVPWGT VYYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSFTILQCUPETLRQLTEIYGGLSAGEFQ LLRQTLLIFFQDLHTRUSMFLKDKVQNNNSRFVLPVSGPVPWGT EVPGLIRMFNNKGESVKRIEFKHGGNYVPAPKEGSFFFYGDRVL KLGTIMMYSVNQPVETHVSGSSKLALSWTGESIAAPNELAKBELNF LARLMGGMEIKKPSGGPEOFFILLSTTGEELGAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM		1		LKQREEVLRKIYTDQLNEEIKLVEEDKHKSEEKKEKEIKLLKLK
ASAPPPRGFSAISCTVEGAPASFGKS FAQKSGYFLCLSSLGSLE NPQENVVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKRMCV KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK APREVPKPRGLSRDMGGLSLDAASQPSKGGLLERTASRLGSRAS TLRRNDSIYEASSLYGISAMDGVFFTLHPRFEGKSCSPLAFSAF GDLTIKSLADIEEYNYGFVVEKTAAARLPPSVS 6642 22 1296 PLEERMMTKMDPNDQAQRDIIFELRR IAFDAESDPSNAPGSGTE KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDVHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPFIVELREKIQPEILELIKQQRLMRLCEGSSFRKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFSLQBKIP ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSEITKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHGSHPLQYIG HDRTWQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKGHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEETLGKDHTLKFVVVTRAFKKAPLLLHYRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMPNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRRKOVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRGTLLIFFQDLHIRVSMFLKVKQNNNGRFVLPVSGDPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTINMYSVNQPVETHVSGSSKLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGEPGFFRLNLFTTDEEEGAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	J	J.	j	YDEKIKNIREEAERNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS
NPQENVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKRMCV KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK APRPVPKRPGLSRDMGGLSLDAASQP SKGLLERTASRLGSRAS TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF GDLTIKSLADIEEETNYGFVVEKTAAARLPPSVS 6642 22 1296 PLEERMMTKMDPNDQAQRDIIFELRR IAFDAESDPSNAPGSGTE KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLINKTWKEMRATAEDFN KVWQVVREQITRALPSKPNSLDQFKS KLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRQERFWYCKLALMHKVLHYGDLDDNPQGBVFFSSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPMKYEKZCIWIDGLSALLGKOMESELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLABKPKMLTRKIKLWDINAHITCRLCSGYLI HDRTMQDIVYKLVFGLQBAEMRKQREFYHKLGMEVFGDIKGGTC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSFNEL DILCNEEILGKDHTLKFVVVTRMFKKKAPLLLHYPRMDLL 6644 1489 290 FRPLATEFRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASINKLNQASMBKLVDLMTMAFKYQVLLCPRRDVL LVTFNHLDTIKGFIRDSPTILQQUETLRQLTEITGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVFGLIRMFNNKGEEVKRIEFKHGNYVPAPKEGSFEFYGDRVL KLGTINMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEGAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	6641	1	894	SAAVGRRSEVRGCAPRPRLRRSARRMDPVPGTDSAPLAGLAWSS
NPQENVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKRMCV KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK APRPVPKRPGLSRDMGGLSLDAASQP SKGLLERTASRLGSRAS TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF GDLTIKSLADIEEETNYGFVVEKTAAARLPPSVS 6642 22 1296 PLEERMMTKMDPNDQAQRDIIFELRR IAFDAESDPSNAPGSGTE KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLINKTWKEMRATAEDFN KVWQVVREQITRALPSKPNSLDQFKS KLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRQERFWYCKLALMHKVLHYGDLDDNPQGBVFFSSLQBKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPMKYEKZCIWIDGLSALLGKOMESELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLABKPKMLTRKIKLWDINAHITCRLCSGYLI HDRTMQDIVYKLVFGLQBAEMRKQREFYHKLGMEVFGDIKGGTC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSFNEL DILCNEEILGKDHTLKFVVVTRMFKKKAPLLLHYPRMDLL 6644 1489 290 FRPLATEFRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASINKLNQASMBKLVDLMTMAFKYQVLLCPRRDVL LVTFNHLDTIKGFIRDSPTILQQUETLRQLTEITGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVFGLIRMFNNKGEEVKRIEFKHGNYVPAPKEGSFEFYGDRVL KLGTINMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEGAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM				ASAPPPRGFSATSCTVEGAPASFGKSFAOKSGYFLCLSSLGSLE
KLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK APRPVPKPRGLSRDMQGLSLDASSQPSKGGLLERTASRIGSRAS TIRRNDSIYEASSLYGISAMDGUPFTLHPRFEGKSCSPLAFSAF GDLTIKSLADIEEEYNYGFVVEKTAAARLPPSVS 6642 22 1296 PLEERMMTKMDPNDQAQRDIIFELRRIAFDAESDPSNAFGSGTE KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRTVLENSSREDKHECPFGRSAIELIKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELRERLJPELLELIKQQELTELIKQSERFKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKKKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKOMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI HDRTMQDIVYKLVEGLORAERKORRFFYHKLGMEVPGDIKGGTC SAKQHLDSHRNGETKADDSSNKEAAEEKPEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKINLSSFNEL DILCNEEILGKDHTLKFVVVTRWFFKKAPLLHYRPKMDLL CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKINLSSFNEL LTATATEPELGKHTLKFVVVTRWFFKKAPLLHYRPKMDLL LVTFNHLDTIKGFIRDSTILQQVDETLRQLTEIYGGLSAGEFQ LRQQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYBRLAHASIMKINQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLDFVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETIVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPBFGFFLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	1:	: .		
APRPVPKPRGLSRDMQGISLDAASQPSKGGILERTASRIGSRAS TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF GDLTIKSLADIEEEYNYGFVVEKTAARLPPSVS 6642 22 1296 PLEERMMTKMDPMDQAQRDIFELRRIAFDAESDPSNAPGSGTE KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGBLD NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSBILBLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLALMHKVLHYGDLDDNPGGEVTFESLQEKIPV ADIKAIVTGKDCPHMEKSAIKQNKEVLELAFSILYDPDETINF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVVHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLBENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQEAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGBTKADDSSNKEAAEEKPEDDNDYHRSDEQVSI CLECNSSKLIRGLKRKWIRGSNKEAAEEKPEDDNDYHRSDEQVSI CLECNSSKLIRGLKRKWIRGSNKEAAEEKPEDDNDYHRSDEQVSI CLECNSSKLIRGLKRKWIRGSNKEAAEEKPEDDNDYHRSDEQVSI CLECNSSKLIRGLKRKWIRGSNKEAAEEKPEDDNDYHRSDEQVSI CLECNSSKLIRGLKRKWIRGSNKEAAEEKPEDDNDYHRSDEQVSI CLECNSSKLIRGLKRKWIRGSNKEAAEKPEDENDYHRSDEQVSI CLECNSSKLIRGLKRKWIRGSNKEAAEKPEDENDYHRSDEQVSI CLECNSSKLIRGLKRKWIRGSNKEAAEKPEDELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LRATMIPDIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPBFGFFLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM			·	1 7 7
TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF GDLTIKSLADIEEEYNYCHTVARAALPPSVS PLEERMMTKMDPNDQAQRDIIFELRIIAFDAESDPSNAPGSGTE KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDMMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFBELFGICIQLLNKTWKEMRATAEDFN KVMQVVRQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETIMF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVEGLGRAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEDDDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWFKKAPLLLHYRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVRTLPLLFINLGGEMLYILDOR LRAQNIPGGKARKVINDIISTMFNRK FMEELFKPQELYSKKARL TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTTNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGESVKRIEFKHGGNYVPAPKEGSFETYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARRMGGMEIKKPSGPEFGFRLNLFTTDEEEGQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM		1	1	
GDLTIKSLADIEEEYNYGFVVEKTAAARLPPSVS 6642 22 1296 PLEERMMTKMDPNDQACRDIIFELRRIAFDAESDPSNAPGSGTE KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAPEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREGITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRGERFMYCRLALNHKVLHYGDLDDMPGGBVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPMKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBREMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWFKKAPLLLHYRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGBKARKVINDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSTTLQOVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEFGFRLNLFTTDEEEGQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM				
PLEERMMTKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTE KRKAMYTKDYKMLGGTINHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRGERFWYCRLALNHKVLHYGDLDDNPQGBVTFBSLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPMKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTYTECLHTFCRSCLVKYLBENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQEAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLCCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRPVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESTAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	1			
KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLIKKTWKEMRATAEDFN KVMQVVGQTQTRALPSKPNSLDQFKSKLRSLSYSETLRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRQEFFWYCRLALNRKVLHYGDLDDNPGGEVTFBSLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNP IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLERIQIPBEAPPPIPKEPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTYTECHHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQEAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRNFKKAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFILNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	1	<u> </u>	l .	+
HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVRQITRALPSKPNSLOPKS KLRSLSYSEILRIRQSES MSQDDFQSPPIVELREKIQPEILELIKQQELINRLCEGSSFRKIG NRRRGERFWYCRLALNHKVLHYGDLDDNPGGEVTFSSLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMODIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFINLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKKKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFFFYGDRVL KLGTMMYSVNOPVETHVSGSSKNLASWTQSSIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	6642	22	: 1296	PLEERMMTKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTE
NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLAINHKVLHYGDLDDNPQGBVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKBPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRWIRCSAQATVLHLKKFIAKKINLSSFNEL DILCNEEILGKDHTLKFVVVTRWFFKKAPLLLHTRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNTVPAPKEGSFEFYGDRVL KLGTMMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM		•		KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV
NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLAINHKVLHYGDLDDNPQGBVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKBPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRWIRCSAQATVLHLKKFIAKKINLSSFNEL DILCNEEILGKDHTLKFVVVTRWFFKKAPLLLHTRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNTVPAPKEGSFEFYGDRVL KLGTMMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	l .		, ,	HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP
KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLMRLCEGSSFRKIG NRRRQERFWYCRLALMHKVLHYGDLDDNPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQEAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEKPEEDDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRRFKKAPLLLHYRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNNYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	1			NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN
MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETINF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQEAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWFKKAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	1			
NRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKBKSALKQNKEVLELAFSILYDPDETINF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLÄEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQEAEMRKQREFYHKLGMEVPGDIKGGTC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWFFKKAPLLLHYRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVVGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM		''.	,	
ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETINF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQEAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWFFKKAPLLLHYPRKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM				
IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLINLSSFNEL DILCNEEILGKDHTLKFVVVTRWFKKAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFINLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM			:	1 -
LDLENIQIPEAPPPIPKEPSSYDFVYHYG 6643 3049 2265 SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQRE FYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDS SNKEAAE EKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWFFKKAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQUTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	1		ĺ	_
SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWFKKAPLLLHYRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	1			
DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWFKKAPLLLHYRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	<u> </u>		<u> </u>	
HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWFKKAPLLLHYRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	6643	3049	2265	SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI
SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWFFKKAPLLLHYRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	1		1	DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG
SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWFFKKAPLLLHYRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM			1	HDRTMQDIVYKLVPGLQEAEMRKQREFYHKLGMEVPGDIKGETC
CLECNSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWFKKAPLLLHYRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	1		1	
DILCNEEILGKDHTLKFVVVTRWFFKKAPLLLHYRPKMDLL 6644 1489 290 FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	ł		1	
FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	1		1	
LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM		1400	 	
TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	5544	1489	290	
LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM				
LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	ł		1	<u>-</u>
EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	1			LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ
EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	[LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT
KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	1		İ	
LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM	I		1	
EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM			1	
l l				ENTAL CAMODOOD CREET AD TMCDDD TODODD, COCKCODI. T. AMM
DEL				
			<u> </u>	DEP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 :	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
,	amino acid	sequence	Codon, /=possible nucleotide deletion,
ţ	sequence	Bequence	\=possible nucleotide insertion)
6645	6530	1646	
9645	6530	4646	FVEGLAGYVYKAASEGKVLTLAALLLNRSESDIRYLLGYVSQQG
	}		GQRSTPLIIAARNGHAKVVRLLLEHYRVQTQQTGTVRFDGYVID
]		GATALWCAAGAGHFEVVKLLVSHGANVNHTTVTNSTPLRAACFD
		·	GRLDIVKYLVENNANISIANKYDNTCLMIAAYKGHTDVVRYLLE
į .	!	İ	QRADPNAKAHCGATALHFAARAGHIDIVKELIKWRAAIVVNGHG
ļ			MTPLKVAAESCKADVVELLLSHADCDRRSRIEALELLGASFAND
l .		{	RENYDIIKTYHYLYLAMLERPODGDNILEKEVLPPIHAYGNRTE
i '			CRNPQELESIRODRDALHMEGLIVRERILGADNIDVSHPIIYRG
			AVYADNMEFEQCIKLWLHALHLRQKGNRNTHKDLLRFAQVFSQM
			IHLNETVKAPDIECVLRCSVLBIEQSMNRVKNISDADVHNAMDN
1			YECNLYTFLYLVCISTKTQCSEEDQCKINKQIYNLIHLDPRTRE
1			GFTLLHLAVNSNTPVDDFHTNDVCSFPNALVTKLLLDCGAEVNA
	!		VDNEGNSALHIIVOYNRPISDFLTLHSIIISLVEAGAHTDMTNK
	.		ONKTPLDKSTTGVSEILLKTOMKMSLKCLAARAVRANDINYODO
i :			1
		<u> </u>	IPRTLEEFVGFH
6646	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
ł			EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL
]		EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL
1			TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD
			FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA
	· ·		GSEEAREKQDSEKPLLEL
6647	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
	i		EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL.
· ·			EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL
			TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD
ļ			FKVLPQEABEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA
	•		GSEEAEEKQDSEKPLLEL
6648	413	897	
0040	413	697	RNCWNCFTKYFNSPPEDIDHKDSYLITRSIMAEPDYIEDDNPEL
1			IRPQKLINPVKTSRNHQDLHRELLMNQKRGLAPQNKPELQKVME
:	·		KRKRDQVIKQKEEEAQKKKSDLEIELLKRQQKLEQLELEKQKLQ
:			EEQENAPEFVKVKGNLRRTGQEVAQAQES :
6649	1357	832	WIPRAAGIRHEVKWDVKEIMSQHNIYVDALLKEFEQFNRRLNEV
;			SKRVRIPLPVSNILWEHCIRLANRTIVEGYANVKKCSNEGRALM
:	`		QLDFQQFLMKLEKLTDIRPIPDKBFVETYIKAYYLTENDMERWI
}			KEHREYSTKQLTNLVNVCLGSHINKKARQKLLAAIDDIDRPKR
6650 .	32	765	LVPLVFSLLVQSCKQVYRSIAMKFVPCLLLVTLSCLGTLGQAPR
		,	QKQGSTGEEFHFQTGGRDSCTMRPSSLGQGAGEVWLRVDCRNTD
	·	*	OTYWCEYRGOPSMCOAFAADPKSYWNOALOELRRLHHACOGAPV
;			LRPSVCREAGPOAHMOOVTSSLKGSPEPNOOPEAGTPSLRPKAT
			VKLTEATOLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAK
·			KKAWEHCWKPFOALCAFLISFFRG
6651	3425	1353	
0021	3425	1353	AKELLKVGDFSLCAGFYQNTADTMENLSKEPLASFVSESFDISA
			CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG
			DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDGYESSLNF
			HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR
			DLHGILRTYANFSITKELKDTMRTSHGLRRHPSFSANCGLPSSW
			TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV
	ŀ		FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP
			RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL
			NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN
			DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA
			CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIEPQHFCQAFHR
			·-
			ENDTLIIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV
			LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG
		İ	RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFQSANIIELLH
			YHQCDSRSSTKAEILKCLLNLQIQHIDARFAVLLTDKPTIPREV

	-		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
! .	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequeines	\=possible nucleotide insertion)
	bequence		FENNGILVTDVNNFIENIEKIAAPFRSSYW
6652		1345	
0052	2	1343	IPGSTISCSCHSRRLRGGSPAPRLSLGAASPRPRPPSLPLPLPL
1	1		PFPLFLPTRPAERAWIRSRRASEWVGKMEVPRLDHALNSPTSPC
			EEVIKNLSLEAIQLCDRDGNKSQDSGIAEMEELPVPHNIKISNI
į			TCDSFKISWEMDSKSKDRITHYFIDLNKKENKNSNKFKHKDVPT
	i		KLVAKAVPLPMTVRGHWFLSPRTEYTVAVQTASKQVDGDYVVSE
			WSEIIEFCTADYSKVHLTQLLEKAEVIAGRMLKFSVFYRNQHKE
l			YFDYVREHHGNAMQPSVKDNSGSHGSPISGKLEGIFFSCSTEFN
1			TGKPPQDSPYGRYRFEIAAEKLFNPNTNLYFGDFYCMYTAYHYV
j	•		ILVIAPVGSPGDEFCKQRLPQLNSKDNKFLTCTEEDGVLVYHHA
	!		QDVILEVIYTDPVDLSLGTVAEITGHQLMSLSTANAKKDPSCKT
			CNISVGR
6653.	170	1910	FFLEPRLRPFPASRARFVPARTRPSPLHPCCFCFEGGGSMLSPQ
i ·			RVAAAASRGADDAMESSKPGPVQVVLVQKDQHSFELDEKALASI
	1		LLQDHIRDLDVVVVSVAGAFRKGKSFILDFMLRYLYSQKESGHS
1 .	· ·	,	NWLGDPEEPLTGFSWRGGSDPETTGIOIWSEVFTVEKPGGKKVA
ł			VVLMDTQGAFDSQSTVKDCATIFALSTMTSSVQIYNLSQNIQED
'			DLOOLOLFTEYGRLAMDEIFOKPFOTLMFLVRDWSFPYEYSYGL
l	ļ		QGGMAFLDKRLQVKEHQHEEIQNVRNHIHSCFSDVTCFLLPHPG
			LOVATSPDFDGKLKDIAGEFKEOLQALIPYVLNPSKLMEKEING
			SKVTCRGLLEYFKAYIKIYOGEDLPHPKSMLQATAEAYNLAAAA
			-
		· ·	SAKDIYYNNMEEVCGGEKPYLSPDILEEKHCEFKQLALDHFKKT
1			KKMGGKDFSFRYQQELEEEIKELYENFCKHNGSKNVFSTFRTPA
			VLFTGIVALYIASGLTGFIGLEVVAQLFNCMVGLLLIALLTWGY
			IRYSGQYRELGGAIDFGAAYVLEQASSHIGNSTQATVRDAVVGR
		, , , , , , , , , , , , , , , , , , , ,	PSMDKKAQ
6654	1	705	RTSLSPSQCSSFNLAMASAGMQILGVVLTLLGWVNGLVSCALPM
		•	WKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQMQCKVYDSLLAL
l			PQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARL
	1		VLTSGIVFVISGVLTLIPVCWTAHAVIRDFYNPLVAEAQKRELG
1 .	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		ASLYLGWAASGLLLLGGGLLCCTCPSGGSQGPSHYMARYSTSAP
	<u> </u>		AISRGPSEYPTKNYV
6655	341	16	KDAYMFKKGLLALALVFSLPVFAABHWIDVRVPEQYQQEHVQGA
l	ĺ	·	INIPLKEVKERIATAVPDKNDTVKVYCNAGRQSGQAKEILSEMG
			YTHVENAGGLKDIAMPKVKG
6656	2	1212	TELPPRPANLATQPPLSPLRALAPLPEKPGAVPPPQKRMAKVAK
1			DLNPGVKKMSLGQLQSARGVACLGCKGTCSGFEPHSWRKICKSC
1			KCSQEDHCLTSDLEDDRKIGRLLMDSKYSTLTARVKGGDGIRIY
			KRNRMIMTNPIATGKDPTFDTITYEWAPPGVTQKLGLQYMELIP
1	İ		KEKQPVTGTEGAFYRRRQLMHQLPIYDQDPSRCRGLLENELKLM
1			EEFVKQYKSEALGVGEVALPGQGGLPKEEGKQQEKPEGAETTAA
			TTNGSLSDPSKEVEYVCBLCKGAAPPDSPVVYSDRAGYNKQWHP
]		TCFVCAKCSEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDEI
1			IFAEDYQRVEDLAWHRKHFVCEGCEQLLSGRAYIVTKGQLLCPT
1			CSKSKRS
6657	830	2120	LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPEYCEP
3037	1 330	2120	LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLKMEH
1			,
			HLEAHKNGHANGHLNIGVDIPTPDGSFSIKIKPNGMPNGYRKEM
			IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER
1			VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL
1			LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK
			LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL
1			TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV
1			AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK
			NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT
6658	35	855	HCCALGAPGSPYRGLYFSSAAPCTAPRKAKHQSTLEGLTKRMLM

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
f	sequence	504444	\=possible nucleotide insertion)
ļ	2042000		FDPVPVKQEAMDPVSVSYPSNYMESMKPNKYGVIYSTPLPEKFF
· .			QTPEGLSHGIQMEPVDLTVNKRSSPPSAGNSPSSLKFPSSHRRA
į			SPGLSMPSSSPPIKKYSPPSPGVQPFGVPLSMPPVMAAALSRHG
1			IRSPGILPVIQPVVVQPVPFMYTSHLOOPLMVSLSEEMENSSSS
ŀ			MQVPVIESYEKPISQKKIKIEPGIEPORTDYYPEEMSPPLMNSV
]			SPPQALLQE
6659	18	523	EPQRGDCETWFQNCSLPKFVCFFCWGFWLWRAHSMSNLHSLPGL
""		343	RGLTSISRNQLQCTNAMRVINNYQRRWKNQNTFLLATFANVVNV
1			CGNPTITCPHNRTLNNCHHSGVQVPLMYCNLTTPSPQNISNCRY
			AQTPANMFYIVACDNRDQRRDPPQYPVVPVHLHTII
6660	514	1707	CAASLDCRHHLCEPDMKLVWPSAKLLQAAAGASARACDSVTSNV
		1 2,0,	LPLLLEQFHKHSQSSQRRTILEMLLGFLKLQQKWSYEDKDORPL
1			NGFKDQLCSLVFMALTDPSTQLQLVGIRTLTVLGAQPDLLSYED
			LELAVGHLYRLSFLKEDSQSCRVAALEASGTLAALYPVAFSSHL
			VPKLAEELRVGESNLTNGDEPTOCSRHLCCLOALSAVSTHPSIV
			KETLPLLLQHLWQVNRGNMVAQSSDVIAVCQSLRQMAEKCQQDP
			ESCWYFHOTAIPCLLALAVOASMPEKEPSVLRKVLLEDEVLAAM
			VSVIGTATTHLSPELAAQSVTHIVPLFLDGNVSFLPENSFPSRF
			QPFQDGSSGQRRLIALLMAFVCSLPRNVSEHIWEVLLFNLDKVT
		,	PG
6661	179	430	GVHAASGTLSATWLAEAKMFDSLAKAGKYLGQAAKLMIGMPDYD
ſ			NYVEHMRVNHPDQTPMTYEEFFRERODARYGGKGGARCC
6662	185	423	RSLPKPAPAQPASIHCARFSGVTPPTAKTAMSDGNTAFNALMYC
			GPKADDGNIFSACAPASSAVKASVSVAQPGQAVIP
6663	3	1005	RPVLSSRVDDFVPPLPETSGRRKKLERMYSVDRVSDDIPIRTWF
1 -	•		PKENLFSFQTASTIMQAISNFRKHLRMVGSRRVKAQTFAERRER
			SFSRSWSDPTPMKADTSHDSRDSSDLQSSHCTLDEAFEDLDWDT
	: :		BKGLEAVACDTEGFVPPKVMLISSKVPKAEYIPTIIRRDDPSII
			PILYDHEHATFEDILEEIERKLNVYHKGAKIWKMLIFCQGGPGH
			LYLLKNKVATFAKVEKEEDMIHFWKRLSRLMSKVNPEPNVIHIM
		` `	GCYILGNPNGEKLFQNLRTLMTPYRVTFBSPLELSAQGKQMIET
<u> </u>		,	YFDFRLYRLWKSRQHSKLLDFDDVL
6664	58	968	PRLLRLPRSVVVMDSPWDELALAFSRTSMFPFFDIAHYLVSVMA
			VKRQPGAAALAWKNPISSWFTAMLHCFGGGILSCLLLAEPPLKF
			LANHTNILLASSIWYITFFCPHDLVSQGYSYLPVQLLASGMKEV
			TRTWKIVGGVTHANSYYKNGWIVMIAIGWARGAGGTIITNFERL
			VKGDWKPEGDEWLKMSYPAKVTLLGSVIFTFQHTQHLAISKHNL
			MFLYTIFIVATKITMMTTQTSTMTFAPFEDTLSWMLFGWQQPFS
			SCEKKSEAKSPSNGVGSLASKPVDVASDNVKKKHTKKNE
6665	171	1278	DERRLACROVVTQQRSELYPGFQKRQRFLPKAGEEAAAQGGRHL
			PGRWLGPGCTQNPCSVHTATGPEPRKLPLLPPDSPNSGYPKEPA
			ALCPGIPSPCRMTHQDLSITAKLINGGVAGLVGVTCVFPIDLAK
1			TRLQNQHGKAMYKGMIDCLMKTARAEGFFGMYRGAAVNLTLVTP
j i			EKAIKLAANDFFRRLLMEDGMQRNLKMEMLAGCGAGMCQVVVTC
			PMEMLKIQLQDAGRLAVHHQGSASAPSTSRSYTTGSASTHRRPS
]]			ATLIAWELLRTQGLAGLYRGLGATLLRDIPFSIIYFPLFANLNN
i I			LGFNELAGKASFAHSFVSGCVAGSIAAVAVTPLDVLKTRIQTLK
<u> </u>			KGLGEDMYSGITDCAR
6666	498	2868	MTTFLPVPQMMAGFSFGTFGNPPMBSPSAWQTIHQPFIVSCLTL
			WSPGCWPQPIQKEGVGLWDIRKPQSSLLRYGGNLSLQSAMSVRF
			NSNGTQLLALRRRLPPVLYDIHSRLPVFQFDNQVYFNSCTMKSC
]			CFAGDRDQYILSGSDDFNLYMWRIPADPEAGGIGRVVNGAFMVL
	1		KGHRSIVNQVRFNPHTYMICSSGVEKIIKIWSPYKQPGCTGDLD
	Ì		GRIEDDSRCLYTHEEYISLVLNSGSGLSHDYANQSVQEDPRMMA
			FFDSLVRREIEGWSSDSDSDLSESTILQLHAGVSERSGYTDSES
L			SASLPRSPPPTVDESADNAFHLGPLRVTTTNTVASTPPTPTCED

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
2.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
	sequence		AASROORLSALRRYODKRLLALSNESDSEENVCEVELDTDLFPR
	,		PRSPSPEDESSSSSSSSSSSEDEELNERRASTWORNAMRROKT
			TREDKPSAPIKPTNTYIGEDNYDYPQIKVDDLSSSPTSSPERST
			STLEIQPSRASPTSDIESVERKIYKAYKWLRYSYISYSNNKDGE
			TSLVTGEADEGRAGTSHKDNPAPSSSKEACLNIAMAQRNQDLPP
			EGCSKDTFKEETPRTPSNGPGHEHSSHAWAEVPEGTSQDTGNSG
		Í	SVEHPFETKKLNGKALSSRAEEPPSPPVPKASGSTLNSGSGNCP
			RTQSDDSEERSLETICANHNNGRLHPRPPHPHNNGQNLGELEVV
			AYSSPGHSDTDRDNSSLTGTLLHKDCCGSEMACETPNAGTREDP
			TDTPATDSSRAVHGHSGLKRQRIELEDTDSENSSSEKKLKT
6667	171	1310	ABEVERLAAMRSDSLVPGTHTPPIRRRSKFANLGRIFKPWKWRK
			KKSEKFKHTSAALERKISMRQSREELIKRGVLKEIYDKDGELSI
, ,		7.	SNEEDSLENGQSLSSSQLSLPALSEMEPVPMPRDPCSYEVLQPS
			DIMDGPDPGAPVKLPCLPVKLSPPLPPKKVMICMPVGGPDLSLV
	· ·	1	SYTAQKSGQQGVAQHHHTVLPSQIQHQLQYGSHGQHLPSTTGSL
			PMHPSGCRMIDELNKTLAMTMQRLESSEQRVPCSTSYHSSGLHS
	1		GDGVTKAGPMGLPEIRQVPTVVIECDDNKENVPHESDYEDSSCL
		·	YTREEEEEEDEDDDSSLYTSSLAMKVCRKDSLAIKPSNRPSKR
			ELEEKNILPROTDEERLELROQIGTKL
6668	714	358	TLAVATGPALTLRCHVCTSSSNCKHSVVCPASSRFCKTTNTVEP
			LRGNLVKKDCAESCTPSYTLQGQVSSGTSSTQCCQEDLCNEKLH
1	,		NAAPTRTALAHSALSLGLALSLLAVILAPSL
6669	459	1207	KDEETRKDYDYMLDHPERYYSHYYHYYSRRLAPKVDVRVVILVS
	i '		VCAISVFQFFSWWNSYNKAISYLATVPKYRIQATEIAKQQGLLK
			KAKEKGKNKKSKEEIRDEEENIIKNIIKSKIDIKGGYQKPQICD
		* *	LLLFQIILAPFHLCSYIVWYCRWIYNFNIKGKEYGEEERLYIIR
	İ		KSMKMSKSQFDSLEDHQKETFLKRBLWIKENYEVYKQEQEEELK
			KKLANDPRWKRYRRWMKNEGPGRLTFVDD
6670	184	594	VARI*GEAAKMSSEPPPPYPGGPTAPLLEEKSGAPPTPGRSSPA
			VMQPPPGMPLPPADIGPPPYEPPGHPMPQPGFIPPHMSADGTYM
		د	PPGFYPPPGPHPPMGYYPPGPYTPGPYPGPGGHTATVLVPSGAA
1			TTVTV
6671	1	763	LPAEKPRSAPNMAGGRCGPQLTALLAAWIAAVAATAGPEEAALP
		1	PEQSRVQPMTASNWTLVMEGEWMLKFYAPWCPSCQQTDSEWEAF
	1	1	AKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFRR
	* 1 · · · · · · · · · · · · · · · · · ·		YRGPGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFS
	l · .		ISGKIWHLHNYFTVTLGIPAWCSYVFFVIATLVFGLSMDLVL*V
		1	ISQCNWDPPYRHVS*/RPSTNLGVHTAHTSEHLRL
6672	304	1089	APGSKPVQFMDFEGKTSFGMSVFNLSNAIMGSGILGLAYAMAHT
		1	GVIFFLALLLCIALLSSYSIHLLLTCAGIAGIRAYEQLGQRAFG
			PAGKVVVATVICLHNVGAMSSYLFIIKSELPLVIGTFLYMDPEG
	1		DWFLKGNLLIIIVSVLIILPLALMKHLGYLGYTSGLSLTCMLFF
	1	1	LVSVIYKKFQLGLCYRATMKQQWESEALVGTPQPRDSTAAVKAQ
ı	1	1	MFHS*LTGVLTQWPIMAFAFVCHPGGAGPSITELCRAFQAQD
	1	i .	
6673	1116	1963	LOTOTHUTHICARVTHI GSHOLL ANACTMI CROOSSSMADARSO
6673	1116	1963	LQIQTHHTHHGARVTHLGSHQLLANAGTMLCRQQSSMAPAFSQ
6673	1116	1963	SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV
6673	1116	1963	SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE
6673	1116	1963	SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE NAVPRP*QG*KVNPSGQERQS\WVLPLPVPGEPLKLPGLPG*NK
6673	1116	1963	SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE NAVPRP*QG*KVNPSGQERQS\WVLPLPVPGEPLKLPGLPG*NK SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL
6673	1116	1963	SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE NAVPRP*QG*KVNPSGQERQS\WVLPLPVPGEPLKLPGLPG*NK SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL ITWH*SAPTPPLKACPAPRPSDPCSSCLSCPCVTQHPRFSDTGW
			SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE NAVPRP*QG*KVNPSGQERQS\WVLPLPVPGEPLKLPGLPG*NK SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL ITWH*SAPTPPLKACPAPRPSDPCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG
6674	1116	1963 440	SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE NAVPRP*QG*KVNPSGQERQS\WVLPLPVPGEPLKLPGLPG*NK SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL ITWH*SAPTPPLKACPAPRPSDPCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL
			SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE NAVPRP*QG*KVNPSGQERQS\WVLPLPVPGEPLKLPGLPG*NK SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL ITWH*SAPTPPLKACPAPRPSDPCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY
			SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE NAVPRP*QG*KVNPSGQERQS\WVLPLPVPGEPLKLPGLPG*NK SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL ITWH*SAPTPPLKACPAPRPSDPCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL

Predicted Predicted Incleotide Incle				
No:		1		
Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequenc	1			
to first amino acid residue of amino acid residue of amino acid sequence se	NO:			
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid sequence 6675 277 1678 1678 277 1678 278 279 1678 277 1678 277 1678 278 277 1678 278 278 277 1678 278 277 1678 278 278 278 277 277 278 278				
amino acid residue of amino acid sequence and acid when the property of the property of the sequence and acid sequence and acid sequence (acid when the property of the proper				
amino acid sequence amino acid sequence 6675 277 1678 1678 277 1678 278 279 277 277 277 278 279 270 270 277 270 270 270 270			******	
amino acid sequence Codon, /-possible nuclectide insertion)		ł .		
sequence Appossible nucleotide insertion]			
1678 CNMPTERNAFLDNPTILJAHIROSHVISDUTGKUEMULDHUVD LEKKHPPSMPODGSETGGSNETGGYVYGNGVUEMULTSSWDFGIR RESNTAQRIERLEKERGNOJICKKNIJOWKERNSKQSQELELSJE KKSLKEKPISGSSETGGSSETGGCLGLINSPPEREYSKPÖKKHV GTTATKKIDVYLPLISSGDDLLPWTVITASARVDDLIGILGVE YTSEGGERKINDWASACKILLERDDGSVDTOFPELDSKEPIHKP GPSTLALVEKYSSPCLITSKGSLFVEINAAHGFGLIQVDNYKVTM KEILLKAVKRKRGSGKVSGSRADGVFEEDSGIDIATVQDLISH HYKSFKVSMIHRIRFTITOVQL/GCALFFGVURRRAAFVDCLBPS ADTWRQBGIGCCGAACAARS TISHKC*FEGISGDKVEIDPVTNQ KASTKWHIKKPISTDSDLLCACYDLABE 6676 277 1678 CNMPTERNAFLINPTILLAHIRGSHVTSDDTGRCEMVLIDHDVD LEKKHPPSMPODGSSETGGSNEETGGVVEANSVITSSWDFGIR RRSNTAQRIERLEKERGNOJKKKNIGWKERNSKQSAGELSJEFE KKSLKEKPPISGGSISVSUGGRCPLQVINNSPREYSKPDGKGHV GTTATKKIDYYLPLHSSGDRLPWTVVINASARVDULIGILGV YTSEGREKKNIDNVSAVCHLABDDGSVDTOFPLDINSPIHKF GFSTLALVEKYSSPGLITSKESLFVRINAAHGFSLIQUDNIKVM KEILLKAVKRKRSGKVUSGRADGVFEBSGJIDHTVQDMLSSH HYKSFKVSMHIRIRFTTTDVQL/GCALFPGVURRRAAPVDCLBSP ADDVRRGGIGCGAACAARS*FOSHKC*BGISGDKVEIDPVTNQ KASTKFWIKKRFISIDSDLLCACYDLABE RESNTAQRIERLEKKRRONGVFEBSGJIDHTVQDMLSSH HYKSFKVSMHRIRRFTTTDVQL/GCALFPGVURRRAAPVDCLBGL KKSHSPPSTGRACACAARS*FOSHKC*BGISGDKVEIDPVTNQ KASTKFWIKKRFISIDSDLLCACYDLABE RESNTAQRIERLEKKRRONGVFEBSGJIDHTVQDMLSSH HYKSFKVSMHRIRRFTTTDVQL/GCALFPGVURRRAAPVDCLBGL KKSHSPPSTGRACHDVANFWESKSCHAVELDDFVTNQ KASTKFWIKKRFISIDSDLLCACYDLABE RESNTAQRIERLEKKRRONGVFEBSGJIDHTVQDMLSSH GRENKTAQRIERLEKKRRONGVFENDVFENDVENDSHGKENDFEDFING GTTATKKLDVYLPLUSSGDRLLPWTVITNAAHGFSLIQUHVTVTM KEILLAAVKRRKGSKVSGSRADGVFEBSGJIDHTVGVMTNSK KSHLKSKPPTSGRASHTVAVAGSGSTLGVFEDSGJIDHTVTVTM KEILLAAVKRRKGSCKVSGSRADGVFEBSGJIDHTVSWFTNG KSHLKFTTAVALDVYLDHTKVTM KEILLAAVKRRKGSCKVSGSRADGVFEBSGJIDHTVSWFTNG GFSTLALVEKYSSPGLTSKSSLPVRINAAHGFSLLGVCH GTTATKKLDTVYLDHTVTVTMAAARVOLLGGLFV KLEHLPWTVATAAARVOLLGGLFFP KSSGSSSSLITUTUTGGSSYMS**INTOTTILRVLSSNFGRQ*LR BFPCSGLDMSGGCCMHLDCCCDWPTIPHQCMRKGRGMMNS* ADDVRRGGGGGCACAALRS**INTOTTILRVLSSNFGRQ*LR GFSTLALVEKYSSPGLTSKSSTHTVLLGGFFYMFTLAGFFLDHTVDG LLGGTLYTSLCTTLVKRVGKSVLVGNINMVVRNETTLIBHGGLD SCYCNKEYNKENHENSLATDJCSCSSGERGCHATUNGSVPDL GEKNITVIKGSTKRSTHAUSGAPGOPP/SPGSSLATDSPTTYBESGLITSS**ALD			sequence	
LEKTHPPSMPODSGSETOGSNETGGYVZNOTHSSMPDTS RESMTAQLIERLEKERRONICKERNIOWERNSKGSQGLEKSIFE RESMTAQLIERLEKERRONICKERNIOWERNSKGSQGLEKSIFE RESMTAQLIERLEKERRONICKERNIOWERNSKGSQGLEKSIFE RESMTAQLIERLEKERRONICKERNIOWERNSKGSQGLEKSIFE RESMTAQLIERLEKERRONICKERNIOWERNSKGSGTLEKERSKERNIOWERSKE		-		
RESNTAQLIERLEKERQNOJICKKNIJOMERNSKQSAGELESSIE KISIKEKEPISGOSIISVALGOCIOLOINNPFEEVSKPOKKHV GTTATKKIDYILPHISSODDILIPMTVITASARVQDLIGICKO YTSEGGERKINDINSAVCHILABODGAVDTPEPLONEPIHKE GPSTLALWEKYSSPOLITSKSI.FVRINAAHGFALIQUINTKVTM KEILLKAVKERKSKOKVGSGRADOKYPERDSIDIJATVQDALSSH HYKSFEVSHIHRLEFTTDVOL/GCALFPGVILKRAAPVDCLARS ADTWRQDQIGCCGARCALRS*DSHKC*BGISGKVEIDPUTUQLISS RASTKWIKKORISTDDLLCAC\DLARE 6676 277 1678 GNWPTERRAFLDNFTIILAHIRGSHVTSDTGKCEMVLIDHDVD KASTKWIKKORISTDDLLCAC\DLARE KRSHTAQKLERLEKERQNOJKKKANIQMERNSKQSAGELESJEE KRSHKARKPPISGOSIISVALGCOLQLUNNFPERSYKDOKKHV GTTATKKIDYILEHISSODRILPMTVUTHASARVQDLIGLICKO YTSEGGERKINDINSAVCHILABDOGEVUTOPPUNGKSH KRSHTAQKLERLEKERQNOJKKKNIQMERNSKQSAGELESJEE KRSHKASKKRPPISGOSIISVALGOCYLQLUNNFPERSKPOKKHV GTTATKKIDYILEHISSODRILPMTVUTHASARVQDLIGLICKO YTSEGGERKINDINSAVCHILABDOGEVUTOPPUNGKSH HYKSFKVSMHIRLERTTTVOL/GCALFPGVURKRAAPVOLLISH KEILLKAVKRKRKOKYSGRADOKYEEDSQIIDTVQDMLSSH HYKSFKVSMHIRLERTTTVOL/GCALFPGVURKRAAPVOLLISH KEILKAVKRKRKOKYSGRADGAVEEDSQIIDTVQDMLSSH HYKSFKVSMHIRLERTTTVOL/GCALFPGVURKRAAPVOLLISH RESNITAQRLERLEKKRONQIKKNIQNKSNSKOSAGELESJEE KKSLKKPPISGOSILSVALDCOLJUNNFPREYSKPOKKEN ADTWRGEJGICGAACAARSH SHIKVOBESSETIGHCEMVLIDHDVD LEKH PPSBMPODESSETIGSNIGETGGYVYAGSVUTITSSWOFGIG TTATKKIDVYLPULSSODRILPMTVUTHASARVQOLIGLICKO YTSEGGERKANDAVSAVCHILABDOGEVUTOPPLOSHBPIHKP GPSTLALWEKYSSPOLITSKSEDYPUTANAHGFSLIOVHKVNTN KRSILKKNPPISGOSILSVALDOCOLJUNNFPREYSKPOKKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKEN KSLKKRPPISGOSILSVALDOCOLJUNNFPREYSKPOKEN KSLKARDON KRSTAGEROMA	6675	277	1678	
KKSLKEKPISGKOSILGVRLEGCEPLOLINPYUTWINSPREYSKPOKHV GTTATKKIDVYLEHASQDRILDPYUTWINSPRAVQDLIGLICUG YTSEGREPKLINDKYSAYCLHIABDDGEVDTOPPPLDENEPIHKE GPSTLALIVEKYSSPGLITKEKSILVVRINAMERICHOVINTKYM KEILLKAVKRKGSQKYSGSRADGVYEEDSQIDIATVQDMLSSH HYKSFKVSMIHRIRFTTTOVL/GCALFFGVLKKRABVOLLEPS ADTWRQEGIGCCGARCAALKS PSIKC'S GISGKVKIDPVINQ KASTKWHIKQKPISIDSDLLCAC'\DLARB 6676 277 1678 GMPTERMAPLDNPTILLAHIRGSHVTSDDTOMCEMVLIDHUVD LEKIHPPSMPODSGSIGGSNGGTGGVYVAQGVDITSGMOFGIR RESHTAQRLEBERKERQQVICKNINQWEMPLEVSKOSQBLESLFE KKSLKSKPISGKOSILSVRLEQCPLQLNMPFNEYSKPOKGHV GTTATKKIDVYLHHSSOORLEMPTVTVMASAQGLEKSLFE KKSLKSKPPISGKOSILSVRLEQCPLQLNMPFNEYSKPOKGHV GTTATKKIDVYLHHSSOORLEMPTVTVMASARAVQDLIGLICUG YTSSGREPKLNDNVSAYCLHIABDDGSVDTDPPPLDSNEPIHKP GPSTLALIVEKYSSPGLITKSKSLEVVINAMERAVQDLIGLICUG YTSSGREPKLNDNVSAYCLHIABDDGSVDTDPPPLDSNEPIHKP GFSTLALIVEKYSSPGLITKSKSLEVVINAMERAVDCLERS ADTWRQEDIGCCGAACAALS*DSINDVINGCALFFGWARAVDCLERS ADTWRQEDIGCCGAACAALS*DSINDVINGCAVLFGWARAVDCLERS ADTWRGEDIGCCGAACAALS*DSINDVINGCAVLFGWARAVDCLERS KKSLKSKPISGKQSILSVRLEGCPLQLNMPFNEYSKPOKGHV GTTATKKIDVYLDHISSODRILDFMVTVMASARVQDLIGLICUG YTSSGREPKLNDNVSAYCLHIABDDGSVDTDFPPLDSNEPIHKP GFSTLALIVEKYSSPGLITKSSLEVVINAMERAVQDLIGLICUG YTSSGREPKLNDNVSAYCLHIABDDGSVDTDFPPLDSNEPIHKP GFSTLALIVEKYSSPGLITKSSLEVVINAMERAVQDLIGLICUG YTSSGREPKLNDNVSAYCLHIABDDGSVDTDFPPLDSNEPIHKP GFSTLALIVEKYSSPGLITKSSLEVVINAMERAVQDLIGLICUG YTSSGREPKLNDNVSAYCLHIABDDGSVDTDFPPLDSNEPIHKP GFSTLALIVEKYSSPGLITKSSLEVVINAMERAVDCLERS KKSIKKSPSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				
TTATKKIDVILLHISQDRILDHTVUTMASARVQDLIGLICMQ YTSEGREPKLANDROSAYCHIARDDGGEVDTOP PIDENTPIHKF GPSTLALVEKYSSPGLTSKESLFVERNAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKYSGSRADGVFEEDSQIDIATQOMLSH HYKSFKVSMIHRLRFTTDVQL/GCALFFGVLKKRARPUDCLBPS ADTWRGDIGCCGAACALKS*DSHKC*EGISGDKVEIDPVTNQ KASTKWHIKQRFISIDSILLGAC\LACAC\LAER 6676 277 1678 CMMPTERNAPIDMPTILLAHIRQSHVTSDDTGMCEMVLIDHDVD LEKHPPSMPFODSGSEIGGSMETGGYYYAGVSDTTSSMPFGIR RSSNTAQRIEBLBKEERQNQIKCNIQWKERNSKQSAQELSLSIFE KKSLKEKPPISGSGSILSVRLEQCPLQNIMPPNEYSKPDGKGHV GTTATKKIDVYLPLHISGORILDHTVUTMASARVODLIGLCWQ YTSSGREPKLANDRVSAYCHLARDGGEVDTPPPDLSNEPIHKF GPSTLALVEKYSSPGLTSKSSLEVPRINAHGFSLIQUDNTKVTM KEILLKAVERKSGSQVISSBAGDOVFEEDSGILCWQ YTSSGREPKLANDRVSAYCHLARDGGEVDTPPDLSNEPIHKF GPSTLALVEKYSSPGLTSKSSLEVPRINAHGFSLIQUDNTKVTM KEILLKAVERKSGSVGISSBAGDOVFEEDSGIVSTDTSOMPFGIR RSSNTAWHIKQRFISIDSILLGAC\DLAG KASTKWHIKQRFISIDSILLGAC\DLAG KASTKWHIKQRFISIDSILLGAC\DLAG KASTKWHIKQRFISIDSILLGAC\DLAG KRSNTARPHIKQRSQVGVGSSGTGGYVYAGGVDTITSSMPFGIR RRSNTARPHIKQRFISIDSILLGAC\DLAG KRSNTARPHIKQRSQVGSGTGGYVAGVGDVDTTSSMPFGIR RRSNTARPHIKQRFISIDSILLGAC\DLAG KRSNTARPHIKQRFISIDSILLGACQDLQAMPPREYSKFDGKGHV GTTATKKIDVYLPLHISGQRLLGPTQLVANDFISSPHFGIRCGWV YTSSGREPKLANDRVSAYCHLARDDGEVDTPPREYSKFDGKGHV GTTATKKIDVYLPLHISGQRLLGPTQLVARDFMEYSKFDGKGHV GFSTLALVEKYSSPGLTSKSSLEVRINAHGFSLIQUDNTKVTM KEILLKAVKRRKGSGVVGGSRTGGVYYAGGVBTGSSWFDGKGFGV HYKSFKVSMHHRLRFTTDVQL/GCALFPGVLRKRAPVDCLRPS ADTWRGDIGCCGAACAALS*DSWFEEDGGVPKFFGROFHEYS HYKSFKVSMHHRLRFTTDVQL/GCALFPGVLRKRAPVDCLRPS ADTWRGDIGCCGAACAALS*DSWFEEDGGVPKFGRGRMEN*QS LLGSDQSSVGLEDLCVPNYFLLHVLLGFF*PHELFLLFVVDLG FLPPLLLQGGCCHALDCCCGNAVYTTGGVHKRGRGRMEN*QS LLGSDQSSVGLEDLCVPNYFLLHVLLGFF*PHELFLLFVVDLG FLPPLLLQGGCHHLDCCCCTHVYTTGGACTHDLGSGSFVSDL SSYCNKEVYNKELIFNSLINYD/SCSQSFEKGHAP*QNONS)PH QBKWIYVHKGSTKRRHGYCTLGBAPNRLDFSGSFVSDL SSYCNKEVYNKELIFNSLINYD/SCSGSFKGRAFCYNDLGQLAN HILPLFLVVGRWADVKHLETVQSGLASLGFFGGPFTTDEBGGFF PKRNSPDTHCPRGGAPFGVFACGGAPGSPFTTTBESGGF PKRNSPDTHCPRGGAPFGVFACGAPGFFTFTDEBGGF PKRNSPDTHCPRGGAPFGVFACGAPGFFTFTDEBGGF PKRNSPDTHCPRGGAPFGVFACGAPGFFTFTDEBGGF PKRNSPDTARGGGPFGGAPGGAPGGPFFTTBEB	1			
TYSEGREPKINDNYSAYCLHIADDGEVDIPPPLDSNPPIHER GPSTLALIMEKYSSPOLTSKESLEVRINANGERICUMTNYKTM KEILLKAVKRRKGSQKYGGSRADGVPEEDSQIDIATVQDMLSSH HYKSFKVSMIHRIRFTTTUVL/GCALFFGVLRKRADGVEDDSYDLAPS ADTWRGDIGCGGAGCALKS*DSIKC*EGISGDKVEIDPVTNQ KASTKWHKQKPISIDSDLLCAC\DLARE 6676 277 1678 GMPTERNAPLDNPTILLAHRGSWYEDDTOMCEMVLIDHDVD LEKIHPPSMPGDSGSIGGSNGSTGGYVYAQSVDITSSMPFGIR RRSHTAQRILERLKRERQNGIKCKNIQWEERBAGVGLEUSIPFE KKSLKEKPPISGKGSILGSVRLEQCPLOLMNPFNETSKFDGKGHV GTTATKKIDVYLHHSSQDRLIBMYVTVMASARVQDLIGLICNQ YTSEGREPKLNDNYSAYCLHLABDDGEVDTDPPPLDSNEPIHKP GFSTLALWEKYSSPGLITSKESLEVRINANAHGFSLIQVDHXVTVM KEILLKAVKRRKSSQKYSGSRADGVPEEDSQIDIATVQDMLSSH HYKSFXVSMIHRIRFTTDVQL/GCALFFGVLKRRAAPVDCLEPS ADTWRGDGIGCGAACAALKS*DSIKC*CEGSQGLEKSIPF ADTWRGDGIGCGAACAALKS*DSIKC*CEGSQGLEKSIPF RRSHTAQRLERLERERQNGIKGKOKYSGDYDFYDDYSWFDFUR RRSHTAGRLERLERRENGNGIKCKNIOWEERBAGDELSSIPF RRSHTAGRLERLERRENGNGIKCKNIOWEERBAGDELSSIPF KKSLKEXPPISGKQSILSVRLEQCPLQLINNPPNEYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLEMTVTWMASARVQDLIGLCNQ YTSEGREPKLANDWSAYCHLHAEDDGSVDTPFPLDSNBPIHKP GFSTLALWEKYSSPGLITSKESLEVRINAHGFSLIQVDHXVIM KEILLKAVKRKSGSKVUSGRADGVFEEDSJGDLIATVQDMLSSH HYKSFKVSBHIRRFPTTOVQL/GCALFFGVLRRAAPVDCLEPS ADTWRGDGIGGGGAGAALRS*DSWFEEDSJCLICKNP ADTWRGDGIGGGGAGAALRS*DSWFEEDSJCLICKP ADTWRGDGIGGGGAGAALRS*DSWFIEDSWFIDPTVN KASTKWHKORPISIDSLLCAC\DLABE GFSTLALWEKYSSPGLITSKESLEVRINAHGFSLIQVDHXVIM KEILLKAVKRKSGSKVUSGRADGVFEEDSJCLIATVODMLSSH HYKSFKVSBHIRRFTTDVQL/GCALFFGVLRRAAPVDCLEPS ADTWRGDGIGGGAGAALRS*DSWFIDPTVT KASTKWHKORPISIDSLLCAC\DLABE GFSTLALWEKYSSPGLITSKSSLEVRINAHGFSLIQVDHXVIT LELLALVSGUTGGAGACALRS*DSKFCTEGGGPGLHXDFOX KASTKWHKORPISIDSLLCAC\DLABE GFSTLALWEKYSSPGLITSKSSLEVRINAHGFSLIQVDHXVIT LELLALVSGUTGGAGAACALRS*DSKFCTEGGGPGLHXDFOX ADTWRGGGGGAGAALRS*DSKFCTEGGGRAFTTHEFULSSNFGQ*LR FERNESSTRICKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			
GPSTLALVEKYSSPEJITSKESLEVEINARHEFSLIQUPIKVTM KEILLKAVKRKSGKYKSSERAGVFEEDSCIDIATVODMLSSH HYKS FKVSMIHEREFTTDVDL/GCALPFGVLRKRAAPVDCLRES ADTWROEGIGCGAACAALRS*DSHKC*EGISGKVEIDPVTNN KASTKWHIKQFISIDSLLCAC\DLAEE ADTWROEGIGCGAACAALRS*DSHKC*EGISGKVEIDPVTNN KASTKWHIKQKPISIDSDLCAC\DLAEE ADTWROEGIGCGAACAALRS*DSHKC*EGISGKVEIDPVTNN KASTKWHIKQKPISIDSPTILAHTGGSEVTSDDFGTGVYVAGAGVGDVITSSWDFGIR RSNTAQRLERLBKERGQGIKCKNIQWKERNSKGSAGELSJFE KKSLKKEPPISIGSGSILSVELGCPLQAMPPNETSKFDGKGHV GTTATKKIDVYLPHHSSQDRLDWTVVTMASARVQDLIGICWQ YTSSGREPKIMBUVSAYCHHAEDGGEVDTDFNETSKFDGKGHV GFSTLALVEKYSSFGITSKSSLEVRINAHGFSLIQUDVKVTM KEILLKAVKRKSGKVGSSFAGAGVFEEDSCIDVTWQTMLSH HYKS FKVSNHHRIRFTTDVQL/GCALPFGVLRKRAAPVDCLRES ADTWROEGIGCGAACAALRS*DSHKC*EGISGKVEIDPVTNQ KASTKWHIKQKPISIDSDLCAC\DLAEE ADTWROEGIGCGAACAALRS*DSHKC*EGISGKVEIDPVTNQ KASTKWHIKQKPISIDSDLCAC\DLAEE KRSNTAQRLEELBKERGWGIKCKNIQWKERNSKGSAGELSJFE KKSIKKKPPISGKSGSISSWESTGGVYVAGAGVDTITSSWDFGIR RRSNTAQRLEELBKERGWGIKCKNIQWKERNSKGSAGELSJFE KKSIKKEVPISGKSGSISSWESTGGVYVAGAGVDTITSSWDFGIR GFSTLALVEKYSSPGLTSKESLEVRINAHGFSLIQUDNTKVTM KEILLJAVKRKSSGKVISGSRAGGVFEEDSCIDVTWDMSSARVGHTOTVQDMLSSH HYKSFYGSMIHRIRPTTDVQL/GCALPFGVLRKRAAPVDCLRES GFSTLALVEKYSSPGLTSKESLEVRINAHGFSLIQUDNTKVTM KEILLJAVKRKSGKVGSSRAGOVFEEDSCIDTVQDMLSSH HYKSFYGSMIHRIRPTTDVQL/GCALPFGVLRKRAAPVDCLRES ADTWROEGIGCCGAACAALRS*DSHKC*EGISGKVEIDPVTNQ KESTKWHIKGRFTITDVQL/GCALPFGVLRKRAAPVDCLRES ADTWROEGIGCCGAACAALRS*DSHKC*EGISGKVEIDPVTNQ KESTKWHIKGRFTSTDVAGAGCHENGROGKERGWERGVPLR HYKSFYGSMIHRIRPTTDVQL/GCALPFGVLRKRGARPHNA*GS ULGSDGSVGLEDLCVPNVFLLGVLRKFGADFTSDAARN HYKSFYGSMIHRIRPTTDVQL/GCALPFGVLRKRGRAPGVPLR HYKSFYGSMIHRIRPTTDVQL/GCALPFGVLRKRGRAPGVPLR GFSTLALVEKYSSPGLTSKESLEVRINAHGFSLIDVONGSVLR HYKSFYGSMIHRIRPTTDVQL/GCALPFGVLRKRGRAPGVPLR HYKSFYGSMIHRIRPTTDVQL/GCALPFGVLRKRGRAPGVPLR HYKSFYGSMIHRIRPTTDVQL/GCALPFGVLRKRGRAPFTONGSVLR HYKSFYGSMIHRIPPTTVVLGCAALRS*DSHCORG HYKSGRAGCHARGAGAARSAFTENGRAFGTBAGAGAACAALRS*DSHCARPATATAPTACAARAGAACAARAAPAARAAPTLESGGSFYSDL SCYCNKGVNRUNDKYRLITBKINTO/SCSGSEKGHABE*QNGNSTSTALDFG PKRNEPTORROEGERFGEVHARGAGFTSAAAAFTLESGGAACAAAAAATAAFTLE				_
REILLKAVERREGSGKYSGSRADGVERSOGLAFEGURERARAPUCLERS HYKS FKUNHERLEFTDUDL, GCALPEGURERARAPUCLERS ADTWRQEQIGCCGAACAALRS*DSHKC*BGISGBKVEIDPVTNQ KASTKWHIKQRISIDSDLCAC\DLABE GF676 277 1678 GNMPTERNAFLDNETI LIAHIRGSHVISDDTGMCEMVLIDHDVD LEKHHPPSNPGDSGSEIQGSNGETGGVVAQSVDITISSDFGIGE RRSNTAQRIBEIRKERRGNICKKNIQWERSKGSAQELKSLFE KISLKEKPPISGKGSILSVRLEQCFLQLANNPFNSTSSHFGIGH GTTATKKIDVYLPLHSSODRILPMTVVTHASARVQDLIGLICKQ YTSEGREPKLNDNVSAYCLHIABDDGSVDTD*PPLDSNPIHKFT GPSTLALVEKYSSDGITSKESLFVRINANFSLJOVDHVVTM KEILLKAVKRRKGSQKVSGSRADGVPEEDSQIDIATVQDMLSSH HYKS FKVSNIRRLFFTTDVQL/GCALPFGVLRRAAPUCLRPS ADTWRCEGLGCGAACAALRS*DSHKC*SEISGBKVBIDPVTNQ KASTKWHIKQRF1SIDSDLCAC\DLABE RRSNTAQRLGGCGAACAALRS*DSHKC*SEISGBKVBIDPVTNQ KASTKWHIKQRF1SIDSDLCAC\DLABE RRSNTAQRLGELREKERGNGIKCKNIQNKRNSKGSAQELKSLFE KKSLKKEPPISGKGSILGSNBETGGVVAQSVDITISSDFGIR RRSNTAQRLERLREKERGNGIKCKNIQNKRNSKGSAQELKSLFE KKSLKKEPPISGKGSILSVRLEQCFLQLANNPFNEYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLLPMTVVMRNSKNSKGSAQELKSLFE KKSLKKERPISGKOSSILGSNBETGGVVAQSVDITJONTKVTM KEILLKAVKRRKSGSKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKS FKVSNIHRLFTTDVQL/GCALFFGVURRBAPVDCLRPS ADTWRCEGIGCGAACAALRS*DSHKC*SIGKWEIDPVTNQ KASTKWHKKNSKYSISIDSDLCAC\DLABE GFSTLALVEKYSSFGLTSKESLFVRI NAAHGFSILJONTKTVGM KEILLKAVKRRKSGSKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSNIHRLFTTDVQL/GCALFFGVURRBAPVDCLRPS ADTWRCEGIGCGGACAALRS*SDSHKC*SIGKWEIDPVTNQ KASTKWHKKNSKYSISIDSDLCAC\DLABE GFSTLALVEKYSSFGLTSKESIGFVURRBAPVDCLRPS ADTWRCEGIGCGGACAALRS*SDSHC*SIGKWEIDPVTNQ KASTKWHKKNSKYSISIDSDLCAC\DLABE GFSTLALVEKYSSFGTAGKTWSTATARSPFGTATLSSRFFRVVV KLISLIAKSQUTSISGGLANLDCCCPWYPIPGQWKTTOGRACHPCDLSSRS HHELPLVVGRADAVKHLETVOSGLASLGFVQDHTSHGPP GEKHITVHKSTSKRRIGVSKVUKONINAWFRIEDEKSGSFYSDL SYCNKEVVNKENLFNSLMYD/SCSQEEKBGHAB*ONGNS\DPH QEKHITVHKSTSRRBGTGKAVARVEREDEKSGSFYSDL SYCNKEVVNKENLFNSLMYD/SCSQEEKBGHAB*CRODQNTTLIR ELLQTLYTSICHCTURGKRRBGFGAVERTURGSGGAGTGTSA*ALD /NOVSPPQPM*GLABERGGGGGGGGGGGGGGGGGTGTSTA*LD- /NOVSPPQPM*GLABERGGGGGGGGGGGGGGGGGGGTGTSTA*LD- /NOVSPPQPM*GLABERGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		,		
HYKS FKVSNIHRLEFTTDVQL/GCALEFGVLRKRAPVDCLRES ADTWREDGIGCGARACALERS DSHKK'S EIGGBKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE 6676 277 1678 CMPPTERNAFLDNETILLAHIRQSHVISDDTGMCEMVLIDHDVD KASTKFWIKQKPISIDSDLLCAC\DLAEE KKSLKKRPJENGDSSEIQGSMGETGGVYVAGVDITSSWFDFGIR RSSHTAQRLEHLRKERGNQIKCKNIQWKERNSKQSAQELKSLFFE KKSLKKRPJESGKSILSVRLEQCPLQLURPSFYSKFDGKGHV GTATKKIDVTLPLHSSQDRLLPMVVTMASARVQDLIGLICKQ YTSEGREPKLNDNVSAYCLHABDDGSVDFPPDSSNFPDSHFDIKF GFSTLALVEKYSSPGLTSKESLFVRINAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQMLSSH HYKSFKVSNHRIREFTTDVJL/GCALEFGVLRKRAAPVDCLRES ADTWRQEQIGCCGAACAALRS*DSHKC*BGISGKVEIDPVTNQ KASTKFWIKQKFISIDSDLLCAC\DLAEE 6677 277 1678 CMPPTERMAFDDNSTIILAHTRQSFVTSDDTGMCEMVLIDHDVD LEKKHPSPSHOGSGSILGSCOSNOETGGVYAQSVDITSSWDFGIR RRSNTAQRLERLRKERQMQIKCKNIQWKERNSKQSAQELKSLFE KKSLKKSKPPISSKQSILSVRLEQCPLQLANNFRISSFFGKGHV GTTATKKIDVTUPLHSSGDRLIPMTVVTHASARVQDLIGLICKQ YTSEGREPKLNDNVSAYCLHTABDDGEVDTDFPIDENBPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAHGFSLIQVDNTKVTM KEILLKAVKRRKGSGKVSGSRADGVFEEDSQIDIATVODMLSSH HYKSFKVSHIRREFTTDVL/GCALEFGRANEAPVDCLRES ADTWRQEQIGCCGAACAALRS*DSHCK*BGISGDKVEIDPVTNQ KASTKFWIKQRPISIDSDLCAC\DLABE GFSTLAGVKYSSPGLTSKESLFVRINAHGFSLIQVDNTKVTM KEILLKAVKRRKGSGKVSGSRADGVFEEDSQIDIATVTODMLSSH HYKSFKVSHIRREFTTDVL/GCALEFGRANEAPVDCLRES ADTWRQEQIGCCGAACAALRS*DSHCK*BGISGDKVEIDPVTNQ KASTKFWIKQRPISIDSDLCAC\DLABE GFSTGSGSGSGGGGVFTCHTAVTDDLAGSRNEN*QS LLGSDGSSVGGLEDLCVFWPILHVLLGLPF*BREIFLEVVDLG FLFPLLLQGGGHCLVLPANLVSQAPQIGKLSCRLOTHDLBGSRN HPLP.FLVVGRMDAVRHLETVJGGLSLGFVQHTSHDE FLFPLLQGGGHCLVLPANLVSQAPQIGKSFGCMRNEN*QS SYCNKEVYNKENLFNSIMTD/SCSGSEREGHAR*GNNS\DPH QEKKIYVHKESTKRRIGVTJGSGLARGFTSADAGFTSADAGFTSADAGFTSADAGFTSADAGFTSADAGFTSADAGFTSATALP /NOVSPPQDM*GAEERGDQRGGKEBAGEELHRSSSCITAAPGFF EVHRNLQTTPGLLSFRAGGGG/GGAGTGGSWAPGEQPF/SLLPAS MQRSQAGLLGWEAGLUESPTHITSALRSGGTAAPGTSADAAGFTSAD				
ADTMROBOIGCCGAACAALRS*DSHKC*EGISGBXVEIDPVTNQ KASTKPHIUQKPISIDSDLLCAC\DLAC 6676 277 1678 GNMPTERNAFLDNPTIILAHTRQSHVTSDDTGMCEMVLIDHDVD LEKIHPPSMPGDSGSEIQGSWAEDTGGYVYAGSVDITSSHDFGIR RRSHTAQRLERIKRERQNQIKCKNIQWKERNSKGSAQELKSLFE KISLKEKPPISSKOSILSVRLEQCPLQLANNPPREYSKFDGKGHV GTTATKKIDVTUPLHSSGDRLLMPTVVTWASARVQDLIGLICWQ TTSEGREPKLNDNVSAYCLHLAEDDGEVDTDPPPLDSNEPIHKP GPSTLALVEKYSSPGLTSKESLFYRINAHGFSLIQUNTKVTW KEILLKAVKRKSGSKVSGSRADGVFSEDSGIDIATVQDMLSSH HYKS FKVSMIRRLEFTTDVQL/GCALFFGVURRAAPDVDCLRES ADTWREGGIGCGGAACAALRS*DSHKC*BISGKVBIDPVTNQ KASTKFWIKQKPISIDDLLCAC\DLAEB 6677 277 1678 GNWPTSRMAFLDNIJGLGCALGACALRS*DSHKC*BISGKVBIDPVTNQ KASTKFWIKQKPISIDDLLCAC\DLAEB KKSLKKRPPISGKOSILSVRLEQCPLQLAUPPREYSKFPGKGHV GTTATKKIDVTLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ YTSSGREPKLNDNVASYCLTABEDGEVDFPNEYSKFPGKGHV GTTATKKIDVTLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ YTSSGREPKLNDNVASYCLTABEDGEVDFPSUSSKPSLEVGHTSWESHFPVKS GFSTLALVEKYSSPGLTSKESLFVRIMAAHGPSLIQUNTKVTM KEILLKAVKRKSGSKVSGSRADGVFEEDSGIDIATVQDMTKVTM KEILLKAVKRKSGSKVSGSRADGVFEEDSGIDIATVQDMTKVTM KEILLKAVKRKSGSKVSGSRADGVFEEDSGIDIATVQDMTKVTM KEILLKAVKRKSGSKVSGSRADGVFEEDSGIDIATVQDMTKVTM KEILLKAVKRKSGSKVSGSRADGVFEEDSGIDIATVQDMTKVTM KEILLKAVKRKSGSKVSGSRADGVFEEDSGIDIATVQDMTKVTM KEILLKAVKRKSGSKVSGSRADGVFEEDSGIDIATVQDMTKVTM KEILLKAVKRRKGSGCWAGLGCCCCCCAVFTPGQWRKGRGNRWF1GS ADTWRGEGIGGCGGAACAALRS*DSHKC*BGISKVEIDPVTNQ KASTKFWINGKPISIDDLCCCCVWFY1FPGQWRKGRGNRWF1GS LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELFLLPVDLG FLPPLLLQGGGHCLVFANLVSGAPGIGKSCRLGFTDLGSGRA HTHELFLVVGKVBLOCCCCWWF1FPGQWRKGRGNRWF1G GFSTLAKGSGTWAGKTVVGGKRFLDESGSFGFOL GFSTANLGVTNKENLFNSLTNDYSCSGEREGGGSFTSATSATSLP ARNEDDTHCPRGERREPCVTLGERAPRELDFSTTALDSRRFNVV RLLELIAKSGLTSLSGIAGNFFMNLIEKVVLKVLEDQQNITLIR ELLQTLYTSSLCTLVKRVGKSVLVONINMVVRMSTLHERQQLN NIGITRVSGQAQPPPGSGSLHRDTGGTRGOFFFTPVTERSGLF P\RKNREDTHCPRGERRERGMFANLFSSGLTAAPGFFP EVHRNLQTTFPGLPSRGGGG/GGGAGGGEGAGGELHRSSGLTSA*ALD /NQVSPPQPM*GAEENGROPGGRGKEAGEELHRSSGLTAAPGFPY FLYRKTGTGFGGGGGGGGGRGRATGARFAPTTCS STYNKETTGFGGGGGGGGGGGRGRATGARFAPTTCS STYNKETTGFGGGGGGGGGGGGGGGGFTSADAGGTFADAGGTFADAGGTFADAGGTFADAGGTFADAG				
RASTKWHIKOKPISIDSDLLCAC\DLAEE				
1678 INMPTERMAPLONPTI LLAHIRGSHYTSDDTGMCERWILDHOVD LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR RRSNTAQRIBERIRKERQNQIKCKNIQWKERNSKQSAQELKSLIPE KKSIKEKPPISKQSILSVRLEQCPLQLINNPFHEYSKPTOKGKN GTTATKKIDVTJPHISSQDRLLBWTVJTMSARVQOLIGLICWQ	ļ			
LEKTHPPSMEGDSGETQGYVYAGSVDITGSMDFGIR RRSNTAQRIERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE KKSLKEKPPISGKOSILSVRLEQCPLQLINNPFWEYSKFDGKGHV GTTATKKIDVTLPLHSSQDRLLLPMTVVTMASARVQDLIGLICWQ YTSEGREPKINDNVSAVCLHIABDGOTPFPPLDSNEPIKKF GFSTLALVEKYSSPGLTSKBSLEVRINAAHGFSLLQVDNTKVTM KEILLKAVKRKSGKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/GCALFFGVLRKRAAPVDCLRPS ADTWRQEQIGCGGACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEB 6677 277 1678 GNWPTERMAFLDNPTILLAHTGSHVTSDDTGMCEWLLDHVDG LEKIHPPSMPGDGSEIQGSNGETGGYVYAQSVDLTSSWDFGIR RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFF KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFWEYSKFPGKKHV GTTATKKIDVTLPLHSSQDELLJPWTVIMASARVQDLIGLICWQ YTSEGREPKINDNVSAVCLHIABDDGEVDTDFPPLDSNRPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRRGSGKVSGSRADGVFEBDSQIDIATVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/GCALFFGVLRRAAPVDCLRPS ADTWRQEGJGCGGACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEB 6678 221 865 GPSNQSSGSLSIVVLEQCPLQKNNPFREDSQIDIATVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/GCALFFGVLRRAAPVDCLRPS ADTWRQEGJGCGGACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEB 6679 2 786 LEFARGAMPFLGGGNSCHEDSQIGKLSCRIQFHDLBGSRN HHPLFLVVQRWDDAVKHLETVQSGLASLGFVQGHTSHGPP QEKMITVHKGSTKRRHCYCTLGBAFNRLDFSTAILDSRRFMTVV RLLELIAKSQITSLSGIAQANFMTLESCELFLLEVVUG RLLELIAKSQITSLSGIAQANFMTLSGERBEHAE*ONDNS\DFH QEKMITVHKGSTKRRHCYCTLGBAFNRLDFSTAILDSRRFMTVV RLLELIAKSQITSLSGIAQANFMTLEAJFGFGTWQTPVGSISEE P\RKNEVNKENLFNSLNTD/SCSGERBEHAE*ONDNS\DFH QEKMITVHGSTKRRHCYCTLGBAFNRLDFSTAILDSRRFMTVV RLLELIAKSQITSLSGIAQANFMTLEAJFGFGGTWQTPVGSISEE P\RKNEPDTHCFRGEARPEV*H.PKHSPSGEGAEIQTSA*ALP P\RVNSPDPHCGAEGRGCP/GGGCTGGSWAGGRDFTSTA*ALP P\RVNSPDPHCGAEGRGP/GGGCTGGSWAGGRDFTSTAFSTCS GGP\PAPPCDPTCLRFGGGSSGGHCTGSWAAGGFTSATAAGTAPPFC PVHRNDCTPFFGGGSSGGGP/GGGCTGGSWAGGRPFTCTLAPGPF PVHTBEGGGGSGGGGPGGGGTGGAGTGAFAAGAQD PQSGGRPTQGTVGTEVILLSGLGSAKACPAARFSPFLEBSPGTTCS GFP\PAPPCGTLGRENGGPRGGREGGFTSATAAGFPFTCS GGP\PAPPCGTLRFGGGGSPGGGPGGGTGTGARAACPAARFAPP*LESDPAS TIFKKGTRGFGGGGPGCGGPGGGPTGGTAAAACGFTSATAAGFPFGW *LAPPLSQPPGATEPQVRACGWAPPSPGTTSATGAAACGFTSATAGATAPPGV *LAPPL	<u></u>			<u> </u>
RRSNTAGRLERLRKERONQIKCKNIQWKERNISKQSAQELKSLIPE KKSLKEKPPISGRQSILSVRLEQCPLQLINDFPNEYSKFDGKGHV GTTATKKIDVTJPLHSSQRLLBWTVVTMASARVQLIGLICWQ YTTSEGREPKLNINNVSAYCLHLABDOGEVDTDFPLDSNEPTLKKF GFSTLALVKKYSSPGLTSKRSLFVRINAAHGFSLIQVDMTKVTM KEILLKAVKRKGSGKVSGSRADGVPEEDSQIDIATVQDMLSSH HYKSFKVSWHIRLRRTTDVQL/GCALFORLRKAAPDDCLRPS ADTWRQEQIGCGAACAALRS+DSHKC*EGISGDXVEIDFVTNQ KASTKFWINQKFISIDSDLLCAC\DLABE GNWPTERMAFIDNPTI ILAHIRGSHVTSDDTGMCEMVLIDHDVD LEKHPPSMPGDSGSEIQGSNGETGGYVYAQSVDITSSMDFGIR RRSNTAQRIERLRKERONQIKCKNIDGMKSKSQSAQELKSLIPE KKSLKEKPPISGRQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV GTTATKKIDVTJPLHSSQDRLLBMTVVTMASARVQDLIGLICW YTSSGREPKLNNNVSAVCHIAEDDGEVJTDFPLDSNEPTHKF GFSTLALVEKYSSPCLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSGKVGSSRADGVESSTGGIDGNCHTSVDLOWDLMSSH HYKSFKVSMIHRLRFTTDVQL/GCALFGCVLRKRAAPVDCLRPS ADTWRQEQIGCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWINGKPISIDSDLLCAC\DLABE 6678 221 865 GPSNQSSGSLSILVTGCSSYWS*INDTCTILKYLSNFGRQ*LR FPFCSQLPMSQGCWHDLCCCPMVPIPTPQQWRKGRQRMKN*QS LLGSDQSSVGLEDLCVFVNFLLHVLLGLFPP PHELFLLFVUDLG FLPFLLLQGGCHCLVJPANLVSQAPD YFPQQWRKGRQRMKN*QS LLGSDQSSVGLEDLCVFVNFLLHVLLGLFPP PHELFLLFVUDLG FLPFLLLQGGCHCLVJPANLVSQAPD YFPQQWRKGRQRMKN*QS LLGSDQSSVGLEDLCVFVNFLLHVLLGLFPP PHELFLLFVUDLG FLPFLLLQGGCHCLVJPANLVSQAPD GHKGRCFLQCHDDBGSN HHPLFLVVGRUDAVMLETVQGGLASLGFVGQNTSHGPP 6679 2 786 LEFARGAMPFLGQDWRSPGGNWKVTDGWKFRDERGRY*LR SYCKKEVNKENLFNSLND/SCSGERHAE*ONNS\DFH QBKMITVHKGSTKRRHGYCTLGBAPNRLDFSTAILDSRFRFNYV RLLBLILAKSQLTSLSGJARQNFNNILDFSTAILDSRFRFNYV RLLBLILAKSQLTSLSGJARQNFNNILDFSTAILDSRFRFNYV RLLBLILAKSQLTSLSGJARQNFNNILDFSTAILDSRFRFNYV RLLBLILAKSQLTSLSGJARQNFNNILDFSTAILDSRFRFNYV RLLBLILAKSQLTSLSGJARQNFNNILDFSTAILDSRRFNYV P\NVSYPPQDPM*CABERBODQSGKERGEHAE*ONNTAGEPFSTTC SYCKKGYVKKENLFNSTQTTGGFRFRYTVESGLF V\NVSYPPQDPM*CABERBODQSGKERGEHAE*SSGCHAAPPAP*LPSDFAS GROPPQDFM*CABERBODQSGKERGEHRSSSGCHAPPAP*LPSDFAS GROPPQTGLRFGGGSSGGCHG*SGSGGGFSGRGFTYTHSDFLARAPFP*LFSDFAS TIFKKTTGFGGGGPGVJCAGENRSKOGGFTSGABAPAP*LPSDFAS TIFKKTGFGGGGPGVJCAGENRSKOGGFTSGABAPAP*LPSDFAS TIFKKTGFGGGGPGVGGRSSGGCGFTTTHSDFLGRAPFSTC *LPAPLSQPPGATERGGSGSGGCGFTTTHS	6676	277	1678	
KKSLKEKP I SGKOS I LSVIRLEQCYLQLIANPPNEYSKFOGKGHV GTTATKKIDVYLPLHSSQDRILPMTVVTMASARVQDLIGLICWQ YTSEGREPKLINDNVSAYCLHLABDDGSVDTOF P PLDSNE P I HKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGSLIQVDNTKVTM KEILLKAVRRKSKGKVSGSRADGVP EEBGSDID IA TVQDMLSSH HYKS FKVSMHHRLRFTTDVQL/GCALFPGVLRRAAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*BGISGDKVEID PVTNQ KASTKFWIKQKPI SIDSDLLCAC\DLABB 6677 277 1678 GNMPTERMAPLDNPTI I LAHTRQSHVTSDDTGMCEMVLIDDVD LEX HMPSMPGDSGSEI QGSNGET QVYAQSVDITSSWDFGIR RRSNTAQRLERLRKERQNQIKCKHIQWKERNSKQSAQELKSLIPE KKSLKXKPPISKQSILSVRLEQCPLQLINNPFNEYSKFDGKGHV GTTATKKIDVYLPLHISSQDRLLPMTVVTMASARVQDLIGLICWQ YTSEGREPKLNDNVSAYCLHTAEDDGSVDTDFPPLDSNEP JHKF GFSTLALVEKYSSPGJITSKESLFYNINAAHGFSLIQVDNTKYTM KEILLKAVKRRKGSQKVSGSRADGVFEEDGSID IAAVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*BGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLABE GFSNGSGSLSLIVTGCSSYWS*STNDTCTILRVLSSNFGRQ*LR HPLFLUQGGCHCLVLPANLVSQAPQIGKLSCRLOFTHDLESSRN HHPLFLUVGGWBDAVKHLBTVQSGLASLGFVGQHTSHGPP CSGRAMPPLGGDWFSPGQNWVFDUKRFDLBSKSGFVSDL SSYCNKEVYNKENLFNSLNYD/SCSQEEKBGHAE*QNQNS\DPH QEKNIYVHKGSTKERRGYCTLGEAFNBLDFSTAILDSRFNYVV RLBLIAKSQLTSLGAIQKNFMILEKVVLKVLEDQQNITLIR ELLQTLYTSICTIVKRVGKSVLVGNINMWYKNETILBRQDLN NIQITRVSGQAQPPBGGSGLRICTGDOFFTATILDSRFNYVV RLBLIAKSQLTSLGAIQKNFMILEKVVLKVLEDQQNITLIR ELLQTLYTSGCTAGFPOGSGSLFGTYORDFFFTYTEBSGLF P\RKNEPDTHCPRGSARPEV*HLEKPRHSFGSGABIGTSA*ALP NQVSYPDQM*GAGERGORDGRGGRERGEBEHRSSSGLTATAFGFP EVHENLQTFPGLPSRGGGP/GGAGTQGSWAPGRQPF/SPLLPAS MQRSQAGLPGWEAGLIVESPTHHIPALRSGTNATGEAPPSTTCS SGP\PAPPGPTCLRPGGSSSGGGF*PGGTWGTPVGSISEE P\RKNEPDTHCPRGBARSGCSSGSGGF*PGTWGTPVGSISEE P\RKNEPDTHCPRGBARSGCSSGSGGF*PGTWGTPVGSISEE FYRKNEPDTHCPRGBARSGCSSGRGGF*PGFTATATGEAPPSTTCS SGP\PAPPGPTCLRPGGGSSSGGGF*PGTYTHSPLGHGRAPCPPF*LDSA MQCPPGAGCWGSQPRGSGCRCPTYTYHSPLGHGRAPCPPRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRFGIRAPGPROP *LPAPLSQPPGAGCWGSQPRGSGCRCPTTYTHSPLGHGRAPCPPRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRFGIRAPGRAPCPPRCWH*				
GTTATKKIDVIJVIPLHISODRILIPMTVUTMSARAVQDLIGLICWQ YTSEGREPKLNDNVSAYCLHLABDDGEVOTDFPPLDNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINARAGFSLIQVDNTKVTM KEILLKAVKRKGSQKVSGSRAGVFEEDSQIDIATVQDMLSSH HYSFFKVSMTHJERFTTDVQL/GEPGVLRFGARAPDVCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*BGISGDKVEIDFVTNQ KASTKFWIKQKPISIDSDLLCAC\DLABB GMPTTERMFLDNPTILBATHGSHVTSDDTGMCEMVLIDHDVD LEKHPPSMPGDSGSEIGSSNGETQGYVYAQSVDITSSWDFGIR RRSNTAQRLERLKERQNQIKCKNIQWKRNSKQSAQELKSLFE KKSLKEKPPISKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV GTTATKKIDVYLPLHSSQDRILIPMTVUTMSARVQDLIGLICWQ YTSEGREPKLNDNVSAYCLHLABDGEVTDFPPLDSNEPTHKFF GFSTLALVEKYSSPGLTSKESLFVRINARAGFSLIQVDNTKVTM KEILLKAVKRRKGSGKVSGSRADEVTEDSQUIDATVQDMLSSH HYKSFKVSMHHLRFTTDVQL/GCALFFGVLRKRAAPVDCLRPS ADTWROEQIGCGSAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFHIKQKPISIDSDLLCAC\DLABE 6678 221 865 GPSNQSSGSLSIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR LIGSDGSVGLEBLCVFVNFILHLDLFP*PHELFLLPVVDLG FLPPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLOTHDLEGSRN HHPLFLVVGRMDAVKHLETVQSGLASLGFVQGHTSHGPP 6679 2 786 LEFARGAMFFLGQDWRSFGQMWKVTVDGWKRFIDEKSGSFVSDL SSYCNKSVYNKENLFNSLNYD/SCSQEEKERLB*CNQNSN DFH QEKNIYVHKGSTKERRGYCTLGBAPNELDFSTALLDSRRFHYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTTSLCTLVKRVCKSV/LVCNINMWYKNETILHENQQLN NIQITRVGQQAPPGSGSLHRIDPSTALLDSRRFHYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQN ITLIR ELLQTLYTTSLCTLVKRVCKSV/LVCNINMWYKNETILHENQQLN NIQITRVGQQAPPGSSSLHRDPSTSGSGBAPPTTEBSGLF P\RKNEPDTHCPRGERRPEV*HLPKPPSGSEGRAECHTASSSSCLTAABGFP EVHRNLQTFPGLPSRGGGP/GGACTQGSWAPGRQPF/SPLLPAS MQNSQAGLDGWABGLVESPTHTHISHPSGSGEAGEIQTSA*ALP /NQVSPPQDM*GAERNGDQRGKERAGEELHRSSSSCLTAABGFP EVHRNLQTFPGLPSRGGGP/GGACTQGSWAPGRQPP/SPLLPAS MQNSQAGLDGWABGLVESPTHTHISHPSGTMATGARPFSTTCS SGP\PAPPGPTGLRPGGSSSGGG**PGLFVGKV\GALGAAQD PQSGGRGPTQGTVGTEMLLSGLGSJKACPAARRAPY*LPSDPAS MQNSQAGLDGWABGLVESPTHTHISHPSGTMATGARPFSTTCS SGP\PAPPGPTGLRPGGGSSGGGC**PTYTHSPLGHGRAPCPRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRFGIRGRAPCPRCCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRFGIRACRPRCCWH*				
TYSEGREPKINDNYSAYCLHIAEDDGEVDTDFPLDSNEPTHKF GFSTLALVEKYSSPGLITSKSLFYRINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEDSQIDIATVQDMLSSH HYKSFKVSMHHRIRFTTDVQL/GCALFPGVLRRAAPVDCLRPS ADTWRQEQIGCCGAACALRS+DGSHKC*EGISGDKVEIDFVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEB 6677 277 1678 GNWFTERMAFLDNPTIILAHTRQSHVTSDDTGMCEMVLIDHDVD LEXIHPPSMFGDDSSEIGCSNSETGGVYVAQSVDITSSWDFGIR RRSHTAQRLERLRKERQNQIKCKHIQWKERENSKQSAQELKSLFE KKSLKSKPDISKGSGLISVRIEGCLOLUNDFPMEYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ YTSEGREPKLNDNVSAYCLHTAEDDGEVDTDFPPLDSNEPTHKF GFSTLALVEKYSSPGITSKESLFYNINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEDSQIDIATVQDMLSSH HYKSFKYSMIHRIRFTTDVQL/GCALFPGVLRRAAPVDCLRPS ADTWRQEQIGCGSACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEB GPSNQSSGSLSILVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR FPPCSQLPMSQGCLHRLDCCCPWVPY LPGQURKGRQNNRR*QS LLGSDQESVGLEDLCVFVNFLLHVLLGLFF*PHELFLLFVVDLG FLFPLLLQGGCICLVLPANLVSQSPQIKSGCRQNNRR*QS HHPLFLVVGRWDAVKHLETVQSGLASLGFVGGHTSHGPP FPPLLLQGGCHCVLPANLVSQAPQIGKLSCRLGTHDLBGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGGHTSHGPP CSSYCNKSVNNKENLFNSLNVJ/SCSQEEKGHAB*QNONS\DPH QEKMIYVHKGSTKERHGYCTLGBAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFFMILEKVVLKVLEDQQNITLIR ELLQTLYTSGCTAPPPGPGGSGLHRIDDFSTAILDSRRFNYVV RLLELIAKSGLTSLSGIAQKNFFMILEKVVLKVLEDQQNITLIR ELLQTLYTSGCTAPPPGPGGSGLHRINDFSTAILDSRRFNYVV RLLELIAKSGLTSLSGIAQKNFFMILEKVVLKVLEDQQNITLIR ELLQTLYTSGCTAPPGPGPGGSGLHGNSGCELHRSSGSABIGTSA*ALP /NQVSPPQPM*GAERGROPGGGSESGGELHRSSCTAAPGFPF EVHRNLQTFPGLPSRGGGPGGAGTQGSWAPGGPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAPPSTTCS SGP\PAPPGFTCLRPGGSSSSGGG*PTGTWGTEMLLSGLGSAKAPPAARPAV*LPESPAS TIFKKGTRGFGSBFGVGGGSSSGGGF*PGGVAGGFTSDAAGTAPPGTV LPAPLSQPPGGTGGRGGGSSGGGG*PGGVAGGATAGGARPSTV*LPSPAS TIFKKGTGGFGSPGVLGSRNRWVGRAQGFTSDAAGTAPPGV* LPAPLSQPPGGTGGRGGGGGGGGGAGGAGARPAPP*LPSPASPAG *LPAPLSQPPGGTGGRGGGGGGGGGAGGAGARPAPP*LPSPASPAG *LPAPLSQPPGGTGGRGGGGGGGGGCGGGAGGAGGAGGARPGTCTGAAVGFIG *LPAPLSQPPGGTGGGGGGGGGGGGGGGGAGGAGGAGGAGGAGGAGGAGG				
GPSTLALVEXYSSPGLTSKESLEVERINAAHGPSLIQUDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVPEEDSQIDIATVQDMLSSH HYKSFKVSMHRRRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRQSQIGCCGAACAALRS*DSHKK*BGISGDKVEIDPVTNQ KASTKFMIKKRPT91BDDLLCAC\DLAEB 6677 277 1678 GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD LEKTHPPSMPGDSGSSIQGSNGETGGYVYAQSVDITTSSWDFGIR RSNTAQRLERLKKERQNQIKKCKNIQWKERNSKQSAQELKSLIFE KKSLKEKPPTSGKQSILSVRLEQCPLQLAINPPNEYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLLEMTVVTMASARVQDLIGLICWQ YTSSGRPBKLIDNWSAYCLHIABDDCEUDTDFPPLDSNEP1HKF GFSTLALVEKYSSPGLTSKESLEVERINAAHGFSLIQVDNTKVTM KEILLKAVKRKSGQKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKAAPVDCLRPS ADTWRQSQIGCCGAACAALRS*DSHKC*BGISGDKVELDPVTNQ KASTKFMIKKRPISIDBLLCAC\DLAEB 6678 221 865 GPSNQSSGSLSLTVTGCSSYWS*INDTCTILEVLSSNBGRQ*LR FPFCSQLPMSQGCLWHLDCCCPWVPILHVLLGLFP*PHELFLLPVVDLG FLPFLLLQGGCHCLVLPANTLVSQAPQIGKLSCRLQTHDLBGSRN HPLPLVVGRWDAVKHLETVQSCAPQIGKLSCRLQTHDLBGSRN HPLPLVVGRWDAVKHLETVQSCAPQIGKLSCRLQTHDLBGSRN HPLPLVVGRWDAVKHLETVQSCAPQIGKLSCRLQTHDLBGSRN HPLPLVVGRWDAVKHLETVQSCAPQIGKLSCRLQTHDLBGSRN HPLPLVVGRWDAVKHLETVGSCAPGERSECHAB*QNDNS\DFH QEKMIYVHKSTKERRGYCTLGFAPMLDFSTALDSRRRMYV RLLELIAXSQLTSLSGIAQKNFMNILEXVULKVLEDQQN ITLIR ELLQTTLYTSCCTLVRVGRSVLVGNINMWVYRMETILHWQQQLN NIQ1TRVSGQAQPPPGSGSLHADTGQTRQDFFFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSGSAPGCQPP;PLPAS MQRSQACLPGWERGLUSSPHHLDTQGTRQDFFFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSGSAPGCQPP;PLPAS MQRSQACLPGWERGLUSSPHHIPALRPSGTNATGEAPFSTTCS GGP\PAPPGPTGLTVGTEMLLSGLSSKAGCGARAPGAPPY*PLPSDPAS MQRSQACLPGWERGLUSSPHHIPALRPSGTNATGEAPFSTTCS GGP\PAPPGPTGLTVGTTEMLLSGLSSKAGCARAPRAPPY*PLPSDPAS TIPKKGTRGFGGEGFGGJUGRSKNRVVGRAGGFTSADAAGTAPPGF EVHRNLQTTFGLBSGRGGGGGGGGGGATGSRAPGCPPP;TLPSDPAS TIPKKGTRGFGGEGFGGGGULGSFRNNVVGRAGGFTSADAAGTAPPGF *LPAPLSQPPGATGCUPGTTGTTMLSGLGSAKACCAPARAPAPP*HPSPDFAS TIPKKGTRGFGGFGGFGGGGGGGGGGRGATGGRAPCPCRRCWH* WQDPPSSPRTGCLPGTTPARQAYSAPRTRSRGIRTGRAAVFIF				
KEILLKAVKRRKGSQKVSGSRADGVPEEDSQIDIATVQDMLSSH HYKSFKVSMHRIRFTTDVQL/GCALFPULRKRAPVDCLRPS ADTWRQSQIGCGAACAALRS PSSHKC*BGISGDXVBIDPVTNQ KASTKFHIKQKP191D3DLLCAC\DLABE 6677 277 1678 GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD LEKKHPPSMPGDSGSSIQGSNGETGGYVYAQSVDITSSWDFGIR RRSMTAGRLERLKKERQNQIKCKNIQWKKRNSKQSAQBLKSLFE KKSLKEKPP1SGKQSILSVRLEQCPJQLNNPPNEYSKPDGKGHV YTSEGREPKLNDMVSAYCLHIABDDGEVDTDFPPLDESBPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSMHHRLRFTTDVQL/GCALFPGVLKRRAPVDCLRPS ADTWRQSQIGGCGAACAALRS*SPSHKC*BGISGDKVEIDPVTNQ KASTKFHIKQKP151D3DLLCAC\DLABE 6678 221 865 GPSNQSSGSLSLIVTGCSSYMS*INDTCTILRVLSSNFGRQ*LR FFPCSQLPMSQGCLWHLDCCCWVPY1PQQWRKGRQRMRN*QS LLGSDQSSVGLEDLCVPVWFLLHVLLGLPP*PHELPFLLPVVDLG FLPPLLLQGGHCLVIPANLVSQAPQ1GKLSCRLQTHDLEGSRN HHPLFLVVGRMDAVKHLETVQSGLASLGFVGQHTSHGGP 6679 2 786 LEFARGAMPFIGQDWRSPGGNWKTYDGKKRFLDEKSGFYSDL SSYCKNEVYNKENLFNSLNYD/SCSQEEKEGHAS*ONNONS\DFH QEKWIYVHKGSTKERRGYCTLGEARNRLDFSTAILDSRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEXVLKVLEDQQNITLIR ELLQTLYTSLCTLYKRVKGKSVLVKVLKVLEDQQNITLIR LELLTLYTSLCTLYKRVKGKSVLVKVLKVLEDQQNITLIR ELLGTLYTSLCTLYKRVKGKSVLVKVLKVLEDQQNITLIR DYNTHEMPTHCPRICRFGARPEV*H.PKPHSPGSSGABIOTSA*ALP /NQVSPPQPM*GAEENGDQRGKERAGBELHRSSSCLTAAPGFP EVHENIQTTFFGLPSRGGGP/GGAGTQSWAPGGFPFSTESGESGF GGP\PNTREDTHCTRGREARPEV*H.PKPHSPGSSGABIOTSA*ALP /NQVSPPQPM*GAEENGDQRGKERAGBELHRSSSCLTAAPGFP EVHENIQTTFFGLPSRGGGP/GGAGTQSWAPGCEPP,SPLPAS MORSQAGLPGWEAGLUSESTHHIPALRPSGTNATGEAPPSTTCS GGP\PAPPGFTGLRPGGGSSSGGHC**POLFVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGGGPGVLQERNRNVVGRAQGFTSADAAGTAP PGV *LPAPLSQPPGATGCMPRQCCHAPPS PFTGSRLVANGRHPGPQV AQCCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGITPARQASAPRTRSRGIRTGRANGFIR WQDPPSSPRTGCLPGITPARQASAPRTRSRGIRTGRANGFIR WQDPPSSPRTGCLPGITPARQASAPRTRSRGIRTGRANGFIR				la contraction of the contractio
HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRGSQIGCCGAACAALRS*DSHKC*FGISGDKVEIDPVTNQ KASTKFMIKQRFISIDSDLLCAC\DLAEB 6677 277 1678 GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD LEKTHPPSMRGDSGSSIGGSNGETGGYVYAGSVDITSSWPFGIR RSSMTAQRLERLKRERQNGIKCKNIQWKERNSKQSAQELKSLFFE KKSLKEREPTISGKQSILSVRLEQCPLQLANNPPNEYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLLEMTVVTMASARVQDLIGLICWQ YTSEGREPKLNDWSAYCLHIABDDGEVDTDFPPLDSNEPTHKF GFSTLALVEKYSSPGLTSKESLEVRINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSGKVSGSRADGVFEDSQIDIATVQDMLSSH HYKSFKVSMHRRRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRGSGIGCGSAACAALRS*DSHKC*BGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEB 6678 221 865 GPSNQSSGSLSLTVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR PPPCSQLPMSQGCLMHLDCCCPWVPYIPGQWRKGRQRMRN*QS LLGSDQESVGLEDLCVFVNFLHVLIGLFP*PHELFPLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSGRLQTHDLBGSGRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 6679 2 786 LEFARGAMPFIGQDWRSFGQNWKVTVDGWKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLMYD/SCSQEEKEGHAB*QNONS\DFH QEKMIYVHKGSTKERRGYCTLGFAYNRLDFSTALLDSRRMYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELQTLYTSLCTLVKRVGKSVLVGNINMVVKMETILHWQQQLN NIQITRYSGQAQPPPGSGSLHRDTGGTRQPFFFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSTGAEIQTSA*ALP /NQVSPPQPM*GAERNEKQWPLA/FGPGTWQTPVGSISEE P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSTGAEIQTSA*ALP /NQVSPPQPM*GAERNEKQWPLA/FGPGTWQTPVGSISEE EVHRNLQTFPGLPSRGGSSGGHG**PGLPGKVVQGWKQGAPPSPLLPAS MQRSQACLPGWEAGLVESTHHIPALRPSGTNATGEAPPSTTCS SGP\PAPPGTGLRPGGGSSSGGHG**PGLPGKVVQGWCAGAGLAQAQD PQSQGRGPTQGTVGTEMLLSGLSGAKACPAARPAVP*LPSDPAS TIPKKGTRGFGGPGVJCSRNMVVGRAQGFTSADAAGTAP FGV *LPAPLSQPPGATEGDAYACGMAPPS PGTSGRLVAMGRHPGPQV AQCCPPGAGCWGSQPRGSQRCPRTYHSPLEGIRFGRAPCPRRCWH* WQDPPSSPRTGCLPGITPARQAYSAPRTRSRGIRTGRAAYGFIR				
ADTWRQEQIGCCGAACAALRS+DSHK+SEGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLABE 6677 277 1678 GNWPTERMAPLDNPTITIAHTRQSHVTSDDTGMCEMULIDHDUD LEKLHPPSMPGDSGSEIGGSMGETGGYVYAQSVDITSSWDFGIR RRSNTAQRLERLRKERQNQIKKKNIQWKRNSKQSAQELKSLFE KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNSYSKPDGKGHV GTTATKKIDVVLPLHSSQDRLLPMTVUTMASARVQDLIGLICWQ YTSEGREPKLNDNVSAYCLHIABDGSEVDTDFPPLDSNEPIHKF GFSTLALVEKYSSFGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRKSGSKVSGSRADGVFEDSGIDIATVQDMLSSH HYKSFKVSMIHRLRFTTDVDL/GCALFPGVLRKRAAPVGCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLABE 6678 221 865 GPSNQSSGSLSIVTGCGSYMS*INDTCTILRVLSSNFGRQ*LR PFPCSQLPMSQGCLWHLDCCCPWVPYIPGQQWRKGRQRMRN*QS LLGSDQSSVGLEDLCVPVNFLLHVLLGLFP*PHBLFLLPVVUGL FLFPLLLQSGGCHCLVLPANFLVOAQAPQIGKLSCRLQTHDLBGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 2 786 LEFARGAMPFLGQDWRSPGQNWWKTVDGWKFFLDEKSGSFVSDL SSYCNKBVYNKBUNKNLFNSLNTVJ/SCSQEKEKBHAR*QNNS\DFH QEKWIYVHKGSTKRRHGYCTLGEAFNRLDFSTALLDSRRNYVV RLLELIAKSQITSLSGIAQKNFFNNILEKVVLKVLDQQNITLIR ELLGTLTTSLCTLVKRVGKSVLVONINMWYSRMSTILHWQQQLN NIQITRVSGQAQPPPGGSSLHRDTGQTRQDFEFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSGGAEIGTSA*ALP /NQVSPPQPM*GAEENGDQRGGKERAGELHRSSSGLTAAPGFP EVHRNLQTFFGLPSRGGBP/GGACTQGSWAPGEQPP/SPLLPAS MQRSQACLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS GPP\PAPPGFTGLPFRGGBSSGGGG**PGLEGAPPSTTCSSADAAGTAPFBTC GGPP\PAPPGFTGLPFRGGBSSGGGG**PGLFGRAPCAFPAPV*LPSDPAS TIPKKGTRGFGGFGGVLQERNRWVVGRAQGFTSADAAGTAPFGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHGPGPV AQCPPGAGCWGSQPRGSQRCQRCTYGTTTHBALRRSTRANAGRHPGPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPGV AQCPPGAGCWGSQPRGSQRCQRCTYTTTHSPLGHGRAPCAFRCWH* WQDPFSSPRTGCLPGTLARQAYSAFRTRSRGGITTGRAAYGFIR				
KASTKFWIKQRPISIDSDLLCAC\DLAEB 6677 277 1678 GNWFTERNAFLDNFTILJAHTRQSHVTSDDTGMCEMVLIDHDVD LEKHPPSMPGDSGSETQGSVYAQSVDITSSWDFGIR RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE KKSLKEKPPISGKQSILSVRLEQCPLQLNNFFNBYSKPDGKGHV YTSEGREPKLNDNVSAYCLHIABDDGEVDTDFPPLDSNEPIHKF GFSTLALVEKYSSFGLTSKESLFVRINAHGFSLIQVDNTKVTM KEILLKAVKRKRGSQKVSGSRADGVFEDBGJDLATVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRGSQIGCCGAACAALRS*DSHKK*EGIGKOSIDIDATVQDMLSSH HYKSFKFVKMFISIDSDLCAC\DLAEB 6678 221 865 GPSNQSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR FPFCSQLPMSQGCLMHLDCCCPWVFY IPGQQWRKGRQRMRN*QS LLGSDQSSVGLEDLCVFVNFILHVLLGLFFP PHELFLLFVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HHPLFLVVGRMDAVKHLETVQSGLASLFVGQHTSHGPP SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNQNS\DPH QEKMIYVHKGSTKSRGYCTLGEAFNRLDFSTAILDSRRINYUV RLLELIAKSQLTSLSGLAGKVFULSVLKVLEDQON ITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF P\CKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKERAGELHRSSSGLTAAPGFF EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGQPPPTTCS SGP\PAPPGFTGLPFGGGSSSGGGH**GGGTGGSRAPGPPFTTTCS SGP\PAPPGFTGLPFGGGSSSGGH**FGLGVGKVQALGAAQD PQSQGRGFTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TTPKKGTRGFGGGGGVLGGRNRWVGGRAQGFTSADAAGTAPFGV *LPAPLSQPPGATEPQVRACGMAPPSPTSGRLVANGRHFGPGV *LPAPLSQPPGATEPQVRACGMAPPSPTSGRLVANGRHFGPGV *LPAPLSQPPGATEPQVRACGMAPPSPTSGRLVANGRHFGPGV *LPAPLSQPPGATEPQVRACGMAPPSPTSGRLVANGRHFGPGV *LPAPLSQPPGATEPQVRACGMAPPSPTSGRLVANGRHFGPGV *LPAPLSQPPGAGTGGSQRCGRACGASAAPATP*LPSDPAS TTPKKGTRGFGGGGSQCPGGSQRCGRACGASAAPATP*LPSDPAS TTPKKGTRGFGGGGSQCPGGSQRCGRACGASAAPATP*LPSDPAS *LPAPLSQPPGATEPQVRACGMAPPSPTTSGRLVANGRHFGPGV *LPAPLSQPPGATEPQVRACGMAPPSPTSGRLVANGRHFGPGV *LPAPLSQPPGATEPQVRACGMAPPSPTTSBGRLVANGRHFGPGV *LPAPLSQPPGATEPQVRACGMAPPSPTTSBGRLVANGRHFGPGV *LPAPLSQPPGATEPQVRACGMAPPSPTTSBGRLVANGRHFGFGFU *LPAPLSQPPGATEPQVRACGMAPPSPTTSBGRLVANGRHFGFGFU *LPAPLSQPPGATEPQVRACGMAPPSPTTSBGRLVANGRHFGFGFU *LPAPLSQPPGATEPQVRACGMAPPSPTTSBFGRLVANGRHFGFGFU *LPAPLSQPPGATEPQVRACGMAPPSPTTSBFGRLVANGRHFGFGFU *LPAPLSQPPGATEPQVRACGMAPPSPTTSBFGRANAVG				
6677 277 1678 GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD LEXTHPPSMPGDSGEIQGSNGETYGYVYAQSVDITSSWPFGIR RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFFE KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV GTTATKKLDVYLPLHSSQDRLLPMTVVTMASARVQOLIGLICWQ YTSEGREPKLNDNVSAYCHLIABDDGEVDTDFPPLOSNPEPHKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSGKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRQEGIGCGGAACAALRS*DSHKC*EGISGDKVBIDPVTNQ KASTKFWIKQRPISIDSDLLCAC\DLABE 6678 221 865 GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR PFPCSQLPMSQGCLWHLDCCCPWYPIPGQQWRKGRQRMRN*QS LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELFLLPVVDLG FLPPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLBGSRN HHPLFLVVGRNDAVHALETVQSGLASLGFVGQHTSHGPP 6679 2 786 LEFARGAMPFLGQDWRS PGQNWKTVDGWKRFLDEKSGS FVSDL SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAB*QNQNS\DFH QEKWIYVHKGSTKERHGYCTLGGAPMLDPSTAILDSRRNYVVY RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNIMMWYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSSGAEIGTSA*ALP NQUSPPQPM*GAEENGDQRGKEBAGEELHRSSSCLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGAGTGGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGGSSSSGGH**PCLVKVQKQLGAAQD PQSGGRGFTDGTVGTGTGTGRAAPGFPSTTCS SGP\PAPPGPTGLRPGGGSSSGGGH**PCLPVKVQGLGAAQD PQSGGRGFTDGTVGTGTGTGRAAPGFPSTTCS SGP\PAPPGPTGLRPGGGSSSSGGH**PCLPVKVQGLGAAQD PQSGGRGFTDGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT				
LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR RRSNTAQRLERIRKERQNQIKCKNIOWKERNSKQSAQELKSLFE KKSLKEKPPISGKQSILSVRLEQCPLQLANPFMEYSKPGKGHV GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ YTSEGRERKLNDNVSAYCLHIABDDGEVDTDFPPLOSNBFIHKF GFSTLALUKKYSSPGLTSKSLFVRINAAMIGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSMHIHRLRFTTDVQL/GCALFFGVLRRRAAPVDCLRPS ADTWRQEGIGCGGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE 6678 221 865 GPSNQSSGSLSLIVTGCSSYWS*INDTCTILVLSSNFGRQ*LR PFPCSQLPMSQGCLWHLDCCCPWVPY1PGQWRKGRQRMRN*QS LLGSDQESVGLEDLCVPVNFLLHVLLGFF*PHELFLLFVVDLG FLPFLLLQGGCHCLVLPANILVSQAPQIGKLSCRLQTHDL8SSRN HHPLFLVVGRMDAVKHLETVQSGLASLGFVGQHTSHGPP 6679 2 786 LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLMYD/SCSQEKEGHAB*QNQNS\DFH QEKWIYVHKGSTKERHGYCTLGBAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIJQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF FLCTIPLMPSALDFGMAGERWEKQWPLA/PGPGTWGTPVGSISEE P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKERAGEBLHRSSSCLTAAPGFP EVHRNLQTFPGLJSRSGGF/GGAGTGGSWAPGEQPP;SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGFTGLRSGGGSSGGGH/*PGLPVGKV\GALGAAQD PQSGRGFTPGGFVGVGTEMLLSGLGSAXACPAARPAY*PLPSDFAS TIPKKGTRGFGGGGGSSCGGH**PGLPVKV\GALGAAQD PQSGRGFTDGGTVGTEMLLSGLGSAXACPAARPAY*PLPSDFAS TIPKKGTRGFGGGGGPGVLQERNRWVVGRAQGFTSADAAGTAPFQV *LPAPLSQPPGATCREGGSSSGGRP**PGLFGRAPARPAY*PLPSDFAS TIPKKGTRGFGGGGGPGVLQERNRWVVGRAQGFTSADAAGTAPFQV *LPAPLSQPPGATCREGMSSQRCPRTYTHSPLGHGRAPCPRCWH** WQDPPSSPRTGCLPGIPRAQAXSAPRTRSRPGIRTGRAAYGFIR				
RRSNTAQRLERLKERQNQIKCKNIQWKERNSKQSAQELKSLFE KKSLKEKPPISGKQSILSVRLEQCPLQLINDPINEYSKFDOKGHV GTTATKKLDVYLDHISQDRLIPMTVVTMASARVQDLIGLICWQ YTSEGREPKLNDNVSAYCLHIABDDGEVDTDFPPLDSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINASHGFSLIQVDDTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/GCALFFGVLRKRAAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLCAC\DLABE 6678 221 865 GPSNQSSGSLSILVTGCSSVWS*INDTCTILRVLSSNFGRQ*LR PFPCSQLPMSQGCLWHLDCCCPWVPY1PGQQWRKGRQRMRN*QS LLGSDQESVGLEBLCVFVNFLLHVLLGLFP*PHELFLLEVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLCYHDLESGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVQOHTSHGPP 2786 LEFRRAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL SYCNKEVYNKENLFNSLNTD/SCSQEEKEGHAE*QNQNS\DPH QEKMIYVHKGSTKERRGYCTLGBAFNRLDFSTAILDSRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNTTLIR ELQTLYTSLCTLVKRVGKSVLVGNINMVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFFFTPVTEBSGLF P\RKNEPDTHCPRGEARPEV*H_PKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKEBAGEELHRSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGACTQGSWAFGEQPP/SPLLPAS MQRSQAGLDGWRAGLUSSPTHHIPALRPSGTNATGRAFPSTTCS SGP\PAPPGPTGLPRGGSSSGGGHC**PGLPVGKV\GALGAAQD PQSGGRGFTGGTVGTTMLLSGLGSAKACPAARPAYP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQURACGMAPPS PGTSGRLVANGRHPGPQV AQCPPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGTFARQAYSAPRTRSRPGIRTGRAAYGFIR	6677	277	1678	
KKSLKERPPISGKQSILSTRLEQCPLQLNNPFNEYSKFDGKGHV GTTATKKIDVYLPLHSSQDRLLPMTVUTMASARVQDLIGLICMQ YTSEGREPKLNDNVSAYCLHIABDDGEVDTDFPPLDSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNIKVIM KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDNLSSH HYKSFKVSMIHRLFFITDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRQEQIGCGGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE 6678 221 865 GPSNQSSGSLSILVTGCSSVWS*INDTCTILRVLSSNFGRQ*LR PFPCSQLPMSQGCLWHLDCCCPWVPYIPGQQWRKGRQRMRN*QS LLGSDQESVGLEDLCVFVNFILHVLLGLFP*PHELFLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 6679 2 786 LEFARGAMPFLGQDWRS*PGONWVKTVDGKKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*ONQNS\DFH QEKWIYVHKGSTKERRGYCTLGEAFNRLDFSTAILDSRRNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLGTLYTSLCTLVKRYGKSVLVCNINMWVYRMETILHMQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQDM*CALERNGDQRGKEEAGEELHRSSSGLTAAPGFF EVHRNLQTFPGLPSRGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS GGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD PQSGGRGFTQGTVGTEMLLSGLGSAKACPARPAYP*LPSDPAS TIPKKGTRGFGEGPGULQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGAMPPSPGTTSGRLVANGTAPPGV *LPAPLSQPPGATEPQVRACGAMPPSPGTTSGRLVANGTAPPGV *LPAPLSQPPGATEPQVRACGAMPPSPGTTSGRLVANGTAPPGV *LPAPLSQPPGATEPQVRACGAMPPSPGTTSGRLVANGTAPPGV *LPAPLSQPPGATEPQVRACGAMPPSPGTTSGRLVANGTAPPGPV *LPAPLSQPPGATEPQVRACGAMPSPSPTTSGRLVANGTAPPGPV *LPAPLSQPPGATEPQVRACGAMPSPSPTTSGRLVANGTAPPGPV *LPAPLSQPPGATEPQVRACGAMPSPSPTTSGRLVANGTAPPGPRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				
GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ YTSEGREPKLNDNVSAYCLHAEDDGEVDTDF PPLDSNEPIHKF GFSTLALVEKYSSEPSGTTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWINQKPISIDSDLLCAC\DLAEE 6678 221 865 GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR PFPCSQLPMSQGCLWHLDCCCPWPFYIPGQQWRKGRQRWRN*QS LLGSDQSSVQLEDLCVFVNFLLHVLLGLFP*PHELFLLPVVDLG FLFPLLLQGGCHCLVFPNLHVLLGLFP*PHELFLLPVVDLG FLFPLLLQGGCHCLVFPNLVSGAPQIGKLSCRLQTHDLEGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP SSYCNKEVYNKENLFNSLNYD/SCSQEEKEBHAB*QNQNS\DFH QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKWFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGGTRQDFEFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSGGALGTGSA*ALP /NQVSPDQPM*GAEENGDQRGKKERAGBELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGGQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGTTGRPSGGSSSGGHG**PGLPVGKV\GALGAAQD PQSGGGFTQGTVGTEMLLSGLSSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGFGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEGPQVRACCMAPPSPGTSGTLVAWGRHPGFQV AQGCPPGAGCWGSQPRGSGRCPGTTYTHSDLGHGRAPCPRCWH* WQDPPSSPRTGCLPGIFARQAYSAPRTRSRPGIRTGRAAYGFIR		• .		
YTSEGREPKLNDNVSAYCLHIABDDGEVDTDFPPLDSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVPEEDSQIDIATVQDMLSSH HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLABE 6678 221 865 GPSNQSSGSLSIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR PFPCSQLPMSQGCLWHLDCCCPWPYIPGQQWRKGRQRMRN*QS LLGSDQESVGLEDLCVPVNFLLHVLLGLFP*PHELFLLPVVDLG FLFPLLLQGGCHCLVLPANLWSQAPQIGKLSGRLQFTHDLBGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 6679 2 786 LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL SSYCNKEVNNKENLFNSLNYD/SCSQESKEGHAB*QNQNS\DFH QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDERFRYVVV RLLELIAKSQLTELSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTERSGLF P\RNEPDTHCPRGEARPEV*HLPKPHSPGSEGABIQTSA*ALP /NQVSPPQPM*GAEENCDQRGGKERGEELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGGQPF/SFLLPAS MQRSQAGLPGWEAGLVESPTHIPPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGRPGGGSSSGGHG**PGLPGVKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQURACGMAPPS PGTSGRLVAWGRHPGPQV AQGCPPGACCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				
GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGSRADGVFEDSQIDIATVQDMLSSH HYKSFKVSMIHRLFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRQEQIGCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE 6678 221 865 GPSRQSSGSLSLIVTGGSSYWS*INDTCTILRVLSSNFGRQ*LR PFPCSQLPMSQGCWHLDCCCPWVPYIPGQQWRKGRQRMRN*QS LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELFLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLBGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP QEKWIYVHKGSTKERHGYCTLGBAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELQTLYTSLCTLVKRVGKSVLVCNINMWYKMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKEBAGEELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGACTQGSWAPGEQPP/SPLLPAS MQRSQAGLDWEAGLVESPTHHIPALRSGTNATGEAFPSTTCS SGP\PAPPGPTGLPFGGGSSSGGHG**PGLVGKV\GALGAAQD PQSGGRGPTGTVGTTEMLLSGLGSAKACPARRAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAACTAPFGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQRCRSQRCPRTTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR		:		
KEILKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSMHRRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE 6678 221 865 GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR PFPCSQLPMSQGCLWHLDCCCPWVPYIPGQQWRKGQRMRN*QS LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELFLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 6679 2 786 LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNONS\DFH QEKWIYVHKGSTKERRGYCTLGEAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQDM*GAEENGDQRGGKERAGEELHRSSSGLTAAPGFP EVHRNLQTFFCLPSRGGBP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGFTGRPGGSSSGGGG**PGLPGVKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGULQERNRWVVGRAQGFTSADAAGTAPFGV *LPAPLSQPPGATEPQVRACGMAPPS PGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLCHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				
HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWRQEQIGCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSLLCAC\DLAEE GPSNQSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR PFPCSQLPMSQGCLWHLDCCCPWVPYIPGQWRKGRQRMRN*QS LLGSDQESVGLEDLCVFVNPLLHVLLGLFP*PHELFLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 2 786 LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLNIVD/SCSQEEKEGHAE*QNQNS\DPH QEKWIYVHKGSTKERHGYCTLGBAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQLN NIQITRVSGQAQPPBGSGSLHRDTGQTRQDFEFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKERAGEELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWAGGLVESPTHHIPALRPSGTNATGEAPPSTTCS GGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGFGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPS PGTSGRLVAWGRHPGPQV AQGCPPGAGGWGSQPRGSQRCPRTYTHSPLCHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR			•	·
ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLABE 6678 221 865 GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR PFPCSQLPMSQGCLWHLDCCCPWVPYIPGQQWRKGRQRMRN*QS LLGSDQSSVGLEDLCVFVNFLLHVLLGLFF*PHELFLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HHPLFLVVGRMDAVKHLETVQSGLASLGFVQQHTSHGPP 6679 2 786 LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLNYD\SCSQEEKBEHAE*QNQNS\DPH QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLLEDQNITLIR ELQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKERAGBELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGP/GGACTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLFVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPFQU AQGCPPGAGGCGSQPRCSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR	1			
KASTKFWIKQKPISIDSDLLCAC\DLAEE 6678 221 865 GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR PFPCSQLPMSQGCLWHLDCCCPWVPYIPGQQWRKGRQRMRN*QS LLGSDQESVGLEDLCVFVNFLLHVLLGLFF*PHELFLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 2 786 LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL SYCHNEVYNKENLFNSLNYD/SCSQEEKEGHAB*QNQNS\DPH QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINNWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKEBAGEELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPFGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR	. :		•	1.
6678 221 865 GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR PFPCSQLPMSQGCLWHLDCCCPWVPY1PGQQWRKGRQRMRN*QS LLGSDQESVGLEDLCVFVNFILHVLLGLFP*PHELFLLPVVDLG FLFPLLLQGGCLCLVLPANLVSQAPQ1GKLSCRLQTHDLEGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 2 786 LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNQNS\DFH QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWYYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTESSGLF P\RKNEPPTHCPRGEARPEV*HLPKPHSPGSEGABIQTSA*ALP /NQVSPPQPM*CABENGDQRGGKERAGEELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGGEGPGVLQERNRWVVGRAQGFTSADAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGFQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR		-		
PFPCSQLPMSQGCLWHLDCCCPWVPY1PGQQWRKGRQRMRN*QS LLGSDQESVGLEDLCVPVNFLLHVLLGLFP*PHELFLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 2 786 LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAP*QNQNS\DPH QEKWIYVHKGSTKERHGYCTLGEAPNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKEBAGEELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGACTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR			·	
LLGSDQESVGLEDLCVFVNFLLHVLLGLFFF*PHELFLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQ IGKLSCRLQTHDLEGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 2 786 LEFARGAMPFLGQDWRSFGQNWVKTVDGNKRFLDEKSGSFVSDL SSYCNKEVYNKKENLFINSLNYD/SCSQEKEGHAE*QNQNS\DFH QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWYXMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKERAGEELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGFTGLRPGGGSSSGGGH**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGGGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR	6678	221	865	1
FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 2 786 LEFARGAMPFLGQDWRS PGQNWVKTVDGWKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNQNS\DFH QEKWIYVHKGSTKERHGYCTLGEAPNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGOTRQDFEFTPVTEESGLF P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKEBAGBELHRSSSGLTAAPGFP EVHRNLQTFFGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGFTGLRPGGSSSGGHG**PGLPVGV\GALGAAQD PQSQRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQENNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPS PGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				1
HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP 6679 2 786 LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNQNS\DFH QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF 6680 1498 2951 PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVGSISEE P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKERAGBELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR	;	·		· ·
LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNQNS\DFH QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFFETTPVTEESGLF PLCTLPLMFSALPGWAGERWEKQWPLA/PGFGTWQTPVGSISEE P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKERAGEELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGBTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR			•	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE+QNQNS\DFH QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF 6680 1498 2951 PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVGSISEE P\RKNEPDTHCPRGEARPEV+HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKERAGBELHRSSGLTAAPGFP EVHRNLQTFPGLPSRGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR	6670	3	706	
QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF 6680 1498 2951 PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVGSISEE P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKERAGBELHRSSGLTAAPGFP EVHRNLQTFPGLPSRGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR	6019	4	. /00	1
RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF 1498 2951 PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVGSISEE P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*CAEENGDQRGGKERAGBELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALQGAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				1
ELLQTLYTSLCTLVKRVGKSVLVGNINMWYYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF 1498 2951 PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVGSISEE P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*CARENGDQRGGKERAGBELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR		,		1 ~
NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF 6680 1498 2951 PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVGSISEE P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKERAGBELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				
PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVGSISEE P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKERAGBELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				1 ~
P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP /NQVSPPQPM*GAEENGDQRGGKERAGBELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR		1400	2000	·
/NQVSPPQPM*GAEENGDQRGGKERAGBELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR	0080	1498	2951	
EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				1 .
MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				1 '
SGP\PAPPGFTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				•
PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				
TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				
LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				
AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				
WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR				
rQGGGGG				
	L			r QGGGGG

PCT/US00/34263 WO 01/53312

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
6601	sequence		\=possible nucleotide insertion)
6681	1169	511	INYIYYNQQQRAFHELK\EKLMSAPALGLPDLTKLFTLHVSERE
			KMTVGVLTQTVGPWSRPGAYLSKQLDGVSKGWPPCPRALAATAL
	1		LAQEADELTLRQNLNRKSPHA\VVTLINTKGHH*LINARLTRYQ
	İ		TLLCENPHKTIEVSNT/LNPATLLLVTESPVKHNCLEVLDSVYS
			SRPNLRDHP*TSVDWELYVDGSGFANPCKVTLKKETSPAPVTPR
			S
6682	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
		·	VRRRIELIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
			YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG
			FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
	1		PLQTDAAENNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL
			D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY
			DLRSDKPLLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK
	1		NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
			GPAPRWCSFLDNLTEELEENPESNE
6683	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALOKKDVD
			VRRRIELIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
			YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG
			FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
	İ		PLQTDAAENNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL
			D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY
		; ·	DLRSDKPLLVKDHOYGLPIKSVHFODSLDLILSADSRIVKMWNK
			NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
	1		GPAPRWCSFLDNLTEELEENPESNE
6684	111	527	GLRGGTSRGRAGREPEFAAGVLCVVAGFCQSPCPPGGRGREAPA
6004	111	527	
	1.		PP\SGRRHA*RPA*WLGGPGGDSGGREEGGS/GELQRAMESKMG
			ELPLDINIQEPRWDQSTFLGRARHFFTVTDPRNLLLSGAQLEAS
6685	350	1475	RNIVQNYR
6665	258	1473	KLLGDNFEGFCNKFELSDSENGSNS*QSPL\FDRLFDPDPQKVL
			QGVIDMKNAVIGNNKQKANLIVLGAVPRLLYLLQQETSSTELKT
, .	. 12		ECAVVLGSLAMGTENNVKSLLDCHIIPALLQGLLSPDLKFIEAC
			LRCLRTIFTSPVTPEELLYTDATVIPHLMALLSRSRYTQEYICQ
			IFSHCCKGPDHQTILFNHGAVQNIAHLLTSLSYKVRMQALKCFS
	1,	4	VLAFENPQVSMTLVNVLVDGELLPQIFVKMLQRDKPIEMQLTSA
		,	KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKERLLEERVEGA
	,		ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK
•			RLDHDLKHAHELRQAAFKLYASLGANDEDIRKKVSLGEGRPPVL
			TASRQGVTST
6686	310	927	DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY
			QLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV
	1		LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN
			SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV
	<u> </u>		VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT
6687	181	915	EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST
			IGETSNRSRDRDRYRRRNSRSRSPGROCRHRSRSWDRRHGSESR
			SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR
			IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIOSV
			PLAIGLTGQRLLGVPIIVQASQAEKNRLAAMANNLQKGNGGPMR
			LYVGSLHFNITEDMLRGIFEPFGKV
6688	1025	1	AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF
		•	SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD
			LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS
			STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE
			VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTC
			TMSELEELFSLFSPAPLLSKLFTSSGSIAICCQDSGPSDTGRLS
			VCQLWLADSDTGKLSDCQEVVTVGDSGGLTCPELSLGRM*MSLL
		•	540
			J*10

·			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residué of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
(amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6689		1200	SSAVIPGYSSSSDSRLNTVPTVDLLCPFQTKSST
0003	640	1299	SSSASYATSATSISDTAFSGSLKLKHGLLSALDSSSRTS*STSS
			AEDSTFRICSPSVSDTSSDSSGSKDNVLILFSKVSI*SCFSLSS FFSDSISFCFSSSSFCKR*FVSSKVSQNALLSSRLSNGPGGSSK
]			QRNSLTARQLAMSL*ATKF*RNACNPNCLSSKKSAL*LSLNQRF
1			GGSASRKPGNISFNSQKCSALSYCCNFVIKPREVSVSSENYPAF
6690	1	442	GTRGKMAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGP
1 3030	*	772	QQVGAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLMGNAMVMTO
1			YIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQGKKNL\H
1			GDGLAIWYTKDRMOP
6691	287	1401	LKTETSEEKARRYKDRPSQLNAVFQEQKKMIQAQESITLEDVAV
	<u> </u>	1201	DFTWEEWQLLGAAQKDLYRDVMLENYSNLVAVGYQASKPDALFK
1		•	LEQGEQLWTIEDGIHSGACSDIWKVDHVLERLQSESLVNRRKPC
		* *	HEHDAFENIVHCSKSQFLLGQNHDIFDLRGKSLKSNLTLVNQSK
1	•		GYEIKNSVEFTGNGDSFLHANHERLHTAIKFPASQKLISTKSQF
· ·	•		ISPKHQKTRKLEKHHVCSECGKAFIKKSWLTDHQVMHTGEKPHR
į .			CSLCEKAFSRKFMLTEHQRTHTGEKPYECPECGKAFLKKSRLNI
			HQKTHTGEKPYICSECGKGFIQKGNLIVHQRIHTGEKPYICNEC
j			/GKGFIQKTCLIAHQRFHTER
6692	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCOVE
		``	RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
1			DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL
	•		IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL:
İ			DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
			SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
6693	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCQVE
}			RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
			DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL
	e United Section		IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
			DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
6694			SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
6694	292	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAAESRQHELPVR
: :			EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
			LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV.
6695	292	013	NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
0095	434	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRQAAESRQHELPVR
			EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
			LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
6696	1	782	PRVRGRVGERWAFLSVPAAMSSEMEPLLLAWSYFRRKFOLCAD
	•	702	LCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQEGIAEMML
			DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL
			RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML
			TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD
			LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREAEKOIKSS
6697	3	782	PPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR
	-	, 44	IPQILTKVIDTLHRHKSEFFEKHGEEGVEAEKKAISLLSKLRNE
	1		LQTDKPFIPLVEKFVDTDIWNQYLEYQQSLLNESDGKSRWFYSP
	1		WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQES
			IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL
	į		SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK
6698	668	754	VGSCACAGSCKCKECKCTSCKKSECRAFP
6699	325	492	EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV
			LLGKRKGSVGAGSFQLPGGHLEFGETWEECAQRETWEEAALHLK
	ļ		NVHFASVVNSFIEKENYHYVTILMKGEVDVTHDSEPKNVEPEKN
			

SEQ	Predicted	Predicted end	Desire and compatible of the compatible
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
140.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	· · · · · · · · · · · · · · · · · · ·
	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion, -possible nucleotide insertion)
	sedgetice		ESKRIIYNHAFFFOESKWSGGILO
6700	1000	1200	
6700	1098	1392	TQCWRSSTPGMRTHFRTQP/RLECGQGFSQQENGHCMDTNECIQ
			FPFVCPRDKPVCVNTYGSYRCRTNKKCSRGYEPNEDGTACVERT
C 701			LLIGLCNLLGK
6701	2	1485	AAAGPRTRVRRAAAFEGQPSPSPGLGPTSDKAAAPRTPKRRRLW
			RQRQ/HPAMLCYVTRPDAVLMEVEVEAKANGEDCLNQVCRRLGI
			IEVDYFGLQFTGSKGESLWLNLRNRISQQMDGLAPYRLKLRVKF
			FVEPHLILQEQTRHIFFLHIKEALLAGHLLCSPEQAVELSALLA
			QTKFGDYNQNTAKYNYEELCAKELSSATLNSIVAKHKELEGTSQ
			ASAEYQVLQIVSAMENYGIEWHSVRDSEGQKLLIGVGPEGISIC
			KDDFSPINRIAYPVVQMATQSGKNVYLTVTKESGNSIVLLFKMI
			STRAASGLYRAITETHAPYRCDTVTSAVMMQYSRDLKGHLASLF
			LNENINLGKKYVFDIKRTSKEVYDHARRALYNAGVVDLVSRNNQ
			SPSHSPLKSSESSMNCSSCEGLSCQQTRVLQEKLRKLKEAMLCM
			VCCEBEINSTFCPCGHTVCCESCAAQLQVGESAAHFCLQPHLSL
			LLTGSRSQVLAR
6702	397	1971	PLAKFLKLDLVNVLCLPMBDVFLFYRTCFCSMGLGSSCHLSLPK
			RAEALLCSRKATVVRDLVAVRMAEEQEFTQLCKLPAQPSHPHCV
			NNTYRSAQHSQALLRGLLALRDSGILFDVVLVVEGRHIEAHRIL
			LAASCDYFKGMFAGGLKEMEQEEVLIHGVSYNAMCQILHFIYTS
			ELELSLSNVQETLVAACQLQIPEIIHFCCDFLMSWVDEENILDV
	. *		YRLAELFDLSRLTEQLDTYILKNFVAFSRTDKYRQLPLEKVYSL
			LSSNRLEVSCETEVYEGALLYHYSLEQVQADQISLHEPPKLLET
			VRFPLMEAEVLQRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ
			SPQTELRSDFQCVVGFGGIHSTPS\MSSATRPKYLNPLLGEWKH
		, ,	FTASLAPRMSNQGIAVLNNFVYLIGGDNNVQGFRAESRCWRYDP
			RHNRWFQIQSLQQEHADLSVCVVGRYIYAVAGRDYHNDLNAVER
			YDPATNSWAYVAPLKREVYAHAGATLEGKMYITCGRKGRIT
6703	45	1244	GVGPRAAAMPLELELCPGRWVGGQHPCFIIAEIGQNHQGDLDVA
			KRMIRMAKECGADCAKFOKSELEFKFNRKALERPYTSKHSWGKT
			YGEHKRHLEFSHDQYRELQRYAEEVGIFFTASGMDEMAVEFLHE
			LNVPFFKVGSGDTNNFPYLEKTAK/TRGWHSVLRDVCGVQLNDE
	1		TSSWDVLGRVRTSKEKVLMVLVLDYSGRPMVISSGMQSMDTMKQ
, ,		1	VYQIVKPLNPNFCFLQCTSAYPLQPEDVNLRVISEYQKLFPDIP
	. :		IGYSCHETGIAISVAAVALGAKVLERHITLDKTWKGSDHSASLE
			PGELAELVRSVRLVERALGSPTKQLLPCEMACNEKLGKSVVAKV
	1		KIPEGTILTMDMLTVKVGEPKGYPPEDIFNLVGKKVLVTVEEDD
	ļ <u>.</u>		TIMEE
6704	82	1007	TMNTRNRVVNSGLGASPASRPTRDPQDPSGRQGELSPVEDQREG
			LEAAPKGPSRESVVHAGQRRTSAYTLIAPNINRRNBIQRIAEQE
		1	LANLEKWKEQNRAKPVHLVPRRLGGSQSETEVRQKQQLQLMQSK
			YKQKLKREESVRIKKEAEEABLQKMKAIQREKSNKLEEKKRLQE
			NLRREAFREHQQYKTAEFL/RQTEHRIARQKCLSKCCLWPTILN
			MGQKLGLQ\DSLKAEENRKLQKMKDEQHQKSELLELKRQQQEQE
		1	RAKIHQTEHRRVNNAFLDRLQGKSQPGGLEQSGGCWNMNSGNSW
			GI
6705	2	786	RLCRNSARVPCGWSASRSLGEGAGFIGPLRGPHPRAGGTGTSFT
		[SYKRKGGIMSTIAAFYGGKSILITVATGFLGKELMEKLFRTSPD
			LKVIYILVRPKAGQTLQHRVFQILDSKLFEKVIEVRPNVHEKIR
		1	AIYADLNQNDFAISKEDMQELLSCTNIIFHCAATVRFDDTLRHA
		1	VQLNVTATRQLLLMASQMPKLEAFIHISTAYSNCNLKHIDEVIY
		1	PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK
6706	130	531	FTHSSSSHSQEMLGKLNMLRNDGHFCDITIRVQDKIFRAHKVVL
	1		AACSDFFRTKLVGQAEDENKNVLDLHHVTVTGFIPLLEYAYTAT
	}	}	LSINTENIIDVLAAASYMQMFSVASTCSEFMKSSILWNTPNSQP
	i		EK
		·	<u> </u>

	taining signal peptide
ID beginning nucleotide (A=Alanine, C=Cysteine	
NO: nucleotide location Glutamic Acid, F=Pheny	
location corresponding H=Histidine, I=Isoleuc	
corresponding to first L=Leucine, M=Methionin	
to, first amino acid P=Proline, Q=Glutamine	
amino acid residue of S=Serine, T=Threonine,	
residue of amino acid W=Tryptophan, Y=Tyrosi	
amino acid sequence Codon, /=possible nucl	
sequence \=possible nucleotide	
6707 2233 1343 YWSGIGYELQHFHWRKFHFEKK	
GMVVVGWTAVNGSW*GGQLRCV	
FFILSQ*KT*SSWENWVFAKYS	
SQAR*SRFCGLCNPCGHCGLDII	-
NRRVFSLLCEGPGHCYQGAVCR	
1 1	CILYNISFNLFSYSF*GVARYA
C*RCHWYFEWLLYNHCGDILVA	
6708 115 . 1729 TVGSWSRSGRSPPVGRQLLLTG	
GEIIRVVHPHRPCKLALGSDGV	
ENFTSEAAFIENLRRRFRENLI'	
QHMERYRGVSFYEEPPHLLAVAI GAGKTDATKRLLOLYAETCPAP	
AKTLRNDNSSRFGKYMDVQFDF	
AKTERNDNSSRFGKYMDVQFDF NHGERNFHIFYQLLEGGEEETLI	· · · · · · · · · · · · · · · · · · ·
VSSINDKSDWKVVRKALTVIDF	
FAANEESNAQVTTENOLKYLTR	
EELLSPINLEOAAYARDALAKA	
ESPSWRSTTVLGLLDIYGFEVF	
ELTLKSEOBEYEAEGIAWEPVO	
LDE\ECLRPGE	
6709 3 894 PPHEHLFPSGERGPFSFLVSRR	GLGPGKMGKKGKKEKKGRGAEK
TAAKMEKKVSKRSRKEEEDLEA	
1 1	GEYFNGOKTFLYNELYVYNIRK
DTWTKVDIPSPPPRRCAHQAVV	
FYHYKDLWVLHLATKTWEQVKS'	
GGFHESTRDYIYYNDVYAFNLD	
IPSLPRAASSVYGGYSKQRVKK	DVDKGTRHSDMF
6710 158 980 RHKMTNYRVESSSGRAARKMRL	ALMGPAFIAAIGYIDPGNFATN
IQAGASFGYQLLWVVVWANLMAI	MLIQILSAKLGIATGKNLAEQI
RDHYPRPVVWFYWVQABIIAMA	rdlaefigaaigfklilgvsll
QGAVLTGIATFLILMLQRRGQK	PLEKVIGGLLLFVAAAYIVELI
FSQPNLAQLGKGMVIPSLPTSE	AVFLAAGVL\GATIMPHVI/YI
WHSSLTQHLHGGSRQQRYSATK	NDVAIAMTIAGFVNLAIMATAA
SELNFYGHTGVA	
6711 3 347 VTECKTMTCKMSQLERNI*TMI	NTLHHYSVKLGHPDTLIHGEFK
ELVRTDLHNILMKENKNDQAI+I	HIMEDLDTNAHMQIIFKELIML
MAMLTWSYHDNMHDADYGPGQQI	
6712 118 578 PHGQKRTRYPQVRAPGQQPQAQI	LAMALCLKQVFAKDKTFRPRKR
FEPGTQRFELYKKAQASLKSGLI	DLRSVVRLPPGENIDDWIAVHV
VDFFNRINLIYGTMAERCS*TS0	CPVMAGGPRYEYRWQDERQYRR
PAKLSAPRYMALLMDWIESLI	
6713 2485 3 QARGSDSEDGEFEIQAEDDARAI	RKLGPGRPLPTFPTSECTSDVE
PDTREMVRAQNKKKKKSGGFQSN	MGLSYPVFKGIMKKGYKVPTPI
QRKTIPVILDGKDVVAMARTGSO	ektacfllpmferlkthsaqtg
ARALILSPTRELALQTLKFTKE	GKFTGLKTALILGGDRMEDQF
AALHENPDIIIATPGRLVHVAVI	EMSLKLQSVEYVVFDEADRLFE
MGFAEQLQEIIARLPGGHQTVL	fsatlpkllvefaragltepvl
IRLDVDTKLNEQLKTSFFLVRE	TKAAVLLHLLHNVVRPQDQTV
VFVATKHHAEYLTELLTTORVSC	
1	CAHIYSALDPTARKINLAKFTL
GKCSTLIVTDLAARGLDIPLLDD	· · · · · · · · · · · · · · · · · · ·
	VINYSFPAKGKLFLHRVGRVA
GKCSTLIVTDLAARGLDIPLLD	VINYSFPAKGKLFLHRVGRVA LHLFLGRSLTLARPLKEPSGVA
GKCSTLIVTDLAARGLDIPLLDI RAGRSGTAYSLVAPDEIPYLLDI	vvinysfpakgklflhrvgrva Lhlflgrsltlarplkepsgva Stlbaslelrglarvadnaqqq
GKCSTLIVTDLAARGLDIPLLDI RAGRSGTAYSLVAPDEIPYLLDI GVDGMLGRVPQSVVDEEDSGLQS	vvinysfpakgklflhrvgrva Lhlflgrsltlarplkepsgva Stleaslelrglarvadnaqqq Elglhplfssrfeeeelqrlrl
GKCSTLIVTDLAARGLDIPLLDI RAGRSGTAYSLVAPDEIPYLLDI GVDGMLGRVPQSVVDEEDSGLQS YVRSRPAPSPESIKRAKEMDLVO	VVINYSFPAKGKLFLHRVGRVA LHLFLGRSLTLARPLKEPSGVA STLEASLELRGLARVADNAQQQ SLGLHPLFSSRPEEEELQRLRL LCSQVMRAKRQKDRKAIARFQQ

Deginning nuclectide location corresponding corresponding corresponding corresponding corresponding corresponding contrasp	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No. nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence s	-L	l		
Cocresponding Coirespondin		, , ,		
Leibeucine, Medethiomine, N-Asparagine, amino acid residue of amino acid residue of amino acid sequence with the sequenc	1.0.			
to first amino acid residue of amino acid amino acid sequence 8-Servine, T-Threonine, V-valine, 4-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop codon, /-possible nucleotide deletion, (-possible nucleotide deletion) 1.51506563AFEQARAGNIJAMEDBAGNITGREGOLEMERKEK FVGOSGOEDKEKIRTESGRYISSSYKRULVOKKUKKUKKUK 19-8-1, 1.51506563AFEQARAGNIJAMEDBAGNITGREGOLEMERKEK FVGOSGOEDKEKIRTESGRYISSSYKRULVOKKUKKUKKUK 19-8-1, 1.51506563AFEQARAGNIJAMEDBAGNITGREGOLEMERADASS LEIKTKOOLIKORRERAQKAALSIORWUPDALLOPD NNOGELDFPPPARMITSSGRAPAGARADROPCYCKVELSVS GONLILDROVYSKSDPPCULFFERMGRRIEVDRETETAINMINPAR SKRYTUVHFERSVKLYRALPHODOLSAMENDROVITUSIAGA RILDKULFANDENSKSDPPCULFFERMGRRIEVDRETETAINMINPAR RILDKULFANDENSKSPPCULFFERMGRRIEVDRETETAINMINPAR RILDKULFANDENSKSPPCULFFERMGRRIEVDRETETAINMINPAR RILDKULFANDENSKSPPTEULIAMERSCHAMERSPRICHTSJORSSI RIKKULDYBREGOLEPYRAGNARMINERVENTETAINMINPAR RILDKULFANDENSKSPPTEULIAMERSCHAMERSPRICHTSJORSSI MCEARBONDERSTENSKELPTYRKODOKHMUNGETEUTYTTJOW KRPTUPLINSLICHEMERSICHTAAGKLSDRWITTSJORSF MCEARBONDERSTENSKELPTYRKODOKHMUNGETEUTYTTJOW KRPTUPLINSLICHEMERSICHTAAGKLSTTOPOGOSGORGSSISTIMI. SAIRAWGOLIOWPSKERPALARDROALPFDEWKRHEFAINFOR TNPPCGGUDDIAQAYSACIP TNPPCGGUDDIAQAYSACIP TNPPCGGUDDIAQAYSACIP TNPPCGGUDDIAQAYSACIP TNPPCGGUDDIAQAYSACIP TNPPCGGUDDIAQAYSACIP TNPPCGGUDDIAQAYSACIP TNPPCGGUDDIAQAYSACIP TNPPCGGUDDIAQAYSACIP TNPPCGGUDDIAQAYSACIP TNPPCGGUDDIAQAYSACIP TNPPCGGUDDIAQAYSACIP TNPPCGGUDDIAQAYSACIP TNPPCGGUDDIAQAYSACIP TNPPCGGUDDIAQAYSACIP TNPCGGUDDIAQAYSACI	1			
amino acid residue of amino acid sequence wytypophan, y-Yrycoshen, X-Whiknown, *-Stop Codon, /-possible nucleotide deletion, Vaposable nucleotide deletion,				
residue of amino acid sequence				
amino acid sequence Codon, /-possible nucleotide cletion,		1		
Sequence Nepossible nucleotide insertion				
LSISGEGAPEQQAAGAVIDLINGBERQOLLTRERQUIXWOPKER, FVGQSQOEDKKIR LTESGRYISSY SKREINJOWKROKI DF SPL GRRRGILITRREPRIEVIGSAPILAQACCI ROPHAPRIPLOARES LELKTRQCILLKORPRAQAALISCORPWRQAALOC GRRRGILITRREPRIEVIGSAPILAQACCI ROPHAPRIPLOARES LEKTRQCILLKORPRAQAALISCORPWRQAALOC GRRRGITERREPRIEVIGSAPILAQACCI ROPHAPRIPLOARES LEKTRQCILLKORPRAQAALISCORPWRQAALOC GOLD HAND CONTROL OF THE WAS AGRAFIADOR OF THE WAS AGR			bequence	
FVGQSGOBKKILTTERGRYISSYYKEDLOVKOQKID'S SYL GRRGTLITRERFETEWGRAPHEADAGCIP OPHARPHIOABEA LEIKTKQOILKORRRAQKAALSIQRWRDQAALCO 169 1416 NCOCGLIPPFARWANT PSGGABLAGARAPGOPYCVCKVEISYS GQMLLDRUYTSISDPCULTPERNORNIEDDRITTAINNIAPPA SKKYVLDYHPEBVQKLKPALFODKSSMRLDBEHDFLGSYSCULG TIVSSKRITRPLLLLKDRAGKGLITTAAQELSDNRVITLISLAG RRLDKKDLFGKSDPFLEFY KRGDDGKMRLUMRTEVIKYTLDYW KPRTVPLVISLICDBMREFIQWCTUDYDMOGGDBIFOERGYTSVSQ MCBARDSYLEPECINPKKQRKKKHYNSGITILRSCKINRDY FLDYILGGCQLBFYCGIDTAKSKOPLDDBISHLTHINBMITMETL SAINANGGITQOYDSDNRWFLDDBISHLTHINBMITMETL SAINANGGITQOYDSDNRWFLDSFLEHTINBMITMETL SAINANGGITQOYDSGSGGSGFPSKAYAG THERMSPHITMMITMANSSCHAPPTFFTANKE SAINANGGITABARDON FENDEPPLIBERIGINDHTWORTTVLHPLKVADGSTMMSHTAKWG THERMSPHITMMITMANTATURPLEVADGSTMMSHTARWG THERMSPHITMMITMANTATURPLEVADGSTMMSHTARWG THERMSPHITMMITMANTATURPLEVADGSTMTFKSGLTFFTDVA VIFTESBLIGHTWORTTVLHPLKVADGSTMTFKSGLTFFTDVA VIFTESBLIGHTWORTTVLHPLKVADGSTMTFKSGLTFFTDVA VIFTESBLIGHTWORTTVLHPLKVADGSTMTFKSGLTFFTDVA VIFTESBLIGHTWORTTVLHPLKVADGSTMTFKSGLTFFTDVA VIFTESBLIGHTWORTTVLHPLKVADGSTMTFKSGLTFFTDVA VIFTESBLIGHTWORTTVLHPLKVADGSTMTFKSGLTFFTDVA VIFTESBLIGHTWORTTVLHPLKVADGSTMTFKSGLTFFTDVA VPTTERSMPHTTDDLKADARSTSGNATHSCHAPHTTHIKLDDFSKNATH LISSEXKADAKKRYTTAARKISLGCOSSYNICSBSTHEDSA		Doquonec		
GRRRGILTRRRPRIEGUSERPLAGAGCI FOPHAPPHPLOARSA LELKTKOGILKORRPAGAAL GLORWPOGALAL GLORWPOGALAL GLORWPOGALAL GLORWPOGALAL GLORWPOGALAL GLORWPOGALAL GLORWPOGALAL GLORWPOGALAL GLORWPOGALAL GLORWPOGALA GLO		Ì		1
LELKTKOJILKORRRAQKAALSLORNWAPGAALCPO				
6714 169 1416 INCORLIDEPTERAMATIPSGGRAPAGARAMPROPYCYCKYCETSUS GORLIDEPTERAMONITESTICANTIMPRAP SRKFYLDYHPEEVQKLKPALFTQUKSSMRLDEHDFLGQFSCSIG TTVSSKKTTRPLILLIMDKPAGKGGITTAAQBLSDNRVITISLAG RELDKULFGKSSPFLEFKYREDDOKMM-VIRFEVIKYTLDFUM KPHTVELVSLCDEMERPTQWCYDYDNDGCHDF1GEFOTSVSQ MCCRARDSVPLEFECINFKKQRKKKYKNGSIGTERAGKIEDFOKGHTUSLAG MCCRARDSVPLEFECINFKKQRKKKYKNGSIGTERAGKIEPTOWSVSQ MCCRARDSVPLEFECINFKKQRKKKYKNGSIGTERAGKIEPTOWSVSQ MCCRARDSVPLEFECINFKKQRKKKYKNGSIGTERAGKIEPTOWSPSGWPT SAMWAGGITQDVDSDMWFPAGFGRQALPPFWGFRATHNPMOTINELL SAMWAGGITQDVDSDMWFPAGFGRQALPPFWGFRATHNPMOTINELL SAMWAGGITQDVDSDMWFPAGFGRQALPPFWGFRATHNPMOTINELL SAWWAGGITQDVDSDMWFPAGFGRQALPPFWGFATHNPMOTINELL SAWWAGGITQDVDSDMWFPAGFGRQALPPFWGFATHNPMOTINELL SAWWAGGITQDVDSDMWFPAGFAGFAGNFFWHATHNPMOTINELL SAWWAGGITQDVDSDMWFPAGFAGFAGNFFANNING GKPKHLGVPMGRWLAVSDGELSSTTGPQGQGGRGSSLSIHSL PSOPSSPPTESGPVASWALSFREAUGOPLALYFTEFLKKEFS ARBWYTHKACGRCQTAAAAASHSPHGGQPPFRGFTLAGGGRAFGAGFAGFAGFATHNPMOTITUTAGTTAGTAGAAAAAAAAAAAAAAAAAAAAAAAAAA	Ĭ		ĺ	1
GQNLLIDDVTSKADPPCVLFTENNGRRIEVDRTSTAINNIMPAP SKKYVLDYHPBEVQKLKFALFDQDKSSMRLDEHDFLQFSCSIG TIVSSKRITRPLILLINDKPARGGIITTAAGALSDNRVITUSIAG RRILDKGDFGKSDPFLEFYKPGDDGKMMVRRTEVIKYTUSIAG RRILDKGDFGKSDPFLEFYKPGDDGKMMVRRTEVIKYTUSPW KPPTVPLVSLGDDMEKPTQUFOXTDVTDNGGHDFIGEPGTSVSQ MCBARDSVPLEFECINKKQRKKNYKNSGIITLARGKINDVS FLDYILGGCQLMPTVGIDFTAGRONDLDPSSLHYINFMGTNELL SAINAVQGIIQDVDSDEMPFALGFGAQLPPDWKVSHEFAINFPP TNPPCSGVDGIAQAYSACLE 6715 32 493 GPAGASSGSLHCLPATVQALAGARHS PHGQPPFRGEPLIGSGMP GKPKHLGPVBROWLAVSDGBLSSTTPQGQGGGGGSSLSIHSL PSGPSSPPPTEBQPVASHALSFERLLQDPLGLAYFTEFLKKEFS ABNVTBWLACERCQIIPADY GKPKHLGPVBROWLAVSDGBLSSTTPQGGGGGGGSSLSIHSL PSGPSSPPPTEBQPVASHALSFERLLQDPLGLAYFTEFLKKEFS ABNVTBWLACERCQIIPADY 6716 1 176 GAGGPAPRSFGSEEPRAALERDKMSARAAAKSTAMEETAIWEQ HTVTLHRVSLCCSK PHDYSQGGFVPPDMQDQPYTGGIYQPTQAYTPASPQPPYGNN FEBEPPLLEBIGLIDNDHIWGKTLTVLHPLKKANDSIKMETDLAG GVSSGCVASVLGCLIPATLUSAGVLTVLHPLKKANDSIKMETDLAG GVSSGCVASVLGCLIPATLUSAGVLTVLHPLKKANDSISMMETDLAG GVSSGCVASVLGCLIPATLUSAGVLTVLHPLKKANDSISMMETDLAG GVSSGCVASVLGCLIPATLUSAGVLTVHLHPLKANDSISMMETDLAG GVSSGCVASVLGCLDFALLSFAVTFSLGAMSSGTENDALSFV FEBEPPLLEBIGLIDPVGRNLYQDVMLHRFRNILISVGHHPFKHDVFL LEXSKLDIMKTATO 6718 290 599 KQSSTVPGTITSLKMINSGLCKPETGGRAFTKGUTFKDVA VIFTEBEIGGLIDPVGRNLYQDVMLHRFRNILISVGHHPFKHDVFL LEXSKLDIMKTATO 6719 1 691 PTPPEEQDREDGKCHKMENNPISGNLNCDPIAMSQCSSDHGCET DLINDDDKJEKFNNFMXDSASQDNGLSFRISRKRVCSSBDSSL QVVKSSSKATFGILBATTRCAATAANKIKLBODGGSVGCVPSEQYACERSKPP DPDSBGSTKVLSGALANDGDSSDDMLSDEHKHRHTNIHKIDAPSK RKSSSVTSG 6720 3 822 HEVABEAGGTVYPGRGTMPGTKRPCHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKAADANIVHLLQCCDAETFQEEGGALSTY QRLYSSSILTTMVQVAKCWELKEPDGGIVVLGGGGTGGRMAP LMSVSFNOLMKGLGGKPLYTYLLAGGDRSVVASREGTEDSALHG LEKKVAAGKKRVLVIGGGAPVAGRGGTSGRMAP VPITEKSNPLTQDLDKAADARNIVHLLGCCDAETFQEEGGALSTY QRLYSSSILTMVQVAKCWELKEPDGGIVVLGGGGTGGRAP VPITEKSNPLTQDLDKAADARNIVHLLGCCDAETFQEEGGGTGGRMAP LMSVSFNOLMKGLGGKPLYTYLLAGGDRSVVASREGTEDSALHG LEKKVAAGKKRVLVIGGAAPVAGRGGTSGRMAP VPITEKSNPLTQDLDKAADARNIVHLLGCCDAETFGEGGTGGRMAP LMSVSFNOLMKGLGGKPLYTYLLAGGGRSVAGRGGTGGTAGHAP VPITEKSNPLTMQVAKCWELKEPDGGLVVLGG	6714	160	1416	1
SKKPVLDYHFEEVQKLKFALFDQDKSSRRLDEHDFLGOFSCSLG TIVSSKITTEPLLLIMDRYDAKGLITIAGDRRYITSLAG RRLDKKDLFGKSDPFLEFYKPGDDGKWMLVHRTEVIKYTLDPVW KPFTVPLVSLCDGWERFICVMFVTYDMDGGHDFTGGRTGVSVG MCEARDSVFLEFECINFKQRKKRYNTKSGTILLBSCKIRRDYS FLDYILGGCQLMFTVGIDFTASKGRKKYNTKNSGTILLBSCKIRRDYS FLDYILGGCQLMFTVGIDFTASKGRKKYNTKNSGTILLBSCKIRRDYS FLDYILGGCQLMFTVGIDFTASKGRKKYNTKNSGTILLBSCKIRRDYS FLDYILGGCQLMFTVGIDFTASKGRKKYNTKNSGTILLBSCKIRRDYS FLDYILGGCQLMFTVGIDFTASKGRKKYNTKNSGTILLBSCKIRRDYS FLDYILGGCQLMFTVGIDFTASKGRKKYNTKNSGTILLBSCKIRRDYS FLDYILGGCQLMFTVGIDFTASKGRKKYNTKNSGTILLBSCKIRRDYS FLDYINGGCASSACLP TNPFCGGVDGITQAGAYSACLP GKPKHLGVPNGRWLAAVSDGLSSTTGPCGCGGGGSSLGIHSL PSGGSSPPTPTEGQVANSHALJSFRLLQDPLGLAYPTEPLKKEFS AENVTFWKACERFCQIPASDT FREGGSPPTTEGQVANSHALJSFRLLQDPLGLAYPTEPLKKEFS AENVTFWKACERFCQIPASDT FREGGSPPTTEGQVANSHALJSFRLLQDPLGLAYPTEPLKKEFS AENVTFWKACERFCQIPASDT FREGGSPPTTEGQVANSHALJSFRLLDQPLGLAYPTEPLKKEFS AENVTFWKACERFCQIPASDT FREGGSPPTTEGQVANSHALJSFRLLDQPLGLAYAPTGALFKKEFS AENVTFWALACERFCQIPASDT FREGGSPPTTEGQVANSHALJSFRLLDQPLGLAYAPTGALFGCANSHALSG GKPKHLGVPNDAMARAAAKTAMEETALWQ FREGGSPPTTAGTTGTTSTTTTHATAGTAGTATAGTTTTHATAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG	0,14	109	1410	
TIVSSKITRPLILLINDRPAGKGLITIAAGKISDNRVITISLAG RRLDKKDIPEKSIPPLEFYKRGDORKMHLIPEVIKYTIDPW KPFTVPIVSLCDGDMEKPIQVMCYDYDNDCGHDFIGEFQTSVSQ MCBARDSVPLEFECINPKKGRKKRIYRNSGIIILBSCKIRDVS PLDYIIGGCQLMFTVGIDFTASKGMPLDPSSLHYINFMGTINELL SAINAVGGIIQDYDSDRWFPALGFGAQLPPDWKVSHEFAINFMP TNPFCSGVDGIAQAYSACL AND TNPFCSGVDGIAQAYSACL FRANCH AND THE SAINAVGGIPPOKRYDHISGMP GKRYHLGYWRORWILAVSDGISSTTGPGGGGRGSSLSIHSL PSGPSSPPPTEEQPVASWALSFERLLQDPLGLAYFTEFLKKEFS AEMVTHNRACERPCGIPASDT 115 896 LFAMSGFERNINTDFYGTSYSIDDOSGOSYDYGGSGGYSKGYAG GAGGAPARPSGSEEPRAALBERDIMSARAAARSTAMEETAIWEQ HTVTLHRVSLCCSK FRANCHFRANTDFYGTSYSIDDOSGOSYDYGGSGGYSKGYAG YDYSOGGRPVPPDMMOPQOPYTGGIYQPTQAYPPASSPOPFYGNN FEDEPPLLEEBLGINFDHIWGXTTLVHLBYGSIMMETDLAG PMVFCLAFGATLLLAGKIQFGYVYGISAIGCLGMFCLLNIMSMT GVSFSGVASVLGYCTLLIMFLLISSFAVIFSLQGMVGIILTAGTIG FRANCHFRANTO FYRPEEQDEEBLEGINFDHIWGXTTLVHLBYGABLISVF GYSASXIFISALAMBGQOLLVAYPCALUSPALISVF 6718 290 599 KGSSTVFGTILFSLKWHNSGLCKFFETGGWTTFFKGGTFFDVA VIFTEBESLGLIDPVCRNLYDQVWLRINFFRINGSHIPPKHDVL LEKKLDIMKTATO FYRPEEQDEEBCGKCHKMRNDFISGALINCDPIAMSQCSSDHGCEFT DLDSDDDXIEKPNNFMKDSASQDNGLSRKISRKRVCSSDSDSSL QVVKXSSKARTGLLBITTRCAATAANKIKLMSDVBDVLBINHT RSKNGKKRPHLACTTAKKKLSDCBGSVHCSVPSRQYACBGKPP DPDSRGSTKVLSQALNGDSDSEDMINSSHKKRRTINIKTDAPSK RSKSSVTSSG 6720 3 822 HEVABERGGTYYPGRSTHPGTKRPOHVIETPEGKWELTGYEAA VPTTEKSSPHITOOLDKARDARNIVRLIGGCABETPGBALHG IEBLKVVAAGKKRVIVIGISVGLASFFVAGGMCCMNNTAVFLP VLUGYRPVSMARRPFPPPRILRSLITYPSURABHTQTISLEFSM SVVTLISS 6721 3 822 HEVABERGGTYYPGRSTHPGTKRPOHVIETPEGKWELTGYEAA VPTTEKSSPHITOOLDKARDARNIVRLIGGCDABIFGEGALHG IEBLKVAAGKKRVIVIGISVGLASFFVAGGMCCMNNTAVFLP VLUGYRPVSMARRPFPPPRILRSLTYPPSURABHTQTISLLFSM SVVTLISS LITTMYOVAGKVQBVLKERDGGJAVT.SGGGTSGRMAP LMSVSFNQLMKGLGGKPLYYTILLAGGDRSVVASGGTSGRMAP LMSVSFNQLMKGLGGKPLYYTILLAGGDRSVVASGGTSGRMAP LMSVSFNQLMKGLGGKPLYYTILLAGGDRSVVASGGTSGRMAP LMSVSFNQLMKGLGGKPLYYTILLAGGDRSVVASGGTSGRMAP LMSVSFNQLMKGLGGKPLYTTLLAGGDRSVVASGGTSGRMAP LMSVSFNQLMKGLGGKPLYTTLLAGGDRSVAVGGGTSGRMAP LMSVSFNQLMKGLGGKPLYTTLAGGDRSVAVGGCTSGRMAP LMSVSFNQLMKGLGGKPLYTTLAGGDRSVAVGCTBABHDGA GEBUSTURINGENSPARABHTGLAGGTSGA				1
RRIDKKDLFGKSDPFLEFYKPGDDOKMMLUHRIEVIKYTLDPUM KPPTVPLINSLCCDMEME IDVOMCTOYDMOEDTGEFOTSVSO MCEARDSVPLEFECINPKKQRKKKNYKNSGIIILRSCKINRDYS PLDYILGSCQUMFUVGIPTASNGBPLDPSSHYINMGTNELL SAIMANGGIIQDVDSDKHFPALGFGQLPPDMKVSHEFAINFNP TNPFCSGVDGIAQAVSACLP GPAGARSSGSHCLPATVQALAGAAHSPHGGQPPRKGPLIGSGMP GKPKHLGVPNGRWLLAVSDGELSSTTGPGGGGEGGSSLSIHSL PSGPSSPPPTEEQPUANSHALSFERLLQDPLGLAYFTEFLKKEFS AZMVTEWKACSRFCQLPASDT 6716 1 176 GAGGPAPRSFGSEEPRALERDKMSARAAAKSTAMESTAIWEQ HTVTLHRVSLCCSK 6717 115 896 LFAMSGFERNINTDFYGTSYSIDDOSQOSYDYGGSGGPYSKQYAG YDYSQGGRPVPPDMMQPQPYTGQIIQPTQAYYPASPQPPYGN FEDEPPLLERLGINFDHIWGRTLTVLHPLKVADGSINMETDLAG PMYFCLAFGATLLLASKIGTGYVYGISACLMFCLLMFLMIMSMT GVSFGCVASVLGYCLLPHILLSSFAVIFSLQGMUGILLTAGIIG WCSPSAKSITSIALMBGQCQLAVAPCALLMFCLLMFLAMIMSMT GVSFGCVASVLGYCLLPHILLSSFAVIFSLQGMUGILLTAGIIG WCSPSAKSITSIALMANGQLUAYPCALLMFCLMFCLLMFLMSMT GVSFGCVASVLGYCLLPHILLSSFAVIFSLQGMUGILLTAGIIG WCSPSAKSITSIALMANGQLUAYPCALLMFCLMFCLMFLLMMSMT GVSFGCVASVLGYCLLPHILLSSFAVIFSLQGMUGILLTAGIIG WCSPSAKSITSIALMANGQLUAYPCALMFCLMFCLMFLLMMSMT GVSFGCVASVLGYCLLPHILLSSFAVIFSLGYGGTLMFFKDVA VITTEERIGLIDPVCRNLYQDVMLANFRNILSVGHHPRKDVFL 6718 290 599 KQSSTVFGTILFSLKWHNSGLCKFFETGGMTTFKSGLTFKDVA VITTEERIGLIDPVCRNLYYDDVMLANFRNILSVGHHPRKDVFL GVSFSAKSITSIALARG CVSKKSKARTGLLRTRCAATAANKIKLMSDVBSVJENVHT RSKNGKKKDLHLACTTAKKKLSDCGGSVHCKPEDGUVENUNGT GNUTSSSILTITMVQVAGKVQEVLKEPDGUVENUNGGGTSGRMAF LMSVSSTNOLKKGLGGGRPLYTTLLAGGDRSVVASRGEFDBAHIG IEBLKVAAGAKRVIVIGISUGLASPFVAGGMCCMNTTAVFLP VLVGYRPVSMARHPFPPRILRSLTVPPSLRAPHYQITSLLFSM SVVTLISB 6721 3 822 HEVAEEAGGTVYPQRGTMFGTKRPGHVIETPEPGKWELTGYEAA VPITEKSNPLITONDOKADAENIVRLLGQCDAEIFQBEGALSTY QRIYSSSILTITMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSTNOLKKGLGGKPLYTTLLAGDDRSVVASRGSTGSAMAP LMSVSTNOLKKGLGGKFLYTTLLAGDDRSVVASRGSTGSAMAP LMSVSFNOLKKGLGGKFLYTTLLAGDRSVVASRGSTGSAMAP LMSVSFNOLKKGLGGKFLYTTLLAGDRSVVASRGSTGSAMAP LMSVSFNOLKKGLGGKFLYTTLLAGDRSVVASRGSTGSAMAP LMSVSFNOLKKGLFGGAFLYTTLAGORGVVAGRADCCMNTTAVFLP VLVGYRPVSMARHPFPPPRILRSLLTVFSLRAPHYQITSLLFSM SVVTLISB 6722 1 390 RSMSKRTWOLKDEGSKEEDAAGSTTTLAGVQGVCCMNTATAVFLP VLVGYRPVSMARHPFPPPRIL	ł	}		1
KPFTVPLVSLCDGDMEKPIQVMCXVDXDGGHDFIGBPQTGSVGO				I
MCCRARDSVPLEFECINPKKQRKKNYYNNSCIIILRSCKINRDYS PLDYIIGGCQLMFYVGLDFTANGNPLDPSSLHYINFMGTNEYL SAIWAVGQIIQDYDSDKMFPALGFQQLFPDWKVSHEFAINFNP TNPPCSGVDGIIQAYSACLP GPÄGÄBSGSIHCLDFTVQALAGARAHSPHGQPPRRGPLIGSGMP GKPKHLGVPNGRMVLAVSDGELSSTTOPQGQGEGRGSLSISHSL SGPSSPPPTEEDVASWALSFERLLQDPLGLAYFTEFLKKEFS AENVTFWKACERFQQIPASDT 115		1		
### PLDY ILGGCQLMPTVGIDETASHONPLDPSSLHYINDMGTNEYL SAINAVGQIIQDYDDRMFPALGPGAQLPPDMKVSHEFAINFND TNPFCSGVDGIAQAYSACLP 6715 32 493 GPÄÄABSGSLHCLPATVQALAGAAHSPHGQDPRRGFLIGSGMP KRPHLGYMPNGRMLANVSDGLISSTTOPQGCGEGRGSSLSIHSL PSGPSSPPPTEEDVASMALSFERLLQDPLGLAYFTEFLKKEFS AENVTFWKACERFQQIPASDT 6716 1 176 GAGGPAPRSFGSEEPRAALERDKHSARAAAKSTAMEETAIWEQ HTVTLHRVSLCCSK LTAMAGGERFANTDFYGTSYSIDDQSQQSYDYGGSGGFYSKQYAG YDYSQQGRRVPPDMMQPQDPYTGQIYQPTQAYTPASPQPPYGNN FEDEPPLLEELGINFDHIWQKTLTVLHPLKVADGSIMNETDLAG PMVFCLARGATLLLAGKIQFGYVVGISAIGCLGMFCLLANLMSMT GVSFGCVASVLGVCLLMTLLSSPAVIFSLQGMVGIILTAGIIG WCSFSASKIFISALAMBGQQLLVAYPCLAYOVALDYSIMNETDLAG PWFCLARGATLLLAGKIQFGYVVGISAIGCLGMFCLLANLMSMT GVSFGCVASVLGVCLLMTLLSSPAVIFSLQGMVGIILTAGIIG WCSFSASKIFISALAMBGQQLLVAYPCLAYOVALDYSIMNETDLAG PWFCLARGATLLLAGKIQFGYVVGISAIGCLGMFCLLANLMSMT GVSFGCVASVLGVCLLMTLLSSPAVIFSLQGMVGIILTAGIIG WCSFSASKIFISALAMBGQQLLVAYPCLAYOVALDYSIMP 6718 290 599 KQSSTVPGTILPSLKWEINSGLCKYPETGGMTTFKEGLTFKDVA VIFTEEBLGLLDPVQRNLYQDVMLKNFRNLLSVGHMPKHDVFL LEEKKLDIMKTATQ 6719 1 691 PTRPEEQDREDGKCHKMENNPISCNLNCDDFLAMSQCSDHGCET DLDSDDDLKJERPNNFRWADSASQDMCLSRKISRKRVCSSDGSSL QVVKKSSKARTGLLRITRRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQVACEGKPP DPDSEGSTKVLSQALANGDSDSEDMLNSEHKHRHTNIHKIDAPSK RKSSSYTSSG 6720 3 822 HEVAEERAGTVYPQGTMMGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKAADAENIVELLGQCDASIFQEBGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGTSGGRAP LMSVSTNQLMRGLGQRPIYTTLIAGSDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFMYVSMARHFPPPPFILRSLTVPFSTRAPHYQITSLLFSM SVVTLISB HEVAEERAGTVYPQGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQUDLRAADAENIVELLGQCDASIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGTSGRMAP LMSVSTNGLMRGLGQRVLTVTLIAGGRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFMYVSMARHFPPPPFILRSLTVFFSTRAPHYQITSLLFSM SVVTLISB FERSKLRTMQALPMAVLFLLLFLCTFQAADAMAQAIYVALGEAVE PGRESSLRLLGNYSLMLBGSKEEDDAGRYWACAVLCQHINTYDNW VCQYCTARMADFGISAGGFVAVWMCKSSPVALKGULOQLTITSLSBLL G723 173 659 VCQYCTARMADFGISAGGFSARGESFTLVAQVQVGRPAPDFGK PGRESSLRLLGNYSLMLBGSKE				· · · · · · · · · · · · · · · · · · ·
SAIMAUGQI I QDVDSDIMPPALGFGAQLPPDMKVSHEFAINFNP TNPPCSGVDG IAQAYSACLP 6715 32 493 GPÄGABSGSILICIPATVQALAGAAHSPHGGQPPRRGPLIGSGMP GKPKHLGVPNGRMVLAVSDGELSSTTGPQQQGGGRGSLSIHSL SGGPSSPPPTEGDVASMALSFERLLQGLAYFTEFLKKEFS AENVTEWKACRFQQI PASDT 6716 1 176 GAGGPAPRSFGSEEFRAALERDKMSARAAAKSTAMEETAIWEQ HTVTLHRVSLCCSK 6717 115 896 LPAMSGFENLHTDPYGTSYSIDDQSQQSYDYGGSGFYSKQYAG JVSSQGRVPPDMMQPQQPYTGQIYQPTQAYTPASPQPPYGNN FEDEPPLLEBLGINFDHIWQKTLTVLHPLKVADGS INNETDLAG PMVPCLAFGATLLLAGK LOFGVSVG1G INCIGNMENTLIMEM GVSFGCVASVLGYCLLPMILLSSPAVIFSLQGMVGIILTAGIIG WCSFSASKI PISALAMEGQOLLVAYPCALLISVPYALLSVP 6718 290 599 KQSSTVPGTIJPSIKWHNSGLCKFFETGGMTTFKEGLITFKDVA VIFTEELGLLDPVQRNLYQDWLKNFRNLLSVGHHPPKHDVFL LEKEKKLDIMTATO 6719 1 691 PTRPEEQDEEDGKCHKKHRNPITSCGNLSVGSDSDSL QVVKKSSKARTGLLRITTRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKRPLHLACTTAKKKLSDCEGSVHCEVPSGYACGGKPP DPDSEGSTKVLSQALANDSDSEDMINSEHHHTTHIKHDAPSK RKSSSTTSG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRPQHVIETPEEGKWELTGYEAA VPITEKSNPLTQUDGKARAGEVILYTVLIAGGTSGTSGRMAP LMSVSTNGDLKKGLGGVINTYLLAGGCDASIFQESGQALSTY QRLYSSSILTTMVQVAGKVQEVLLEPDGGUVLSGGTSGRMAP LMSVSTNGDLKKGLGGVINTYLLAGGCDASIFQESGQALSTY QRLYSSSILTITMVQVAGKVQEVLLEPDGGGVAGGGTSGRMAP LMSVSTNGDLKKGLGGVINTYLLAGGCDASIFQESGQALSTY QRLYSSSILTTMVQVAGKVQEVLKEPDGGGVAGGGTSGRMAP LMSVSTNGDLKKGLGGVINTYLLAGGTSGRWAF LMSVSTNGDLKKGLGGVINTYLLAGGCDASIFQESGQALSTY QRLYSSSILTTMVQVAGKVQEVLKEPDGGGVAGGGTSGRMAP LMSVSTNGDLKKGLGGVINTYLLAGGCDASIFQESGQALSTY QRLYSSSILTTMVQVAGKVQEVLKEPDGGGVAGGGTSGRMAP LMSVSTNGDLKKGLGGVINTYLLAGGCDASIFQESGQALSTY QRLYSSSILTTMVQVAGKVQEVLKEPDGGGVAGGGTSGRMAF LMSVSTNGDKKGLGGVINTYLLAGGCDASIFQESGALSTY QRLYSSSILTTMVQVAGKVQEVLYTLIPSGARSVASRGGTEGBALHG IEELKKVAAGKKRVIVIGISVGLAPPVAGQMDCCMNTAVPLP VLUGFPPVSMARHPFPPPRILRSLTVFPSLRAPVGTSLLFSM SVVTLISB 6722 1 390 RSMSKFTMGALPMAVLFLLEGCTPGAADAMQAIYVALGEAKP PGRESELRLLGNYSLMLEGSKEEDAGRYWGAVALGALTGVALGGCTGALTY GNGGKVYENIKGLLGGARGESPAAKGSLGUTGKALGALTT GNGGKVYENIKGLLGGARGESPAALKGLOVALGALTGCHNYGNM	1			
6715 32 493 GPAGAESGIHCLPATVQALAGAHS PHGGQP PRRGPLIGSGMP GKPKHLGVPNGRMVLAVSDELISTTGPQGGEGGSSIS INSL PSGPSSPFPTEQPVASWALSFERLLQDPLGLAYFTEFLKKEFS ARNITWKACERFGQI PASDT 6716 1 176 GAGGPAPRSFGSEBFRALERDKMSARAAAKSTAMEETAIWEQ HTVTLHRVSLCCSK 6717 115 896 LPAMSGFEMLNTDFYQTSYSIDDGQQSYDYGGSGGPYSKQYAG YDYSQGGRFVPPDMMQPQQPYTGQIYQFTQAYFDASPQPFYGNN FEDEPPLERELGINFDHIWGKTLTVLHPLKVADGS INNETDLAG PMVPCLAFGATLLLAGKIQFGYVYGISAIGCLGMFCLLNIMSMT GVSFGCVASVLGYCLLDMILLSSFAVIFSLGGWGIILTAGIIG WCSFSASKIFISALAMBGQQLLVAYPCALLAGWFALLISVF 6718 290 599 KQSSTVPGTILPSLKWINSGLCKFPETGSKMTTKSGLTFKDVA VIFTEEEGLLDPVGYNIVQDVMLRNFRNLLSVGHHPFKDVFA LEKEKKLDIMKTATO 6719 1 691 PTRPEEGDREDGKCHKMEMNP YSGNLNCDFIAMSQCSSDHGCET DLDSDDDAKIERNNFRMDSASQONGLSKKISRKRVCSSDSDSSL QVVKKSSKARTGLRITRCAATAANKIKLMSDVEDVSLENVHT RSNGRKRULHLACTTAKKKLISDGSVICEVPSEGGVACGKFP DPDSEGSTKVLSQALNGDSDSEDMINSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTODLDKADABNIVRLLGGCDABIRGESGGALSTY QRIYSESILTTTMQVAGKVQDLKEPDGGIVVLSGGGTSGNAP LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEBLKVAAGKKRVIVIGISVGLSAPFVAGMCCNNINTAVELP VLUGFRPVSMARHPPPPPRILRSLTVPPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTODLDKADABNIVRLLGGCDABIRGEGGALSTY QRIYSESILTTIMVQVAGKVQDUKEDPGGIVVLSGGGTSGNAP, LMSVSFNQLMKGLGGKPLYTYLIAGGDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGMCCNNINTAVELP VLUGFRPVSMARHPPPPPRILRSLTVPPSLRAPHYQITSLLFSM SVVTLISE 6721 3 900 RSWSKTWGADENAVYLGGGRSTTULAQUGGRSGTGGRAPF LMSVSTNOLMKGLGGCKPLYTYLLAGGDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGMCCNNINTAVELP VLUGFRPVSMARHPPPPPRILRSLTVPPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKTWGADPMAVFLFLLGGGDRSVVASREGTEDSALHG IEBLKKVAAGKRVIVIGISVGLSAPFVAGMCCNNINTAVELP VLUGFRPVSMARHPPSPSTLARSGTTILVAQVQVGRPAPDFGK PGRSSLRLLGNYSLMLEGSKEEDAGRTWCAVLOGHHNYONW VCQYCTARMADFGISAGGFVAVVAVWDKSSPVEALKGLUGKLGLDT GNGGRVSVENIKQLLGSAHESSFTILLSGLVFGSTTLIKSABIL				_
6715 32 493 GPAGAESGSLHCLPATVQALAGARHSPHGGOPPRRGPLIGSGMP GKRKHLGVPNGRMVLAVSDGELGSTTGPCGGGEGRGSSLSIRLS PSGPSSPPTEGEVAWALSFERLQOPLGLAYFTEFLKKEFS AENVTEWKACERFQQIPASDT 6716 1 176 GAGGPAFRSFGSEEPRALERDKMSARAAAKSTAMEETAIWEQ HTVTLIRVSLCCSK 6717 115 896 LFAMSGFERLINTDFYGTSTSIDDGSQOSYDYGGSGGPYSKQYAG YDYSQGRFVPPDMWQPQPTTGJTQPTQAYFTASFQPFYGNN FEDEPPLLERLGINFDHIWGKTLTVLHPLKVADGSIMNETDLAG PMVFCLAFGATLLLAGKIQFGYVYGISATGCLGMFCLLNLMSMT GVSFGCVASVLGYCLLDMILLSSFAVIFSLGGMGILLTAGGIG WCSFSASKIFISALAMRGQQLLAYPCALLDAYVPALLISVP 6718 290 599 KQSSTVPGTIFSLGKMINSGLCKFPFTGGKMTTFKSGLTFKDVA VIFTEEELGLLDPVGRNLYQDVMLRNFRNLLSVGHHPFKHDVFL LEKEKKLDIMKTATQ 6719 1 691 PTRPERGDEDGKCHKMEMBPISGNLNCDPTAMSQGSDHGCET DLDSDDDKIEKFNNFFMKDSASQDNGLSRKISRKVCSSDSDSSL QVVKKSKARTGLLRITRCAATAANKIKMSDVEDVSLENVHF RSKNGRKKPLHLACTTAKKKLSDCGSVHCCVSPSEGYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMLNSEHKRHTNIHKIDAPSK RKSSTVTSG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKMELTGYEAA VPITEKSNPLINGGLGGKPLYTYLIAGGDRSVVASREGTEDSALHG LELKKKVAAGKKRVLVIGISVGLGSPTGGRAPA LMSVSFNQLMKGLGGKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVLVIGISVGLGSPVAGGMDCCNNTAVELP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLITVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGGKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSABFVAGGMDCCNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLITDQLDKAADAENIVRLLGCDAEIFQEEGGALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGGKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSABFVAGGMDCCNNTTAVFLP VLVGFNPVSMARHPPPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSMSKRTWQALFGARSFTTIVAQVQVGRPAPDFGK PGRSSLRLLGNYSIMLBGSKEDAAGSFTTIVAQVQVGRPAPDFGK PGRSSLRLLGNYSIMLBGSKEDAAGSFTTIVAQVQVGRPAPDFGK PGRSSLRLLGNYSIMLBGSKEDAAGSFTTIVAQVQVGRPAPDFGK PGRSSLRLLGNYSIMLBGSKEDAAGSFTTIVAQVQVGRPAPDFGK PGRSSLRLLGNYSIMLBGSKEDAAGSFTTIVAQVQVGRPAPDFGK PGRSSLRLLGNYSIMLBGSKEDAAGSFTTIVAQVQVGRPAPDFGK PGRSSLRLLGNYSIMLBGSKEDBAAGSFTTIVAQVQVG				l fight and the second
GKPKHLGVPNGRMVLAVSDGELSSTTGPQGQGEGRGSSLSIHSI PSGPSSPFPTEGQVASWALSFERLLQDPLGLAFFTEFLKKEFS ARNITWKACERFQQIPASDT 6716 1 176 GAGGPAPRSFGSEBFRALERDKMSARAAAAKSTAMEETAIWEQ HTVTLHRVSLCCSK 6717 115 896 LFAMSGFENLNTDFYQTSYSIDDGSQGSYDYGGSGGPYSKQYAG YDYSQGGRFVPDDMWQPQQPYTGQIYQFDGAYTPASPQPFYCNN FEDEPPLEBELGINPDHIWGKTLTVLHPLKVADGS IMNETDLAG PMVFCLAFGATLLLAGKIQPGYVGISATGCLMFCLLALMSMIT GVSFGCVASVLGYCLLPMILLSSPAVIFSLGMVGILLTAGIIG WCSFSASKIFISALAMSGQQLUVAPPCALLKGWFALISVF 6718 290 599 KQSSTVPGTILFSLKWINSGLCKFFETGGKMTTFKGGLTFKDVA VIFTEEEGLLDPVGCNRLYQDVMLRNFRNLLSVGHHPFKRDVFL LEKSKKLDIMKTATO 6719 1 691 PTREEGLLDPVGCNRLYQDVMLRNFRNLLSVGHHPFKRDVFL LEKSKKLDIMKTATO PYPEEGDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET GLASSKATGLLRITRCAATAANKKLMSDVEDVSLENVHT RSNGRKKPLHLACTTAKKKLSDSGVICSVPSGQYAGGKPP DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEERGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLITDDLDKADABNIVRLLGCCDABLFQEEGQALSTY QRIYSSSILTTMVQVAGKVQEVLKEPDGGUVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLLAGCDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFRPVSMARHPFPPPFRILRSLTVPFSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEERGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADABNIVRLLGCCDABLFQEEGGALSTY QRIYSSSILTTMVQVAGKVQEVLKEEDGGIVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLLAGCDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFRPVSMARHPFPPPFRILRSLTVPFSLRAPHYQITSLLFSM SVVTLISE 6721 3 90 RSMSKRTWGALPMAVLFLLLFLCADDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFRPVSMARHPPPPPPRILRSLTVPPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSMSKRTWGALPMAVLFLLLFLCSDFQAADMQAIVVALGGRTSGRAVE LPCPSSPSTLHGDEHLSWFCSPAAGSSTTILVAQVQVGRPAPDDGK PGRSSLRLLGNYSLWLGGGSTGTTLVAQVQVGRPAPDDGK PGRSSLRLLGNYSLWLGGGSTTLVAQVQVGRPAPDDGK PGRSSLRLLGNYSLWLGGGSTTLVAQVQVGRPAPDDGK PGRSSLRLLGNYSLWLGGGSTTLVAQVQVGRPAPDDGK PGRSSLRLLGNYSLWLGGGSTTLVAQVQVGRPAPDDGK PGRSSLRLLGNYSLWLGGGSTTLVAQVQVGRPAPDDGK PGRSSLRLLGNYSLWLGGGSTTLVAQVQVGRPAPDTGK PGRSSLRLLGNYSLWLGGGSTTLVAQVGVGRPAPDGK PGRSSLRLLGNYSLWLGGGSTTLVAQVGVGRPAPDGK PGRSSLRLLGNYSLWLGGGSTTL	6715	32	407	
PSGPSSPPPTEGDVASNALSFERLLQDPLGLAYFTEPLKKEFS ARNVTPKKACERFQQIPASDT 6716 1 176 GAGGPAPRSFGSEEPRAALEERKKNSARAAAKSTAMEETAIWEQ HTVTLHRVSLCCSK 6717 115 896 LPAMSGFENLINTDFYQTSYSIDDOSQOSYDYGGSGPYSKQYAG YDYSQGGRVPPDMWDPQQPYTGQIYQPTQAYTPASPQPFYGNN FEDEPPLLEELGINFDHIWQKTLTVLHELKVADGSIMNETDLAG PMVPCLAFGATLLLAGKIGFGYVYGISAIGCLGMFCLINLMSMT GVSFGCVASVLGYCLLPWILLGSPAVIFSLGWMGTLITAGIIG WCSFSAKIFISALAMBGQQLLVAYPCALLYGVFALISVF 6718 290 599 KQSSTVPGTILFSLKWHNSGLCKFPETGGKMTTFKKEGLTFKDVA VIFTEEBLGLIDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVFL LEKEKKLDIMKTATO 6719 1 691 PTRPEEQDREDGKCHKMEMINPISGNLNCDPIAMSQCSSDHGCET DLDSDDDKLEKPINTMKDSASQDMGLSRKISRRVCSSDSDSSL QVVKKSSKARTGLLRITRCAATMIKIKLMSDVEDVSLENNHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACGGKPP DPDSEGSTKVLSQALINGDSDSEDMINSEHHRHTNILKDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMFGTKRFCHVIETPEFGKWELTGYEAA VPITEKSNPLTQDLKADAENIVELLGGCDABIFQEEGGALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGTSGRMAP LMSVSFNQLMKGLGQKPLYTTLIAGGDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGGMCCNNITAVSLP VLVGFRPVSMARHPPFPPRILRSLTVPPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMFGTKRFCHVIETPEFGKWELTGYEAA VPITEKSNPLTQDLKAADAENIVELLGGCDABIFQEEGGALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTTLIAGGDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGGMCCNNITAVSLP VLVGFRPSMARHPPPPPRILRSLTVPFSLRAPHYQITSLLFSM SVVTLISE 6721 3 90 RSWSKRTWQALGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEBLKKVAAGKRRVIVIGISVGLSAPFVAGGMCCNNITAVSLP VLVGFRPSMARHPPPPPRILRSLTVFFSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALFMAVLFLLLFLCGTPQAADMQAIYVALGEAVE LPCPSPSTLHGBEHLSWFCSPAACSFTTLVAQQVGRPAPDEGK PGRESKLRLLGNYSLMLEGSKEEDAGRYWCAVLGQHHNYQNW GNGRVSVSNINGLLGSAAAGSFTTLVAGQVGCRPAPDEGK PGRESKLRLLGNYSLMLEGSKEEDAGRYWCAVLGQHHNYQNW GNGRVSVSNINGLLGSAAGGFTTLHSABIL	3,13	' '	423	
ABINTTEWKACERFQQIPASDT 6716 1 176 GAGGPAPRSFGSEEPRAALERDKMSARAAAKSTAMEETAIWEQ HTVTLHRVSLCCSK 6717 115 896 LPAMSGPENLNTDFYQTSYSIDDQSQQSYDYGGSGGPYSKQYAG YDYSQQGRFVPPDMMQPQQPYTGQIYQPTQAYTPASPQPFYGNN FEDEPPLLERLGINPDHLWQKTLTVLHPLKVADGSIMMSTDLAG PMVPCLAFGATLLLAGKIQFGYVYGISAIGCLGMFCLLAMSMT GVSPGCVASVLGYCLLPMILLSGPAVYFSLQMVGIILTAGIIG WCSPSASKIPISALAMKGQQLLVAYPCALLYGYPALISUF 6718 290 599 KQSSTVPGTILPSLKWHMSGLCKFFETGGRWTFFKDVA VIFTEEBLGLLDPVQRNLYQDVMLKNFRNLLSVGHMPFKHDVFL LEKEKKLDIMKTATQ 6719 1 691 PTRPEEQDEEDCKCHKMENNFISCHLDSVGRKTSFKRVCSSDSDSL QVVKKSSKARTGLLRITRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKHLHACTTAKKKLSDCESSVHGEVET QVVKKSSKARTGLLRITRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKHLHACTTAKKKLSDCESSVHGEVEPSGYACEGKPP DPDSEGSTKVLSQALNGSDSDEDDMINSEHKHRTNIHKTDAPSK RKSSSVTSGG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLITQDLDKADAENIVELLGQCDAEIFQSEGGALSTY QRIYSESILITMVQVAGKVQEVLKEPDGGIVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLTYTLLAGGDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLUGFMPVSMARHPFPPPRILRSLTVPFSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLITQDLDKADAENIVELLGQCDAEIFQSEGGALSTY QRIYSESILITMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLTYTLLAGGDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLUGFMPVSMARHPFPPPRILRSLTVPFSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLITQDLDKADAENIVELLGQCDAEIFQSEGGALSTY QRIYSESILITMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLTYTLAGGDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLUGFMPVSMARHPFPPPPRILRSLTVPFSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALEGSCEPGAGSTTTLVAQQVGRPAPDEGK PGRESKLRLLGNYSLMLEGSKEEDAGRYWCAVLGQHHNYQNW CYCYTARMAPGISAGQFVAVWWNSCSPVEALKGLVDKLGALT GNEGRVSVENINGLLGSAHEEDSGFTTLVAGQVGVARAPDEGK PGRESKLRLLGNYSLMLEGSKEEDAGRYWCAVLGQHHNYQNW CYCYTARMAPGISAGQFVAVWWNSCSPVEALKGLVDKLGALT GNEGRVSVENINGLLGSAHEESSFDIILSGLVPGSTTLHSAEIL			•	
6716 1 176 GAGGPAPRSFGSEEPRAALERDKMSARAAAAKSTAMEETAIWEQ HTVTLHRVSLCCSK 6717 115 896 LFAMAGGFENLINTDFYQTSYSTDDGSQGYDYGGSGGPYSKQYAG YDYSQQGRFVPPDMMQPQQPYTGQIYQPTQAYTPASPQPFYGNN FEDEPPLLEELGINFDH+WQKTLTVLHPLKVADGSIMMSTDLAG PMVPCLAFGATLLIAGRTGFGYGSGSASLGYGGTGLANIMSMT GVSFGCVASVLGYCLLPWILLGSFAVIFSLQGWGTILTAGTIG WCSFSASKIFISALAMGQQLLVAYPCALLIGYGFALISVF KQSSTVPGTILPSLKWHNSGLCKFPETGGRWTTFKEGLTFKDVA VIFTEEELGLDPVQRNLYQDVMLRNFRNLLSVGHHPFKHDVFL LEKEKKLDIMKTATQ LEKEKKLDIMKTATQ LOUVKKSSKARTGLLRITRCAATAANKIKLMSDVEDVSLENVHT RSKNGKKKLHLACTTAKKKLSDCGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK RKSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEFGKWELTGYEAA VPITEKSNPLTODLDKADAENIVRLLGGCDAEIFQEEGAALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGGKPLYTTLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMCCMNNTAVSLP VLVGVFRPVSMARHPFPPPRILRSLTVPFSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVPQRGTMPGTKRFQHVIETPEFGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGGCDAEIFQEGGALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGGKPLYTTLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMCCMNNTAVSLP VLVGFRPVSMARHPFPPPRILRSLTVPFSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVPQRGTMPGTKRFQHVIETPEFGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGGCDAEIFQEEGALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLIGGKPLYTTLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMCCCNNNTAVSLP VLVGFNPVSMARHPFPPPRILRSLTVFFSLRAPHYQITSLLFSM SVVTLISE 6721 3 990 KGRSTUSNINGLIGGKPLYTTLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGGMCCCNNNTAVSLP VLVGFNPVSMARHPFPPPRILRSLTVFFSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSMSKRTWQALPMAVLPLLFLCGTPQAADNMQAIVVALGEAVE LPCPSPSTLHGDELLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESSLERLIGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW CPGRESSLERLIGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW CPGRESSLERLIGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW CPGRESSLANGLGANDAGAIVALGGALT GNEGRYSVENNINGLLGSAGGFVAVWNOSSSPCALKGLVDKLGALT GNEGRYSVENNINGLLGSAGFVAVWNOSSSPCALKGLVDKLGALT GNEGRYSVENNINGLLGSAGFTTLHSAEIL			ļ	1
6717 115 896 LPAMSGERNINTDFYQTSYSIDDQSQQSYDYGGSGGPYSKQYAG LPAMSGERNINTDFYQTSYSIDDQSQQSYDYGGSGGPYSKQYAG YDYSQQGRYVPPDMMQPQQPYTGQIYQPTQAYPASPQPFYGNN FEDEPPLLEELGINFDHIWQKTLTVLHPLKVADGSIMNETDLAG PMVFCLAFGATLLLAGKIQFGYYYGISAIGCLGMFCLLNILMSMT GVSFGCVASVLGYCLLPMILLSSPAVJFSLQGMVGILITAGIIG WCSFSASKIFISALAMEGQQLLVAYPCALLYGYPALISVF 6718 290 599 KQSSTVPGTILFSLKWHNSGLCKFPETTGKWTTFKEGLTFKDVA VIFTEEBLGLIDPVQRNLYQDVMLRNFRNLLSVGHHPPKHDVFL LEXEKKLDINKTATQ 6719 1 691 PTPPEEQDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET DLDSDDDKIEKPNNFMKDSASQDNCLSRKISKRKVCSSDSDSSL QVVKKSSKARTGLIRITRRCAATAANKKIMBDVBDVSLENNHT RSKNGRKKPLHLACTTAKKKLSDCEGGVHCEVPSEQVACEGKPP DPDSEGSTKVLSQALMGDSDSEDMINSEKKHHTNIHKIDAPSK RKSSSVTSG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRIYSESILTTMYQVAGKVQEVLKEPDGGLVVLSGGTSGRMAF LMSVSFNDLMKGLGQKPLVTLAGGDRSVVASRGSTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRIYSESILTTMYQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNDLMKGLGQKPLVTYLLAGGDRSVASRGSTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRIYSESILTTMYQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNDLMKGLGQKPLYTYLLAGGDRSVASRGSTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPPILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQQVQGRPAPDPGK PGRESRLRLLGNYSLULEGSKEEDAGRYWCAVLGQHHMYQNW CQYCTARMADFGISAGGFVAVWDKSSPYEALKGLUDKLQALT GNBGRVSVENIKQLLQSAKKESFDIILSGLPVGSTTLHSAEIL GNBGRVSVENIKQLLQSAKKESFDIILSGLPVGSTTLHSAEIL	6716		176	
6717 115 896 LFAMSGFENLNTDFYQTSYSIDDQSQQSYDYGGSGGFYSKQYAG YDYSQQGRFVPPDMMQPQQPYTQGTIQPTQATPASPQPFFGNN FEDEPPLIEBIGINFDHINGKTLTVLHPLKXADGSIMMETDLAG PMVFCLAFGATLLLAGKIQFGYVYGISAIGCIGMFCLLNLMSMT GVSFGCVASVLGYCLLPMILLSSFAVIFSLQGMVGILITAGIIG WCSFSASKIFISALAMSQQLLVAYPCALLYGVFALISVF 6718 290 599 KQSSTVPGTILPSLKWHNSGLCKFFETGGKMTFKEGLTFKDVA VIFTEEBIGLDPVQRNLYQDVMLRNFRNLLSVGHHPPKHDVFL LEKEKKLDIMKTATQ 6719 1 691 PTRPEEQDREDGKCHKMEMNPISGNLNCDPTAMSQCSSDHGCET DLDSDDDKJEKFNNFRKDSASQDNCLSRKISRKRVCSSDSDSSL QVVKKSSKARTGLIRTTRRCAATAANKIKIMSDVBVDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALMGDSDSEMINSEKKHTHTHIHLDAPSK RKSSSVTSSG RKSSSVTSSG RKSSSVTSSG FRASSSVTSSG UPVEXESSILTTMYQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAFFVAGQMDCCMNNTAVFLP VLVGFNPVSMARPPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE FRAMSGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARPPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE FRAMSGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGGALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARPPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE FRAMSKRTWQAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLLAGGDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGMDCCMNNTAVFLP VLVGFNPVSMARPPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE FRAMSKRTWQAGLMAVLFLLLFLCGTPQAADNMQATYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESKLRLLGNYSLWLBGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADPGISAGGFYAVVADVLGCHNYQNW GNGGRVSVENIKQLLQSARKESSFDIILSGLVPGSTTLHSAEIL GNGGRVSVENIKQLLQSARKESSFDIILSGLVPGSTTLHSAEIL	8,10	1 -	1/6	· ~ 1
TOTSQQGRFVPPDMMDPQQPYTGQTYQPTQAYTPASPQPFYGNN FEDEPPLLERIGINFDHIWQKTLTVLHPLKVADGS IMMETDLAG PMVPCLAFGATLLIAGKIGYVYGI SAIGCLGMFCLLNIMSMT GVSFGCVASVLGYCLLPMILLSSFAVIFSLQMYGILITAGI IG WCSFSASKIFISALAMBQQLLVAYPCALLYGVPALISVF 6718 290 599 KQSSTVPGTILPSLKWHNSGLCKFFETGGMTIFKEQLTFKDVA VIFTEEBLGLIDEVQRNLYQDVMLMNFRNLLSVCHHPPKHDVFL LEKEKKLDIMKTATQ 6719 1 691 PTRPEEQDREDGKCHKMEMNPISGNLNCDPIAMSQCSDHGCET DLDSDDDKIRKPNNFMXDSASQONGLSRKISRRRVCSSDSDSSL QVVKKSSKARTGLLRITRCAATAANKIKLMSDVEDVSLBNVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMINSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRFGHVIETPEPGKWELTGYEAA VPITEKSNPLTOQLDKADAENIVELLGGCDABIFDEEGGALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEBLKKVARAKKRVIVJGISVGLSAPFVAGGMDCCMNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVPPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVELLGGCDAEIFQESQALSTY QRLYSESILTTMVQVAGKVQBVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEBLKKVARACKKRVIVJGISVGLSAPFVAGGMDCCMNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 1EBLKKVARACKKRVIVIGISVGLSAPFVAGGMDCCMNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 1EBLKKVARACKKRVIVIGISVGLSAPFVAGGMDCCMNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSMSKRWQALPMAVLFLLLFLCGTPQAADMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLMLEGSKEEDAGRYWCAVLGQHINYQNW CQCYCTARMADFGISAGGPVAVWDKSSSPYBALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	6717	115	000	
FEDEPPLLEELGINFDHIWQKTLTVLHPLKVADGSIMNETDLAG PMVFCLAFGATILLIAGRIQFGYVYGISAIGCLGHFCLLNIMSMT GVSFGCVASVLGYCLLPMILLISSFAVIFSLGMVGIILIMAGNT WCSFSASKIFISALAMEGQQLLVAYPCALLYGVPALISVF 6718 290 599 KQSSTVEGTILPSLKWEINSGLCKFFETGGKMTTFKEGLTFKDVA VIFTEBELGILDPVORNLYQDVMLRNFRNLLSVGHHPFKHDVFL LEKEKKLDIMKTATQ 6719 1 691 PTRPEEGDREDGKCHKWEINFISGLINCDDIAMSQCSSDHGCET DLDSDDDKILBKPNNFMNSDASQDNGLSRKISRKPVCSSDSDSSL QVVKKSSKARTGLLRITRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQVACEGKPP DPDSEGSTKVLSQALNGDSDSEDMINSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKKRCHVIETFEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDABIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFRPVSMARHFFPPSFILRSLTVPPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVGISVGLSAPFVAGGMDCCMNNTAVFLP VLVGFRPVSMARHFFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 1 390 RSMSKRTWQALPMAVLFLLEFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESKLRLLGNYSLWLEGSKEEDDARFWCAVLGQHINYQNW 6723 173 659 VCQYCTARMADFGISAGGTVAVWADKSSPYBALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	6/1/	115	896	
PMVFCLAFGATLLLAGKIQFGYVYGISAIGCLGMFCLLNLMSMT GVSFGCVASVLGYCLLPMILLSSFAVIFSLQMVGILITAGIIG WCSFSASKIFISALAMGQQLLVAYPCALLIYGVPALISVF 6718 290 599 KQSTVPGTILPSLKWHRSGLCKFPETGGKMTTFKEGLTFKDVA VIFTEEELGLLDPVQRNLYQDVMLRNFRNILSVGHHPFKHDVFL LEKEKKLDIMKTATO 6719 1 691 PTRPEEGDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRRRVCSSDSDSSL QVVKKSSKARTGLLRITRRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACBGKPP DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRFCHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVGISVGLSAPFVAGQMCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFCHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGGKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 1EELKKVAAGKKRVIVIGISVGLSAPFVAGQMCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE SVVTLISE 6722 1 390 RSMSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRURLLGNYSLMLEGSKEEDAGRYWAVLGQHRIVYDNW 6723 173 659 VCQYCTARMADFGISAGGFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	1.			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
GVSFGCVASVLGYCLLPMILLSSPAVIFSLQGMVGIILTAGIIG WCSFSASKIFISALMRGQQLLVAPYCALLTYGFALTSVF 6718 290 599 KQSTVPSTIJPSLKWHNSGLCKFPETGGMTTFKEGITFKDVA VIFTEEELGLLDPVQRNLYQDVMLRNFRNLLSVGHHPFKHDVFL LEKEKKLDIMKTATQ 6719 1 691 PTRPEEQDREDGKCHKMEMNPISGNLNCDDIAMSQCSSDHGCET DLDSDDKIEKPNNFWKDSASQDNGLSRKISRRKVCSSDBDSSL QVVKKSSKARTGLLRITTRCAATAANKIKLMSDVEDVSLRNVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMINSEHHRRITNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMFGTKRFQHVIETPEFGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGETESALHG IEBLKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAYFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE SVTTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMFGTKRFQHVIETPEFGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEBLKKVAAGKKRVIVGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE LELKKVAAGKKRVIVGISVGLSAPFVAGQMCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE LELKKVAAGKKRVIVGISVGLSAPFVAGQMCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRURLLGNYSLWLEGSKEEDAGRYWCAVLGQHINYQNW 6723 173 659 VCQCTARMADFGISAGGFVAVVWDKSSFYEALKGLDVKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	1			· · · · · · · · · · · · · · · · · · ·
WCSFSASKIFISALAMBGQQLLVAYPCALLYGVPALISVF	1			
6718 290 599 KQSSTVPGTILPSLKWHNSGLCKFPETGGKMTTFKEGLTFKDVA VIFTEEBLGLLDPVQRNLYQDVMLKNFRNLLSVGHHPFKHDVFL LEKEKKLDIMKTATQ 6719 1 691 PTRPEEQDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKRVCSSDSDSSL QVVKKSSKARTGLLRITRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALMGDSDSEDMINSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGGALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLIGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFYAVWMDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL			;	· ·
VIFTEEBIGLLDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVFL LEKEKKLDIMKTATQ 6719 1 691 PTRPEEQDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET DLDSDDDKIEKPNNFMKDSASCDNGLSRKISRKRVCSSDSDSSL QVVKKSSKARTGLRITRRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAERIVRLLGQCDAEIFQEEGQALSTY QRLYSESILITTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAERIVRLLGQCDAEIFQEGGQALSTY QRLYSESILITTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTTLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADMQAIYVALGEAVE LPCPSPSTLHGDEHLSMFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGGFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	6710	200		1
6719 1 691 PTRPEEQDREDGKCHKMEMNPTSGNLNCDPTAMSQCSSDHGCET DLDSDDKIEKPNNFKDSASQDMGLSRKISKKRVCSSDSDSSL QVVKKSSKARTGLIRITRRCAATAANKIKIMSDVEDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMINSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMFGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILITMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMFGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILITTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGGFVAVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	6/18	290	599	
6719 1 691 PTRPEEQDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGGET DLDSDDDKIEKPNNFMKNDSASQDNGLSRKISRKRVCSSDSDSSL QVVKKSSKARTGLLRITRCAATAANKIKLMSDVEDVSLEBVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTXVLSQALNGDSDSEDMINSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMFGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEQQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHFFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMFGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLLAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHFFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVSFNQLMKGLGQKPLYTYLLAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHFFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSMSKRTWQALPMAVLFLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDFK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGGFVAVWDKSSFVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	1	:		
DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKRVCSSDSDSSL QVVKKSSKARTGLLRITRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMINSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLFLCGTPQAADNMQAIYVALGEAVE PGRESRLRLLGNYSLWLEGSKEEDAGSTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	6710	ļ		
QVVKKSKARTGLLRITRRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMINSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVABEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVABEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQBEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQATYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLIGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGUVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	6/19	. 1	991	
RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLNLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL				I
DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTYYPQRGTMFGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMFGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKFLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	1			
RKSSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLLAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	1			· · · · · · · · · · · · · · · · · · ·
6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAFFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVPPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPPPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWKRTWQALPMAVLFLLLFLCGTPQAADMMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	1			~
VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	6722	3	000	
QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	8/20	. 3	522	
LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	1 .	1		· · · · · · · · · · · · · · · · · · ·
IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	1			1
VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	1			
SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL				F
6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	1]		1
VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	6701			
QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	0/21	3	822	,
LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	-			
ieelkkvaagkkrvivigisvglsapfvagqmdccmnntavflp vlvgfnpvsmarhpfppprilrsltvfpslraphyqitsllfsm svvtlise 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIyvalgeave Lpcpspstlhgdehlswfcspaagsfttlvaqvqvgrpapdpgk pgresrlrlgnyslwlegskeedagrywcavlgqhhnyqnw 6723 173 659 Vcqyctarmadfgisagqfvavvwdksspvealkglvdklqalt gnegrvsvenikqllqsahkessfdiilsglvpgsttlhsaeil	1			
VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL				1
SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	t			<u> </u>
6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADMQATYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	1			1
LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	<u> </u>			
PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	6722	1	390	
6723 173 659 VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL				,
GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL				
	6723	173	659	
AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL	1			
				AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL

Molecuted Medication Content of the content o	SEQ	Predicted	Predicted end	
No: not.leot.ide				Amino acid segment containing signal peptide
Costion Corresponding Coffred				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of residue of amino acid residue of amino acid sequence				Giutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid residue of service of service, T-Threenine, V-Aviline, amino acid sequence of service, T-Threenine, V-Aviline, W-Trystophan, Y-Tyxcosine, X-Unknown, *-stop code, /-spossible nuclectide deletion, coden, /-spossible nuclectide deletion, v-possible nuclectide insertion) 100				n=histidine, l=isoleucine, k=Lysine,
amino acid residue of anino acid sequence			b.	Debeucine, Memethionine, Neasparagine,
### ### ### ### ### ### ### ### ### ##	ļ		ľ	S-Corine M-Mhraenine, R-Arginine,
amino acid sequence Codon, /ppossible nucleotide insertion Veyveloreplipervosveminement Veyveloreplipervosveminement Comeanument Veyveloreplipervosveminement Comeanumen	-			Sestine, Territorine, Vevaline,
Sequence		1		Codon / codhla muslantida dalatica
6724 173 659 VCQCCTRAMADRISTAGQVAYAVDESSYVERLICADKIQALT GREGRYSVENIKQLLQSAKKGSSPTLISGLVEGSTTLISGLA ARIARILAPGCLPIKEPVETAVDKSSYVERLICADKIQALT GREGRYSVENIKQLLQSAKKGSSPTLISGLVEGSTTLISGLA ARIARILAPGCLPIKEPVETAVDKNSKYTTASKLCSALTLSGL VEVKELQREPLTPEBVQSVREHLGHESDNIL 6725 356 722 REPTEVTLATMODDIMLALICAGSENICGREADBRQESLELVO ASMELUDETPOLQALFVGNODFWGQLBAUFVKSVAMTLCQS 1CSYECKGGMCSTIRLSEPLLKAPREKLEVEGSMINGLEFTOQCKICKSTTAMTLAVG ASMELUDETPOLQALFVGNODFWGQLBAUFVKSVAMTLCQS 1CSYECKGGMCSTIRLSEPLLKAPREKLEVEGSMINGLEFTOQCKICKSTTAMTLAVG AVIATIONQCITARISPETICLET TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE T TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDFISK ISS REBECQLT PRETIFILE TOMBORQGURI FCMAPDRI FCM			bequence	\=possible nucleotide deletion,
6724 173 659 VCQVCTARMADFGISAGGFVAVVWIKSSPFELLKGLUDGLAGAT GREGRUSVENIKGLLGSANKSSPFELLKGLUDGLAGT GREGRUSVENIKGLLGSANKSSPFELLKGLUDGANT AREATLARGGCLPLLEPUSTAVDANSKYTASKLCSALTLSGL VEVERLIGARE PUTTEREVGSVENHIGHESON. 6725 356 722 RERTPEVTLAMMODDIMLALRIGGERWIGASERDHAGESLSJVD ASMELVOPPTPOLOGAFVENIGASERDHAGESLSJVD ASMELVOPPTPOLOGAFVENIGASERDHAGESLSJVD ASMELVOPPTPOLOGAFVENIGASERDHAGESLSJVD ASMELVOPPTPOLOGAFVENIGASERDHAGESLSJVD ASMELVOPPTPOLOGAFVENIGASERDHAGESLSJVD ASMELVOPPTPOLOGAFVENIGASERDHAGESLSJVD ASMELVOPPTPOLOGAFVENIGASERDHAGESLSJVD ASMELVOPPTPOLOGAFVENIGASERDHAGESLSJVD ASMELVOPPTPOLOGAFVENIGASERDHAGESLSJVD ASMELVOPPTPOLOGAFVENIGASERDHAGESLSJVD ASMELVOPPTPOLOGAFVENIGASERDHAGESLSJVD ASMELVOPPTPOLOGAFVENIGASERDHAGESLSJVD ASMELVOPPTPOLOGAFVENIGASERVENITUNG GYLJTOKQVILVTEYDTITLSGUTUNKTLCEPDAGMYFTDROGTYTING GYLJTOKQVILVTEYDTITLSGUTUNKTLCEPDAGMYFTDROGTYTING CYLVSKSRLDGPEBES ISSNITIGKYFTIK FRAMSKELVILVENIGAGGFARVILVTENDSGGGRTGVADGAFVENIKK VLEYFRIVKASSLVLLEFECTPTPOLOVENGAGTVILVTINARSS RDERYYKOPCVOFFKNIKGVABVULRDDCAAVLIPSKPLARGFY FAHAYKGVLUVANSTTYLEGGSKSKNITULVTINARSS RDERYYKOPCVOFFKNIKGVABVULRDDCAAVLIPSKPLARGFY ARHAYKGVLUVANSTTYLEGGSKSKNITULVTINARSC RDERYKOPCVOFFKNIKGVABVULRDDCAAVLIPSKPLARGFY ARHAYKGVLUVANDTITLGGSKSKNITULVTINARSC RDERYKOPCVOFFKNIKGVABVULRDGCAAVLIPSKPLARGFY ARHAYKGVLUVANDTITLGGSKSKNITULVTINARSS RDERYKOPCVOFFKNIKGVABVULRDGGSKRITULVTINARSS RDERYKOPCVOFFKNIKGVABVULRDGGSKRITULVTINARSC ROFT VLOVOMARHAVENOPTOVATORT SEGNETIVEN FRANKETPAGRAFY AVIDONOMARHAVEN FRANKETPAGAFTAMAGES LIPPODBRQULNATTHPBETRKENMKETFKYFLEEPRTSPRGKK HVSSALKBADSLARKFILLUGTVTVGFLAGSV AUGUSKPLATULVOGFLAGAGRAFYGVAGRAGRAGPGGPGGPGGGAGGAFGAFGAGGGAFGAFGAGGAGAGAGA		- Joquonoo		VENNET OPEN TREEVOLUBERT GUEGOWY
GNEGRUSVENIKOLLOSAHKESSPDITLISGILVPOSTITLISABIL ABLARILA PROGCIPILA PROGCIPILA PUTTAVONNSKYRTASKLOSALTISGI VEVKEL GREPTUTES VOSVENIGHESESDI. ABRIT PER VOSVENIGHESESDI. ASKELVDET IKAR PER KOLVEVE PV LOSVESKING SER PLIKAR PER KOLVE PV PV LOVING STRICK SER PLIKAR PER KOLVE PV PV LOVING STRICK SER PLIKAR PER KOLVE PV PV LOVING STRICK SER PLIKAR PER LOVE PV PV LOVING STRICK SER PLIKAR PER LOVE PV PV LOVING STRICK SER PLIKAR PER LOVE PV PV LOVING STRICK SER PLIKAR PER LOVE PV PV LOVING STRICK SER PLIKAR PER LOVE PV PV LOVING STRICK SER PLIKAR PER LOVE PV PV LOVING SER PLIKAR PER LOVING STRICK SER PLIKAR PER LOVE PV LOVING SER PV LOVING SER PV	6724	173	659	VCOVCTARMADECT CACOEURING DESCRIPTION OF THE CALE
AELARILAPGGCIPILEPUTAVDMINKVATASKLCSALTISGI VEVKELQREPUTEBUGSVERHIGHESINI 6725 356 722 RRETPEVILATMODDIMIALRICOERNICGREEDHAGESLEJVD ASMELVDPT-PUDLOALPVORHOOPPWGGLBAVEVKWSVEMTLCAG ICSVEGKGGMCSIRLSEPLLKLPFKROLVEVFFV 6726 98 714 HLGKMERKIRKEREKEFEGKRINSLEDIDGGKNCKSTIMTLING GYLITUKGYLITEVPTFLESTVINKELLCPBAGGHIFTDRGGL LFRIVLINFLRNGELLIPEGGRENOLLAGRAEFFOLKGLAEBEVKS RWERECLTPRETTFLEITOHNERSGGRIFTOHAGHTYFTDRGGL LFRIVLINFLRNGELLIPEGGRENOLLAGRAEFFOLKGLAEBEVKS RWERECLTPRETTFLEITOHNERSGGRIFTOHAGHTYFTDRGGF REMEGGLTPRETYFLEITOHNERSGGRIFTOHAGHTYFTDRGGF REMEGGLTPRETYFLEITOHNERSGGRIFTOHAGHTYFTDRGGF REMEGGLTPRETYFLEITOHNERSGGRIFTOHAGHTYFTDRGGF REMEGGLTPRETYFLEITOHNERSGGRIFTOHAGHTYFT SKITKSRI VLUSKSRILDGFPEFSISSNILGFKYFIK FUNGNGERPHYVKKHTFOKYDFTKGGFTUNGAGTDIICCVFLL LATUGYVANGIILAMTHGDPEKVITPTDSRGEFCGGKGTKNINKE YLFYFNIVKASIPLULEFFCTPPTOICVEKCPTPTIVLTVINARSS RDFFYYKOFCVGFFKNINGVARVLEBGGCAGATLIPSKPKATKYFT RGMITMGILVILGY RGMITMGILV RGMITMGILV RGMITMGILV RGMITMGILV RGMITMGILV RGMITMGILV RGMITMGILV RGMITMGILV RGMITMGILV RGMITMGILV RGMITMGILV RGMITMGILV RGMITMGILV RGMITMGILV RGMITMGILV RGMITMGILV RGMITMGILV RG	1	1 -73	033	CNECENCIANTE OF THE CONTROL TO A STATE OF TH
VEVERLÖREPLTPERVÖSVREHLIGHESDNIL 6725 356 722 RRRTPPVILARDDIMMARIKDERWINGBRENDHAGESLSLVU ASWELUDPTPDLQALFVOFNLOPFROGLERVEVANSVRHTLCAG ICSYECKGUMS ITLS.BEJLKLEPPKILARDEVANSVRHTLCAG ICSYECKGUMS ITLS.BEJLKLEPPKILARDEVANSVRHTLCAG ICSYECKGUMS ITLS.BEJLKLEPPKILARDEVANSVRHTLCAG ICSYECKGUMS ITLS.BEJLKLEPPKILARDEVANSVRHTLANDG ILFRIVIARIERKREELEREROOLLAQUER FPLOKGLABEVKS RWEKEQLTPRETITLE ITOMPDESOGIRT FOLKGLABEVKS RWEKEQLTPRETITLE ITOMPDESOGIRT FOLKGLABEVKS RWEKEQLTPRETITLE ITOMPDESOGIRT FOLKGLABEVKS RWEKEQLTPRETITLE ITOMPDESOGIRT FOLKGLABEVKS RWEKEQLTPRETITLE ITOMPDESOGIRT FOLKGLABEVKS RWEKEQLTPRETITLE ITOMPDESOGIRT FOLKGLABEVKS RWEKEQLTPRETITLE ITOMPDESOGIRT FOLKGLABEVKS RWEKEQLTPRETITLE ITOMPDESOGIRT FOLKGLABEVKS RWEKEQLTPRETITLE ITOMPDESOGIRT FOLKGLABEVKS RWEKEQLTPRETITLE TOMPDESOGIRT FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS REPETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQLTPRETITLE FOLKGLABEVKS RWEKEQ				AFTADIL DOCCOL EL VEDUETA UDADICIONED CULTOCAL EN COL
6725 356 722 RRETPEVILATMENDEMIALRICISEMENDERSEISTUD 6726 98 714 RAYBEVDETPEDIOALPYOPINOPPROGRESISTUD 6726 98 714 HIGGMERKTURREKEKEYEGKINSLEDTDQGKNCKSTLMTLING GYLYITQKQTLTKYPDTFLBGIUNGKILLGPPADGHYFIDRDGL LFRRVLINFLRRIGHELLBERGFRENGLIAGEASFFOLKBLAEVKS RMERGLITRETTFLBITIONBENGGLAFFOLKBLAEVKS RMERGLITRETTFLBITIONBENGGLAFFOLKBLAEVKS RMERGLITRETTFLBITIONBENGGLAFFOLKBLAEVKS RMERGLITRETTFLBITIONBENGGLAFFOLKBLAEVKS RMERGLITRETTFLBITIONBENGGLAFFOLKBLAEVKS RMERGLITRETTFLBITIONBENGGLAFFOLKBLAEVKS RMERGLITRETTFLBITIONBENGGLAFFOLKBLAEVKS RMERGLITRETTFLBITIONBENGGLAFFOLKBLAEVKS RMERGLITRETTFLBITONBENGGLAFFOLKFOLKYLIK 6727 1 831 FROMGDER PHYTYGKHTPGKYDTFFKGPT JYRRGCTDITCCVFLL LAIVGYVANG ILANTHGDPRKVITYDGSGFFCOKKTNENKS RDFSYKOPCVPGFKNKKVARVLRDGDCPAVLIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTTON LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY ROMINITEDTYTVON WARTHEN LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY PAHAKKGULWKONETTYSCHOPTSTON LIPSK PLARRCY PARACKACHA VIDOVARACHA PLARRCY PARACKACHA VIDOVARACHA PLARRCY PARACKACHA VIDOVARACHA PLARRCY PAHAKACHA VIDOVARACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PLARRCY PAHAKACHA PAHAKACHA PLARRCY PAHAKACHA PAHAKACHA PLARRCY PAHAKACHA PAHAKACHA PAHACHA PAHAKACHA PAHACHA PAHAKACHA PAHACHA PAHAKACHA PAHACHA PA				
ASWELDDPTPDLQALEVQRNDQFFWGQLEAVEVMSVRMTLCAG 1CSYECKGGMCSIRLSEPLLKLRRRRDLUEVFFV 6726 98 714 HLGMMERK KINREREKREYSGKINSLEDTDGKNCKSTIMTLAVQ GYLYLTQKGTLTKYPDTFLEGIVMGKILCPPDAGGFT LFRIUNIPLRNGELLIPEGFRENGLLAGAEFFCLKGLAEEVKS RWEEGLTPRETTFLEITDNIERSOGLRIFCNAPDFISKIKSR VLYSKSRLDGFPERFSISINITIGKYKTI 6727 1 831 PROMGDERPHYYGRHOFPKONTIPTYGSTGFCGQKGTKNENKR YLFYFNIVKCASPLVLLEFQCPTFGICVEKPDRYLTINARSS RDFEYYKGPCVPGFKNKSVAEVLRDGCCPAVLIFSKLARCF PAHAPKGVALVKONETTYEDGHGSRNTIDLVKGAKKANGVLEA RGLMMRIFEDTTVSWWDIISLGIAMAMSLLFILLRTJAGIMS RGMIIMSILVLGY 6728 486 935 PCSSWLRSLADSSLSKKMFLVGLTGGLASGKSSVJQVFQGLCA RGMIIMSILVLGY 1191 VGLTGAGGGRAVAGEMERVVGCHGFGKPGYBTLLKGDGNRKVLGD LIFNGPDRRGLLINATHPBIRKEMMKETFKYFLREPRTSPRGKK HVPSALKEADSLARENT 6729 259 1191 VGLTGAGGGRAVAGEMERAPGVTGKGNGVARGVAGFGADGI PGHFGGGGGRAVAGFALRRULLIGTVTVGFLAGSV LAGVKKFDVPCGGRCCYPRKGGRGGPGPVGGNGGP GLGGFFGLGGKKGKGEMERAPGVTGKKGNGVARGVGGFGADGI PGHFGGGGFRGRPGVGCKGTGCGSGPQCOPPGSEGFTGPDFQG GLGFFGLGGKKGKGEMERAPGVTGKKGNGVARGVGGFGDGTGDFGCG PFGLGGGFGRGRPGFGGKGCGCCPFRKGGRGGPGPVGGNGGP GFGSGGKGKGMERAPGFGFGGGGGGPGFGFGGPGGTGGGGG PFGLGGGFGRGRPGFGGKGKGGKGGGGGPGFGPGFGGPGGGGG GISPDTLHBILIATTGVTFRPDQYKGKKGGSGGPGFGPGPGGGG GISPDTLHBILIATTGVTFRPDQYKGKKGGSGGFGGGFGFGFGGGG GISPDTLHBILIATTGVTFRPDQYKGKKGGSGGFGGGFGGGGG GISPDTLHBILIATTGVTFRPDQYKGKKGGSGGFGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6725	356	722	
CISYECKGOMCSILLSEPLLKLRPRKOLLEVEPFY			7.2.2	ASWELVIDETEDLOAL EVOENDOREWOOL PAVENTING CADE
HIGMERKINRERKEYSCHINGLEDTDOCKNIKSTIMITIANG GYLITOKOUTLEKYDPTELEGITUNGKILOPAGHYFIDROGL LPRIVLINFLANGELLIPEGFERNOLLAQEAEFPOLKGLAEEVKS RWEKEQLTPRETTFLEITONHORSQGLRIFCNAPPTISKIKSRI CONTROL				TCSVEGEGGMCGTDLGEDLLELDDDEDLUEUEU
GYLITTQKOTLIKYPDTFLEGIVNOKILICPPDADGHYFIDDOGL LPRIVLINFLRNOELLIPEGFRENQLIAGABEFPOLKGLABEVKS RWEREQLTRESTTILEITDMHDESGGLRIFCNAPDFISKIKSRI VLVSKSRLDGFPEBFSISSNIIQFKYFIK 6727 1 831 FROMGDERBHYYGKHGFPÇKYPDTFKEGTDIICCVFIL LAIVGVVANGIIAMTHODPRKVIYPTDSRGEFGGKGTKMENKR YLFYFRIVKCASPLVLIBETGCTPFGICVEKCPRVLITTUARSS RDFFYKGCFVFFKNKGVASVIVTDSRGEFGGKGTKMENKR PAFHYKGKJLWGMENTFYBGGHGSKUTIDLWGGAKKANGVLER, RQLAMRIFEDYTVSWYWDIISIGIAMAMSLLFIILLRFLAGIMG RGMIIMGILVLGY 6728 486 935 FCSSWLRSLADSSISWKMFLVGLTGGIASGKSSVIQVFQQLGCA VIDVDVMARHVVQFGYPAHRRITUSVFGTEVLLENGDINRKVLGD LIFNQPRORQLINAITHPEIREMMKETFKYFLREPRTSPRGKK HVPSALKEADSILMRRDT 6729 259 1191 VGUTGAGSGGTASMGRDQRAVAGPALRRWLLLGTVTVGFLAGSV LAGVKKFDVPCGGGRGCTASMGRDQRAVAGPALRRWLLLGTVTVGFLAGSV LAGVKKFDVPCGGGRGCSGGCCYPEKGGRGQPGPVGPCGVGNGFP GLOGFFGLQRKGGKGERGAPGVTGPKGDVGARGVGFPGADGI PGHPGGGGFRGRPGYDGCGGGGGCCYPEKGGRGQPFGPGGADGI FGHPGGGGFRGRPGTYGCRGTGGDSGTQGPFGSGFTGTDPQG GLOGFFGLQRKGGKGERGAPGVTGPKGDVGARGVGGPPGGDCG GPVGAPGFGFGFGFGTGGTGGSGTGGGSGGGPGFGGGADGI FGHPGGGGFRGRPGTGCGGGGGGGCTYGFKGGGGGGFGGGGG GPVGAPGFGFGFGFGTGGTGGGGGGGGGFTGGGGGGGGGGGGG	6726	98	714	HIOKMERK I NEDENENE SANCTED CONTOUR MET AND
LFRIVLINFLRNGELLLPEGFERNOLLAGEAEFFOLKGLAEEVKS RWEEGLITPETTTILE TIDNHDRSGLAF FROADPISKIKKRI VLVSKSRLDGFPEFFS ISSNI LGFKYFIK 6727 1 831 FROMGDERPHYYGKGTGFQKYDFTKGG INTRGCTDI ICCVFLL LAIVGYVANGI LAMTHODPRKVIYDTDSRGEFGGKGKYKNENKY YLFYFNIVKCASPLVLLEFGCFTPGICVEKCPDFLITTLINARSS RDFSYKKOFCVEGFKKNKGYABVLRDGDCPAVLJESKG PLARGCF PAHHAYKGULMVGNETTYEDGHGSKKNITDLVEGAKKANGVLEA RQLAMRIFEDYTVSWYMDI ISLGIAMAMSLLFI ILLERLAGING RGMI INGILVLGY 6728 486 935 FCSSWLESLADSSLSWKMFLVGLTGGIASGKSSVIQVFOQLGCF LIFNOPDRROLLNAITHPEIREMKKETFKYFLREPRTSPRGKK HVPSALKRADSLMREDY LIFNOPDRROLLNAITHPEIREMKKETFKYFLREPRTSPRGKK HVPSALKRADSLMREDY GROWFFGFFGFFGFGALDGTGGFGFGADGI FGHFGGGFBRGRFOYDGCGFCCCYPEKGGRGCPGFDGOYDGGVNGPP GLOGFFFGLGGKREDKREGRAGPGVTDFKDDWGARGVSGFFGADDI FGHFGGGFBRGRFOYDGCGFCTCGDSGPQEPCSGSFTGPPGDPQ PKGGKGFYALDKEERDFYRGFCREPGEDLUFGCBFTGPPGDPQ PKGGKGFYALDKEERDFYRGFCREPGEDLUFGCBFTGPPGPQ GIPSDTLHPILAPTGVTFHPDYKKEKGSSEFGFGIRGISLKGEE GIM NMUDYYEVIGLQRYASFEDIKKAYHKVALKMHPDKNPENKEEAE RKFKEVAGAYSVLSNDEKEDI VDKYGTGGLAFGFGRICHSLKGEE GIM 6730 784 1015 NMUDYYEVIGLGRYASFEDIKKAYHKVALKMHPDKNPENKEEAE RKFKEVAGAYSVLSNDEKEDI VDKYGTGGLAFF GIRGGGFPGFPSPPFNCLOFGGGSDFQCPOSSEFTGPPDPQC GIPSDTLHPILAPTGVTFHPDYKGEKGBFGFGTRGISLKGEE GIM 1015 CRWGRRFPPFSPPFNCLOFGGGSDPQCDCTGLHCHSLTHEGTAKEATY NDLQVEYGKCQLGMKELMKKFKELTQTMYSLLTNROGSLKKNISA LIKTARVEINNKDEI GROWFFFPFSPPFNCLOFGGGSDPQCDCTGLHCLSHSPDDTFW AGROUCYTAATTOAAAPATENCLPDHSGHFPPSPSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRORLAPQNGSSDAPAYRTPPSSQGRREWGSVEPPPSWGDFE PLVAKERSPVCKRTRREFERSDSAKEEVRSSAYYLRSRQRROPR PQSTEMKTRRTTRLQCGPSSQPPLAYMRGRLLDSSISSE DEASSGTDLSGTISKKTWSS (GRAPAVSEDLVIRLRPPLRYPR YEATSVQCONSOPPLOGPSGPPLOTGREKESSEDEN VKKKSNRKEDDVAASGTVKRHLKTSGECERKTKKSLELSGEDLI QLISTMEEGLQAREDVIRMLKTEKTÇEBULGHGSSEPEKVLR VLHRDAILAGGKSIGEDVYKPF1SELDRLEEKKGKTYRRMLEQL LLAEKCHRRTVYELENEKKHTTDYMMSCDDFTNLLEGGERKKKSLELSGEDLI QLISTMEEGLGARDVIRMLEKTSDFTNLLEGGERKSKEEDLI QLISTMEEGLGARDVIRMLEKTSTDFTNLLEGGERKTKRSLELGKEL LLEGKKAYQARKE 6734 189 551 SAAMFPUVSGCFGELGEKNKSLELVSFEWAVHFTWEEMQDLDD				GYLYITOKOTI,TKYPDTFI.FCIIMGKTI.GBDDADGUUETDDGG
RWEKEQLTPRETTFLEITONHURSGGLRIFCNAPPTSKIKSRI (19727 1 631 FRGMGDEPERFSISNIIOFEPERSISNIIOFERSISNIIOFEPERSISNIIOFERSISSEE DERSSOTOLSOTIISKTYRSIOPERSISSEE DERSSOTOLSOTII	_		•	LFRHVLNFI.RNGET.I.DEGFRENOT.AOFAFFFOT.KOTAFFIRE
VLUSKSRLDGFEERSISSNIIGFKYFIK	1			RWEKEOLTPRETTFLEITONHOPSOCIATECNA DORTCET PORT
6727 1 831 FRGMGDERPHYGKKGTFOKXDPTFKGPTINGCTDIICCUFLL LAIVGVVAVGILAWTGDPRAVIYPTDSRGFCGQKGTKNENKP YLPYFNIVKCASPLVLLEFQCPTPGICVEKCPDRYLTYLMARSS RDFSYYKQPCVPGFKNNKGVAEVLRDGDCPAVIIPSKPLARRCF FAIHAVKGVLMVGNSTTYTED-MSGRKNITDLVEGGKKANGVLEA. RQLAMRIFEDYTVSWYWDIISLGIAMAMSLLFIILLRFLAGIMG RGMIIMGILVLGY 6728 486 935 FCSSWLRSLADSSLSWKMFLVGLTGGIASGKSSVIQVFQQLGCA- VIDVDVMARHVVQPGYPAHRRIVEVPGTEVLLENGDINRRVLGD- LIFNOPDRRQLLINATTHPEIRKEMKETFKYFLREPRTSPRGKK HVPSALKEADSLMRRDT 6729 259 1191 VGLTGAQSGRTASMGTQGAVAGFALRRWLLLGTVTVGFLAGSV LAGVKKFDVPCGGRDCSGGCQCYPEGGGRGDGPGVGPGQGYNGPP GLQGFPGLGGRKGDFVGGCNGTGGARGVSGFDGADGI PGHPGGGGFRGPFVGGGRRGDFGDFGDFGDFGGRGPGPFGPGGYNGPP GLQGFPGLGRKGDKGRGAPGVTPKGBVGARGVSGFDGADGI PGHPGGGGFRGPFQDFPGRGGRGGPGPFGPGGGRGPGP PKGQKGEPVALPKEERDRYRGEPGBPGLVGPGPGRGRGVGGPGP GIVADPGRPGDPGPGPGPGPGGRGRGGPGPFGPGGGRG GIRSDTLHHILAPTGVTFHPDQVKGEKGSGEGPGPRGPGPGPG PKGQKGEPVALPKEERDRYRGEPGBPGLVGFQGPGPG GIRSDTLHHILAPTGVTFHPDQVKGEKGSGEGPGIRGISLKGEE GIM 6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVABAYEVLSNDEKRDIYDKYGTEGLMEP 6731 1 446 GIRKRLHGAVVPRVEVGCVWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVDSASKSCVPSRNCLDLYEEILTEEGTAKEATY NDLQVEYGKCQLQMKEIMKKFKEIQTQNFSLINENGSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWGRPPPFSPPLNCLQFGGGSDPQQLTQLRHCLSHSPQDTFW AGRQVCYTAATTQAAAPATRNCLPPESGHRPFPRSHRHRGEN LGSIKFSSGYTATTMAGDGRRARGEWGFGWGFWGFPP PQSTEEMKTRTTTLQQGHSGPPLQPSFVMTRGIRGDSHSSEE DEASSGTDLSGTISKKTVRSIQBAPAVSEDGYPSRDGRSDBSG DKTTRSSSGYTESFW VARATSVQKVMFSEEGSGFTEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSGYTESFW RSCRQVGNFSRNGGESASDGHTSCFKPSTIGNAGEKSLSEDAK KKKSNRKEDDVMASGTVKRHLKKTSGECERKTKKSLELSKEDLI QLLSIMEGELQARBUVHHMKTEKTKPBVLGAHYGSAEPEKVLR VHENDAILAQEKSIGEDVVEKUPISLDRLERKYREPLERMLEGU LLABKCHRRTVYELENEKKHCTUMNKSDDFTNLLEQERELKK LLEGKANQARKB LLAGKKGTGEDVYEKUPISLDRLERKOFTRMLEDQ LLABKCHRRTVYELENEKKHCTUMNKSDDFTNLLEQERGRLKK LLEGKKANQARKB SAAMFPVSGCCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				VLVSKSRLDGEPEEFSISSNTTOFKVFTK
LAIVGYVAVGIIAWTHGDPRRVITPTDSRGFFCGCKGTKNERNRY YLFYFNIVKCASPLVLLEFQCPTPGICVEKCPDRYLITYLNARSS RDFEYYKQFCVPGFKNNKGVAEVLRFDGCPAVLIPSKPLARKCF PAHHAYKGVLWGNETTYEDDHGSRKNITDLVEGAKKANGVLEA RQLAMKIFEDYTVSWYWDIISLGIAMAMSLLFIILKFLAGIWG RGMIIMGILVLGY 6728 486 935 FCSSWLRSSLSWKMFLVGLTGGIASGKSSVJQVFQQLGCA VIDVDUMARHVVQPGYPAHRRIVEVFGTEVLLENGDINRKVLGD LIFNOPDRRQLLMATTHPEIRKEMMKETFKYFLREPRTSPRGKK HVPSALAKEADSLMREDT 6729 259 1191 VGLTGAQSGRTASMGRDQRAVAGFALRRWLLLGTVTVGFLAGSV LAGVKKFDVPCGGRDCSGGCQCYPEKGGRGQPGVPGQGYNGPG GLQGFFFGLGARKGNGKREGAPGVTGPKGDFKGQGVRGP GLQGFFGLGARKGNGKREGAPGVTGFGFFGAPGHVCGM GPWGAPGRPGPPGPEGRKGQGGNRGGFYGGPFGPGPGPGPGPG GIRSDTLHPIIAPTGVTFHPDQVKGEKGSGEFGIRGISLKGEE GIM 6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKKEVBEAYSVLSNDEKRDI YDKYGTEGIMEF 6731 1 446 GIRKRLHGAVVPFEVECGPWETEESGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEEGTAKEATY NDLQVEYKKCQLQMKELMKKKFKEIGTQNFSILINENGSLKKNISA LIKTARVEINRKDEII 6732 102 1205 GRWGRFPPFSSPLNCLQPGGGSDPQOLTOLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGRFPTPPRSHRHHQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYTPRAPIRE GRGRLAPQNGGSSDAPAKTPPSRGRREVESSEYVTVKARSRQRGQFF PDETKERRSPVGKRTRLEEPRSDSAKEWRSAYYLKRSRQRGQFF PDETKERRSPVGKRTRLEEPRSDSAKEWRSAYYLKRSRGRROPR PORTEMKTRRTTRLQQDHSGQFSASDGHISCPKPSIGNAGSKSCDAF TRESTVQQKVMFSSEGGTEEDDDQDSSHSSVTTVKARSRDSBSG DEASSQTDLSQTISKKTVRS 1QEAPAVSEDLYTLRKRPPLRYPR YEATSVQQKVMFSSEGGTEEDDDDGSSHSSVTTVKARSPDSBSG DKTTRSSQYIESFW RSCQVGWSSRRQGGESADGHISCPKPSIGNAGEKSLSEDAK KKKSNRREDDVMASGTVKRHLKTEGGCERKTKKSLELSEADAK KKKSNRREDDVMASGTVKRHLKTERGCERKTKKSLELSEADAK KKKSNRREDDVMASGTVKRHLKTERGECERKTKKSLELSEADAK KKKSNRREDDVMASGTVKRHLKTERGECERKTKKSLELSEADK LLAEKCHRRTVYFLENEKKHTTDYMNKSDDFTNLLEQERERLKK LLAEKCHRRTVYFLENEKKHTTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVESGCFQELGEKNKSLELVSFEEVAVHFTWEEWQDLDD	6727	1 .	831	FRGMGDER PHYYGKHGTPOKYDDTEKCDTVNDCCTDTTCCVETT
### ##################################	1			LAIVGYVAVGIIAWTHGDPRKVTYPTDGRGRECGOKGTKNENKD
RDFEYYKOFCYPGFKNIKGVAEVAEVAERGEDCAPALI PSKPLARRCF PAIHAYKGVLMVGNETTYEDGHGSKKNITDLVEGAKKANGVLEA RQLAMRIFBDYTVSWWDI ISLGIAMAMSLLFI ILLRFILAGING RGMIIMGILVLGY RGMIIMGILVLGY FCSSWLESLADSSLSWKMPLVGLTGGIASGKSSVJQYFQQLGCA VIDVDVMARHVVQPGYPAHRRIVEVFGTEVLLENGDINKKVLGD LIFNQPDRRQLLNAITHPBIRKEMMKETFXYFLREPRTSPRGKK HVPSALKEADSILMRRDT 6729 259 1191 VGLTGAGSGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAQSV LAGVKKFDVPCGGRDCSGGCCYPEKGGRGQPGPVGPQFVGPG GLGGFFGLGGRKGDKGERGAPGVTGPKGDVGARGVSGFPGADGI PGHPGGGGFRGRPGTDGCNGTTGDSGPQGPGGPGFGPGFQGG GLGGFFGLGGRKGDKGERGAPGVTGPKGDWGARGVSGFPGADGI PGHPGGGGFRGRPGTDGCNGTTGDSGPQGPGFGFGFGHVGQM GPVGAPGRPDPDFDKGQQGNRGLGFYGVKGKGKDVQDPGN GIRSDTLHFILAPTGVTFHPDQYKGEKGSGEFGIRGISLKGEE 6730 784 1015 NMVDYYEVLGLQRYASPBGIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYEVLSNDEKRDIYTDKYGEGLINEF 6731 1 446 GIRKRLHGAVVPRVEVGCPMETRESEGVHLERFTSFLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYBEILTEGTAKEATY NDLQVSYGKOCLQMKELMKKPKEIQTONFSLINENGSLKKNISA LIKTARVEINRKDESI 6732 102 1205 GRRQRFPPPFSPFLNCLQPGGGSDPQQLTQLHCLSHSPQDTPW AGRQVCYTAATTOAAAPATRRCLPDHSGHPTPPPRSHRHHRGEN LGSIKPSSPSKRTATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRRGLAPQNGGSSDAPARTTPPSSQCREWERPSDEPBEYDGFP PLVAKERSPVGKRTELEFFRSDSKKEVERSAYYLRSRGRRQPR PQGTEEMKTRRTTRLDGQHSSQPPLQPSPWITRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YRATSVQKVNFSEEGGTEBDQDSSHSSVTTVKARSRDSDESG DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YRATSVQKVNFSEEGGTEBDDQDSSHSSVTTVKARSRDSDESG DKTTTSSSSYIESFW 6733 613 1311 RSCGQVGMSSRNGGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKYKKSLELSERDAL QLLSIMEGELQAREDVHIMLKTEKTKFEVLAHYGSAPPEKVLR VHENDAILAQEKSIGEDVYERFJ SELDGLEEKOKETYRMLBGQL LLAEKCHRRTVYELENEKHKHTDYMKSDDFTNLLEQERERLKK LLEQEKAYQARKB 6734 189 551 SAAMFFVFSGCFQELQEKKSLELVSFEEVAHYFWEEWQDLDD	1			YLFYFNIVKCASPLVLLEFOCPTPOTCVEKCPDRVLTVLMADGG
PAHRYKGVLMVGNETTYPDCHGGSRKNITDLVEGAKKANGVLEA RQLAMRIFEDYTVSWYMDIISLGIAMAMSLLFIILLRFIAGIMG RGMIIMGILVLGY FCSSWLRSLADSSLSKKMFLVGLTGGTASGKSSVIQVFQQLGCA VIDVUMARHVVQPGYPAHRRIVEVFGTEVLLENGDINRKVLGD LIFNQPDRRQLLNATTHPSIRREMMKETFXYFLREPRTSPRGKK HVPSALKEADSLMRRDT G729 259 1191 VGUTGAQSGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAQSV LAGVKKFDVPCGGRDCSGCQCYPEKGGRGPCPVGPQGYNGPP GLOGFFGLOGRKGDKGRGAPGVTGPKGUDGARGVSGFPGADGI PGHFGQGGPRGRGPGYDGCCGTGDSGPQGPGSGEFTGPPGPQ PKGQKGEPYALPKEERDRYRGEPGBPGLVGFQGPPGRPGHVCQM GPVGAAFGRPPPDPDCPKGQQGNRGLGFYGVKGCKGDVQPQFGN GIRSDTLHPILAPTGVTFHPDQYKGEKGSGSGPFGPBGPQ PKGQKGEPYALPKEERDRYRGEPGBPGLVKGPKGGBGRGPGFPGBPQ GIRSDTLHPILAPTGVTFHPDQYKGEKGSGSGPFGFBGPGPG GIRSDTLHPILAPTGVTFHPDQYKGETGSGFPGFBGFGFGFGFG GIRM 6730 784 1015 MWDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNFENKEEAE RKFKEVAEAYEVLSNDERRDTYDKYGTEGINEF GIRRLHGAVVPRVEWGCPWETRESEGVHLERPTSPLKNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYBEILTEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTONFSLINENGSLKKNISA LIKTARVEINRKDESI GRGRAPPPPSPPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPFRSHRHHRGEN LGSIKPSSRSTKATSTIMAGDGRAEAVREGWGVYTPPAPIRE GRGRLAPQNGGSSDAPAXTFDPSQRREWFSBEPPEVYGFPE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRQPR PQGTEEMKTRRTTRLQQQHSEQPPPLQPSPTWTRGLRDSHSSEE DEASSTOTLSGTISKKTVRS 1GEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEBDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYLESFW AKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMGEBLQAREDVIHMLKTEKTKPBVLATYGSABPEKVLR VUHRDAILAQEKSIGEDVYERF JSELDRLEEKOKETYRRMLEGU LLAEKCHRTTVYELENKKHETTYPBUTEAHYGSABPEKVLR VUHRDAILAQEKSIGEDVYERF JSELDRLEEKOKETYRRMLEGU LLAEKCHRTTVYELENKKHETDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKB 6734 189 551 SAMFFVFSGCGPGELQEKMKSLELVSFEEVAHYFWEEWQDLDD				RDFEYYKOFCVPGFKNNKGVAEVI.RDGDCPAVI.IPSKPI.ARRCR
RQLAMRIFEDYTVSWYNDIISLGIAMAMSLLFIILLRFLAGIMG RGMIIMGILVLGY FCSSWLRSLADSSLSWKMFLVGLTGGIASGKSVIQVFQQLGCA VIDVDUVARRHVQDGYPAHRRIVEVFGTEVILENGDINRKVLGD LIFNOPDRRQLLANATHPBIRKEMMKETFKYFLREPRTSPRGKK HVPSALKEADSLMRRDT 6729 259 1191 VGLTGAQGGRTASMGRDQRAVAGGALRWLLLGTVTVGFLAQSV LAGVKKRDVPCGGGRCCSGCCYPBKGGRGQPGPVGPQGYNGPP GLQGFPGLQGRKGDKGERGAPGVTGPKGDVGARGVSGFPGADGI PGHIGGGGRRGBYGDCGCCYPBKGGRGQPGPVGPQGYNGPP GLQGFPGLQGRKGDKGERGAPGVTGPKGDVGARGVSGFPGADGI PGHIGGGGRRGBYGTMCGETGCDSGFQFGPGFPGFPGPQG GPVGAPGRPGPPGPPGPGGGGRCGGCAPBKGGRGQPGPVGPQGYNGPP GLQGFPGLQGRKGDKAFGLGTGCDSGFQFGPGPGFGGPGPG GPVGAPGRPGPPGPPGPGKGQQGNRGLGPYGVKGBKGDVGQPGPN GPVGAPGRPGPPGPPGPKGQQGNRGLGPYGVKGBKGDVGQPGPN GPVGAPGRPGPPGPPGPKGQQGNRGLGPYGVKGBKGDVGQPGPN GPVGAPGRPGPPGPPGPKGQQGNRGLGPYGVKGBKSDVGQPGPN GPVGAPGRPGPPGPPGPKGQQGNRGLGPYGVKGBKSDVGQPGPN GPVGAPGRPGPPGPPGPKGQQGNRGLGPYGVKGBKSDVGQPGPN GPVGAPGRPGPPGPPGPKGQQGNRGLGPYGVKGBKSDVGBEG GFM AMDDYYEVLGLQRYASPEDIVKNALKHPDKNPENKEEAE RKFKEVAEAYEVLSNDEKKDITDKYGTEGLNFP 6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEILTREGTAKEATY NDLQVEYGKCQLGMKELMKFLGTQNFSLITNENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWGRFPPPSPPLWCLQPGGGSDPQQLTQLRCLSHSPQDTFW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVEGWGVVYTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRGGRREVFSDEPPEVYCDFE PLVAKERSPVGKRTRLEEFRSSAKEEVESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQGISEQPPLQPSPWTTRGLRDSHSSEE DEASSQTDLSGTJISKTVRSIQGEAPAVSEDLVIRRRPPLRYPR YEATSVQQKVNFSEEGETEEDQDSSHSSVTTVKRRSRDSESG DKTTRSSSQYISSFW OKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLISIMEGGLQAREDVIHMLKTEKKPSPULGHTGSABPEKVLR VLHRDAILAQERSIGEDDVYRSILDLALERKOKSTTYRRMLEQU LLAEKCHRTVVELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE LLEQEKAYQARKE 6734 189 551 SAMMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD		'		
RGMIIMGILVLIGY		·		
VIDVDVMARHVVQPGYPAHRRIVEVFGTEVLLENDDINKKVLGO LIFNQPDRRQLLNAITHPEIRKEMKETFKYFLREPRTSPRGKK HVPSALKEADSLMRRDT OGLTGAQSGRTASMGRDQRAVAGFALRRWLLLGTVTVGFLAQSV LAGVKKRDVPCGGRDCSGGCCYPSKGGRGQFGYGPQGYNGPP GLOGFPGLQGKRGDKGBRGAPGVTGPKGDVGARGVSGFPGADGI PGHPGQGFRGRKGPKGRGAPGVTGPKGDVGARGVSGFPGADGI PGHPGQGGPRGRPGYDLCNGTQGDSGPQGPGSGFTGPPGPGQ PKGQKGEPYALPKEERDRYRGEPGEGGLVGFQGPPGREGHVGOM GPVGAPGRPGPPGPGPGKQQGNRGLGFYGVKGKBKGWQDFGPN GIPSDTLHPIIAPTGVTFHPDQYKGEKGSEGPGIRGISLKGEE GIM 6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYEVLSNDEKRDIYDKYGTEGLNEF 6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSANDSASKSVPSNCLULYERILTREGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWGRPPPPSPPFLWCLOPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHQEN LGSIKPSSRSTKATSTTMAGDGRABAVREWGGYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGREWFFSDEPPSVYGDFE PLVAKERSPVGKETRLEEPRSDSAKEEVRESAYYLRSRQRQPR PQETEEMKTRRTTRLQQQHSEQPPLGPSPVMTRGLRDHSSEE DEASSGTDLSQTISKKTVRSIQEAPAVSEDLVIRLRPPLRYPR YEATSVQQKVNFSEEGGTEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCCQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYKPPISELDKLEKEKKETTRRMLEQL LLAEKCHRRTVYSLENEKKHHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD			*	
VIDUDWARHVUÇPGYPAHRRIJENGÜINRKVIGD LIFNQPDRRQLINAITHPEIRKEMMKETFKYFLREPRTSPROKK HVPSALKEADSLMRRDT 6729 259 1191 VGLTGAGGGRTASMGRDGRAVAGPALRRMLLIGTTVGFLAGSV LAGVKKFDVPCGGRDCSGGCCYPEKGGRGGPGPVGPGYNGPP GLOGFFGLQGRKGDKGRGAPGVTGPKGDVGARGVSGFFGADGI PGHFGQGGPRGRPGYDGCNGTQGDSGPQGPPGSSGFTGPPGPQG PKGQKGEPYALPKEERDRYRGEPGBPGLVGFQGPPGRFGHVCQM GPWGAPGRPGPPGPPGPKGQQCNRGLGFYGVKGEKGBUQQPGPN GIPSDTLHPIIAPTGVTFHPDQYKGEKGSGSGFPGISISKGEE GIM 6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAVEVLSNDEKRDIYDKYGTEGIMEF GIRKILHGAVVPRVEVGCPWETRESEGVHLEFPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRCLDLYEEILTEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHQEN LGSIKPSSRSTKATSTIMAGDGRAEAVREGWVVYTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGREWFFSDEPPEVYGDFE PLVAKERSPVGKETRLEEFRSDSAKEBWRSAYYLRSRQRRQPR PQETEEMKTRRTTLQQQHSGDPPLQPPPWTRRGLRDSHSSEE DEASSGTDLSQTISKKTWSIQEAPAVSEDLVIRLRPPLRYPR YEATSVQQKVNFSEEGGTEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGSSASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDWASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VUHRDAILAQEKSIGEDVYEKPISELDELEEKQKETTRRMLEQL LLAEKCHRRTVYSLEENEKHKHTDYMNKSDDFTNLLEQERERLKK LLLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCRGELEKWKSLELVSFEEVAVHFTWEEWQDLDD	6728	486	935	FCSSWLRSLADSSLSWKMFLVGLTGGIASGKSSVIOVFOOLGCA
LIFNOPDRRQLINAITHPEIRKEMMKETFKYFLREPRTSPRGKK HVPSALKEADSLMRRDT VGTTGAGGGRTASMGRDQRAVAGPALRRWLLIGTVTVGFLAGSV LAGVKKFDVPCGGRDCSGGCQCYPEKGGRGQPGPVGPQGYNGPP GLQFFGLQGRKGDKGERGAFGVTGPKGDUGARGVSGFPGADGI PGHFGQGGPRGRPGPVGCCGTGCDSGPQGPDSSEGFTGPADGIG PGHGQGGPRGRPGPVGCCGTGCDSGPQGPDSSEGFTGPADGIG PGHGQGGPRGRPGPVGCCGCGNGLGFYGVKGGRGDVQQPGPN GFVGAPGRPGPPGPPGPRGQCGNGLGFYGVKGRKGDVQQPGPN GISPDTLHPILAPTGVTFHPDQYKGEKGSEGPGIRGISLKGEE GIM 6730 784 1015 NMMDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKPKEVABAYEVLSNDEKKRITYDKYGTEGLMEF 6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTHEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTONFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWGRPPPPSPPLWCLQPGGGSDPQQLTQLHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREWGGVYVTFRAPIRE GRGRLAPQNGGSSDAPAYRTPPSQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKTRLEEFRSDSAKERVRSAYLRSGRQRPR PQETEEMKTRRTTRLQQCHSEQPPLQSPPWTRTGLKRDSHSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGGTEEDDDDSSISSVTTVKARSRDSDESG DKTTRSSCQVISFFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHTSCPKPSTIGNAGEKSLSEEDAK KKKKSNRKEDDWASGTVKRHLKTSCBCERKTKKSLELSKEDLI QLLSIMEGELQAREDVTHRLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGBDVYEKPISELDRLEEKCKETTRRNLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFFVFSGCRCELQEKNKSLELVSFEEVAVHFTWEEWQDLDD		*	' · · ·	VIDVDVMARHVVQPGYPAHRRIVEVFGTEVLLENGDINRKVLGD
HVPSALKBADSLMRRDT VGLTGAQSGRTASMGRDQRAVAGFALRRWLLLGTVTVGFLAQSV LAGVKKFDVPCGGRDCSGGCQCYPBKGGRGQPGPVGPQGYNGPP GLQGFPGLQGRKGDKGERGAPGVTGPKGDVGRGVGPPGDGG PGHPGQGGPRGRPGYDGCMGTGDSGPQGPPGSEGFTGPPGPGG PKGQKGGPYALPKERGDRYRGEPGBPGLVGPQGPPGRPGHVQM GPVGAPGRPGPPGPPGPKGQQGNRGLGFYGVKGCKGDVGQPGPN GIPSDTLHPILAPTGVTFHPDQYKGEKGSVGGPGPRGHVQM GIPSDTLHPILAPTGVTFHPDQYKGEKGSVGGPGPNGENGL GIM NMYDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYPVLSNDEKRDIYDKYGTEGLNEF 6731 1 446 GIRKRLHGAVVPRVEVGCPWETTESEGVHLERFTSPLKNNDEGS LDTYAGLDSAVSDASAKSCVPSRNCLDLYREILTEGGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENGSLKKNISA LIKTARVEINRKDESI 6732 102 1205 GRWQRPPPPPSPLNCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHRQEN LGSIKPSSRSTKATSTIMAGDGRAEAVREGWGVYVTPRAPIRE GRGRLAPQNNGGSDAPAXTRTPSRQGRREVRFSDEPEVYGDFE PLVAKERSPVGKTRTLEFFRSDAKEBVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQOHSEQPPLQPSPVMTRRGLRDSHSSE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDQDSSHSSVTVKARSRDSDESG DKTTRSSQYIESFW DKTTRSSQYIESFW OKKKKSNRKEDDVMASGTVKRHLKTGGECRKKTKKSLELSKEDLI QLLSIMEGELQARRDY HIMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYSLENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKB 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				LIFNOPDRRQLLNAITHPEIRKEMMKETFKYFLREPRTSPRGKK
LAGVKKPDVPCGGRDCSGGCCYPEKGGRGQPGPVGPGYMGPP GLOGFPGLOGRXGDKGERGAPGVTGPKGDVGRAGVBPP GLOGFPGLOGRXGDKGERGAPGVTGPKGDVGRAGVSGFPGADGI PGHPGQGGPRGRYGYDGCMGTQGDSGPQGPPGSEGFTGPPGPQG PKGGKGEPYALPKEERDRYRGEPGBPGLVGFQGPPGREGHVGQM GPVGAPGRPGPPGPPGPKGQQGNRGLGPYGVKGEKGDVGQPGPN GIPSDTLHPIIAPTGVTFHPDQYKGEKGGSGGPFGINGISLKGEE GIM 6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKPKEVABAYEVLSNDEKRDIYDKYGTEGLNEF GIRKRLHGAVVPRVEVGCPWTTEESGGYHLERPTSPLKNNDEGS LDIYAGLDSAVSDASKSCVPSRNCLDLYEEILTEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWGRPPPPSPPLWCLQPGGGSDPQQLTQLHCLSHSPQDTFW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRAEAVREGWGVYVPPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVFFSDEPPVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEBVRESAYYLRSQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSGTDLSGTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVMFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMRSERNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNKEDDVMASGTVKRHLKTSGECERRTKKSLELEKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEERKYSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAMMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				
LAGVKKFDVPCGGRDCSGGCQCYPEKGGRQPGPVGPQGYNGPP GLQGFPGLQGRKGDKGERGAPGVTGPKGDUGARGVSGFPGADGI PGHFGQGGPRGPKGPVGTQCNGTOGDSGPQGPPGSGFTGPPGPQG PKGQKGEPYALPKEERDRYRGEPGEPGLVGFQGPPGPGPGPGPGPGPGPGPGPGPGPAGPGPGPGPGPGPG	6729	259	1191	VGLTGAQSGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAOSV
GLQGFPGLQGRKGDKGBRGAPGVTGPKGDVGARGVSGFPGADGI PGHPGQGGPPGCNGTQGDSGPQGPPGSEGFTGPDGPQG PKGQKGFPYADFKERDRYRGFPGBPGLVGFQGPPGRPGHVGQM GPVGAPGRPGPPGPGPGPGPGPGRPGHVGQM GPVGAPGRPGPPGPGPGPGPGRYGKGBKGDVGQPGPN GIPSDTLHPIIAPTGVTFHPDQYKGEKGSEGEPGIRGISLKGEE GIM 6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYEVLSNDEKRDIYDKYGTEGLNEF 6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDASSKOVPSRNCLDLYEEILTEGTAKEATY NDLQVEYGKQCLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAPATRNCLPPHSGHPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRARAAVREGWGVVVTPAPAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVFFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEBVRSSAYYLRSRQRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPWTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSABPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELEEMEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD		,	*	LAGVKKFDVPCGGRDCSGGCQCYPEKGGRGQPGPVGPOGYNGPP
PGHPGQGGPRGRPGYDGCNGTQGDSGPQGPPGSEGFTGPPGPQG PKGQKGEPYALPKEERDRYRGEPGEBEDLVGFQGPPGPHGRUGQM GGPVGAAPGRPGPPGPBGRQQQGNRGLGFYGVKGEKGDVGQPGPN GIPSDTLHPILAPTGVTFHPPQYKGEKGSEGEPGIRGISLKGEE GIM 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPPKNPENKEEAE RFKFKVAEAYEVLSNDEKRDIYDKYGTEGLMEF 6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEGTAKEATY NDLQVEYGKCQLQMKELMKKPKEIQTQNF5LINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCTTAATTQAAAPATRNCLPPHSGHPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGREWFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRQPR PQGTEEMKTRRTTRLQQQHSEQPPLQPSPWMTRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGGTEBDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVCMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELEMEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKB 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				GLQGFPGLQGRKGDKGERGAPGVTGPKGDVGARGVSGFPGADGI
GPVGAPGRPGPPGPPGPKGQQGNRGLGFYGVKGEKGDVGQPGPN GIPSDTLHPIIAPTGVTFHPDQYKGEKGSEGPGIRGISLKGEE GIM 6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYEVLSNDEKRDIYDKYGTEGLNEF 6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEBVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDATLAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEGL LLAEKCHRRTVYELENEKKKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD		٠.	:	PGHPGQGGPRGRPGYDGCNGTQGDSGPQGPPGSEGFTGPPGPQG
GPVGAPGRPGPPGPPGPKGQQGNRGLGFYGVKGEKGDVGQPGPN GIPSDTLHPIIAPTGVTFHPDQYKGEKGSEGPGIRGISLKGEE GIM 6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYEVLSNDEKRDIYDKYGTEGLNEF 6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEBVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDATLAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEGL LLAEKCHRRTVYELENEKKKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD			and the second s	PKGQKGEPYALPKEERDRYRGEPGEPGLVGFQGPPGRPGHVGQM
6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYEVLSNDEKRDIYDKYGTEGLNEF 6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEBVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEBDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYERPISELDRLEEKQKETYRRMEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKB	1 1			GPVGAPGRPGPPGPRGQQGNRGLGFYGVKGEKGDVGQPGPN
6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYEVLSNDEKRDIYDKYGTEGLNEF 6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDASKSCVPSRNCLDLYEEILTEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDESGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVVVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEBVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD		1 1 31 1		GIPSDTLHPILAPTGVTFHPDQYKGEKGSEGEPGIRGISLKGEE
RKFKEVAEAYBULSNDEKRDIYDKYGTEGLNEF 6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRPPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGYVYTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEBVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEBDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				GIM
6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	6730	784	1015	NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE
LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEBVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEBDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWQDLDD				RKFKEVAEAYEVLSNDEKRDIYDKYGTEGLNEF
NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEBVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEBDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	6731	1	446	
LIKTARVEINRKDEEI 6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEBDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				
6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEBVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEBDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	1 . 1	1		
AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				
LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEBDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	6732	102	1205	
GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				
PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEBDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				
PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEBDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD		İ		
DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEBDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	1			
YEATSVQQKVNFSEEGETEBDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD		j		
6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				
6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD] 1			
KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	6723	613		
QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	0,33	013	1311	
VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD			1	
LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				
LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				VLHKDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL
6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	1			
JOHNSTEIN STEEN AND TWEE WOODEDD	6734	100		
AQKTLYRDVMLETYSSLVSLGHCITKPEMIFKLEQGAEPWIVEE	0134	103	551	SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD
	<u> </u>			ACKILIKDVMLETYSSLVSLGHCITKPEMIFKLEQGAEPWIVEE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 .	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TLNLRLSGGSKKQVFSGICHRSLVELQEVHLV
6735	280	558	
1 0,33	200	330	KSRRAGVTKMSNPFLKQVFNKDKTFRPKRKFEPGTQRFELHKKA
1 .			QASLNAGLDLRLAVQLPPGEDLNDWVAVHVVDFFNRVNLIYGTI
6736	105		XDGCT
6/36	195	808	MNYELNFKREMPNIKSLGLTNLNFLLKRLSSVLPLITDYVYFEN
İ			SSSNPYLIRRIEELNKTASGNVEAKVVCFYRRRDISNTLIMLAD
		}	KHAKEIEBESETTVEADLTDKQKHQLKHRELFLSRQYESLPATH
		1	IRGKCSVALLNETESVLSYLDKEDTFFYSLVYDPSLKTLLADKG
	<u> </u>		EIRVGPRYQADIPEMLLEGTFFCVFAVL
6737	150	1209	PVIMPLHFSPGDIVRPSCCVSSSPKLRRNAHSRLESYRPDTDLS
			REDTGCNLQHISDRENIDDLNMEFNPSDHPRASTIFLSKSQTDV
		1	REKRKSLFINHHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTIK
1		Ī	CVALAIYYHIKNRDPDGRMLLDIFDENLHPLSKSEVPPDYDKHN
	\$4.55	I * * * * * * * * * * * * * * * * * * *	PEQKQIYRFVRTLFSAAQLTAECAIVTLVYLERLLTYAEIDICP
			ANWKRIVLGAILLASKVWDDQAVWNVDYCQILKDITVEDMNELE
			ROFLELLQFNINVPSSVYAKYYFDLRSLABANNLSFPLEPLSRE
		•	RAHKLEAISRLCEDKYKDLRRSARKRSASADNLTLPRWSPAIIS
6738	148	653	CACAEQPARAEVGAATALPVRWASGEMAPSGSLAVPLAVLVLLL
	1	""	WGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACONL
l			
i .)		QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHC
6739	3		KDGEFRRYQGPRTKKDFINFISDKEWKSIEPVSSWF
8/39] 3	631	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
1	1		ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKP
[VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
		;	REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
6740			TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6740	3	631	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
J			ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
			VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
	1 :		REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
			TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6741	141	960	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
			HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM
j l		'.	YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI
		,	WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW
		<u> </u>	DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
		i	PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ
			LIPKTKIP
6742	141	960	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
			HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM
j l			YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI
<u> </u>			WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW
<u> </u>			
			DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
			PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ
		410	LIPKTKIP
. m/a2	1 1	412	MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK
6743		,	ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN
6/43			UNDERSTRUCTURE OF THE PROPERTY AND THE PROPERTY OF THE PROPERT
6/43		•	FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL
		, 	LQNIR
6744	95	1343	•
	95	1343	LQNIR
	95	1343	LQNIR RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGQBELT
	95	1343	LQNIR RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT
	95	1343	LQNIR RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFQESVEEFPE
	95	1343	LQNIR RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT

SEQ	Predicted	l Drodietad and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
,	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 :	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
!	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
			CEQYGLQNVDGEMLEEVFHNLDPDGTMSVEDFFYGLFKNGKSLT
			PSASTPYRQLKRHLSMQSFDESGRRTTTSSAMTSTIGFRVFSCL
1	}		DDGMGHASVERILDTWQEEGIENSQEILKALDFGLDGNINLTEL
6745	 		TLALENELLVTKNSIHQACI
6745	1	588	TFRDQGWAQRRRWLLGCASWESWEAAIAAGPGLPSSTARQQNNP
			AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERRRDP
	1		ELPVTSFDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNKWTC
			PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMRAHI RTCQKYIDKYGPLQELEETA
6746	110	492	GATGAMAESAPARHRRKRRSTPLTSSTLPSQATEKSSYFOTTEI
3,40	110	774	GATGAMAESAPARHRRKRRSTPLTSSTLPSQATEKSSYFQTTEI SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCEKMA
			VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN
6747	247	484	EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLSVGH
1 1			QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC
6748	201	665	MTTFKEAVTFKDVAVVFTEEELGLLDPAQRKLYRDVMLENFRNL
			LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIEMET
1 .			VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGDVPC
			QIEARLSISXVQQXPYRCNECKQ
6749	95	719	RREVKGGDGVCPRARGSPQSQQFPSCAGGGEGLQQSGEALDGAM
	;		SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFDKAF
			VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQSVSQ
			INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQLQL
			HAKTGQSADSGTIKAKLSGPSVEELERELKAN
6750	3	428	SCESRRPGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRATMGT
]			TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERMFTR
			EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSRRKS
6751			RSSQLSSRR
0,21	152	1417	PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIV
	grade the state of		NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGEEML
			QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLCEDL
1 :- 1			FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE HDLLGDYVEDLSKLAVTSYNDIODI MDSGNVARMVAAMDAATERG
		:	HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETS SRSHAVFNIIFTQKRHDAETNITTEKVSKISLVDLAGSERADST
; . [•	GAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNKKKKKTD
1 : 1			FIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLR
] :]			YADRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLGD
			ITDMTNALVGMSPSSSLSALSSRNV
6752	24	1834	RNCVPPLGCYRSRVKFHSDIKMQYSHHCEHLLERLNKQREAGFL
1	1		CDCTIVIGEFQFKAHRNVLASFSEYFGAIYRSTSENNVFLDQSQ
			VKADGFQKLLBFIYTGTLNLDSWNVKEIHQAADYLKVEEVVTKC
	}		KIKMEDFAFIANPSSTEISSITGNIELNQQTCLLTLRDYNNREK
	1		SEVSTDLIQANPKQGALAKKSSQTKKKKKAFNSPKTGQNKTVQY
	}		PSDILENASVELFLDANKLPTPVVEQVAQINDNSELELTSVVEN
	İ		TFPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPYEAE
	,		NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV
	1		CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF
	İ		HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR
	ľ	ĺ	CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR
			KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED
1 1		ļ	HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV
6753			TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY
0/33	2	1305	VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS
			PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG
1			SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV
l l			AHPGPPPASSQTPAPEHDKAANKMPLAQKPALAPKPTSQTPPAS

C 080	need at all a		
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first		L=Leucine, M=Methionine, N=Asparagine,
J	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	1	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
			PLSKLSRPYLVELLSRRAGRPDPEPSEPSKEDQESSDRRPPSPP
1			GPEERKGQKRDEEEEATERKPASPPLPATQQEKPSQTPEAGRKE
l .			KPMLQSRHSLDGSKLTEKVETAQPLWITLALQKQKGFREQQATR
			EERKQAREAKQAEKLSKENVSVSVQPGSSSVSRAGSLHKSTALP
			EEKRPETAVSRLERREQLKKANTLPTSVTVEISYSSPAAPLVKE
			VSKRFSSPDDAPVSSEPAWLALAKRKAKAWSDCPLIIK
6754	2	413	FVRRRRRLGGPEVNTMSSLHKSRIADFQDVLKEPSIALEKLRE
			LSFSGIPCEGGLRCLCWKILLNYLPLERASWTSILAKQRELYAQ
			FLREMIIQPGIAKANMGVSREDVTFEDHPLNPNPDSRWNTYFKD
			NEVLL
6755	298	1343	PGLQLQVALEADWFLDMPGGRRGPSRQQLSRSALPSLQTLVGGG
			CGNGTGLRNRNGSAIGLPVPPITALITPGPVRHCQIPDLPVDGS
			LLFEFLFFIYLLVALFIQYINIYKTVWWYPYNHPASCTSLNFHL
1	,	* **	IDYHLAAFITVMLARRLVWALISEATKAGAASMIHYMVLISARL
Ĭ,			VLLTLCGWVLCWTLVNLFRSHSVLNLLFLGYPFGVYVPLCCFHQ
			DSRAHLLLTDYNYVVQHEAVEESASTVGGLAKSKDFLSLLLESL
			KEQFNNATPIPTHSCPLSPDLIRNEVECLKADFNHRIKEVLFNS
			LFSAYYVAFLPLCFVKVSGYLTFMCFLDLCVNYINWVFLV
6756	180	754	IERALGSLPLSIPVSWGSLRTLKYQQQPLRPKVLLCQTRVQCHD
Ì			LRSLQPQPPGLKQSFCLRVLGLQTGATTPGLRDLTCKELIILTE
1 .			REAQKRKKRKEKESGMALTQGPLTFRDVAIEFSQEEWKSLDPVQ
	, ,	* * *	KALYWDVMLENYRNLVFLGKDNFALEVKICPRVFLYFLCCLSWE
			PFHYLTETEALLTHK
6757	2	459	NSRVEAPEAHSRESQGSDAMRKHLSWWWLATVCMLLFSHLSAVQ
1			TRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRKLDID
	·	,	FGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQ
			AANQGEFQKPDNKLHQQVLW
6758	1	1008	ASGPELPGRRFRDRAPWLPARLLRGVLAVWVSLSALGPGSFCRR
1	-		RVPSLAQLGHSEAAPSPDDVRWSRVPDRCPEERDRAWPPPPPPS
1			LPPSFRRNMANNSPALTGNSQPQHQAAAAAAQQQQQCGGGGGATK
1			PAVSGKQGNVLPLWGNEKTMNLNPMILTNILSSPYFKVQLYELK
.	÷ .		TYHEVVDEIYFKVTHVEPWEKGSRKTAGQTGMCGGVRGVGTGGI
			VSTAFCLLYKLFTLKLTRKQVMGLITHTDSPYIRALGFMYIRYT
l			QPPTDLWDWFESFLDDEEDLDVKAGGGCVMTIGEMLRSFLTKLE
			WFSTLFPRIPVPVQKNIDQQIKTRPRKI
6759	1	513	RKHNFHSLDGTSTRAFHPQTGLPLLSSPVPQRKTQSGCFDLDSS
1	,		LLHLKSFSSRSPRPCLNIEDDPDIHEKPFLSSSAPPITSLSLLG
			NFEESVLNYRFDPLGIVDGFTAEVGASGAFCPTHLTLPVEVSFY
	•		SVSDDNAPSPYMGVITLESLGKRGYRVPPSGTIQVVCVL
6760	239	606	VLSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGIT
1			AMSVKEVLOSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLE
			VLESQLSEGSQKHASLQKSIBKAKIGRCETEERT
6761	29	1733	ERTLRGLREVAAPSDVADAAVSRRGRCCCCLHCTOTOVAODCPS
1			SSSSVQRCELSLFQSLHTMTSKKLVNSVAGCADDALAGLVACNP
			NLOLLOGHRVALRSDLDSLKGRVALLSGGGSGHEPAHAGFIGKG
			MLTGVIAGAVFTSPAVGSILAAIRAVAQAGTVGTLLIVKNYTGD
			RLNFGLAREQARAEGIPVEMVVIGDDSAFTVLKKAGRRGLCGTV
			LIHKVAGALAEAGVGLEEIAKQVNVVTKAMGTLGVSLSSCSVPG
I			•
!			SKPTFELSADEVELGLGIHGEAGVRRIKMATADEIVKLMLDHMT
			NTTNASHVPVQPGSSVVMMVNNLGGLSFLELGIIADATVRSLEG
			RGVKIARALVGTFMSALEMPGISLTLLLVDEPLLKLIDAETTAA
	į		AWPNVAAVSITGRKRSRVAPAEPQEAPDSTAAGGSASKRMALVL
			ERVCSTLLGLEEHLNALDRAAGDGDCGTTHSRAARAIQEWLKEG
			PPPASPAQLLSKLSVLLLEKMGGSSGALYGLFLTAAAQPLKAKT
1			SLPAWSAAMDAGLEAMQKYGKAAPGDRTMLDSLWAAGQEL

770	
SEQ Predicted Predicted end Amino acid segment containing ID beginning pucleotide (A=Alanine C=Cysteine D=Aso	signal peptide
	artic Acid, E=
NO: nucleotide location Glutamic Acid, F=Phenylalaning location corresponding H=Histidine, I=Isoleucine, K=1	
corresponding to first L=Leucine, M=Methionine, N=As	
to first amino acid P=Proline, Q=Glutamine, R=Arg	
amino acid residue of S=Serine, T=Threonine, V=Valin	
residue of amino acid Warryptophan, Yarrosine, XaU	
amino acid sequence Codon, /=possible nucleotide of	
sequence \=possible nucleotide insertic	
6762 3 613 ASTISWRLCVAGAEARRPVPVAGERAGGG	
QVAFITLAVAAGLYYLAELIEBYTVATSR	
LYVFERFPTSMIGVGLFTNLVYFGLLQTF	
LVVVNHYLAFQFFABEYYPFSEVLAYFTF	CLWIIPFAFFVSLSA
GENVLPSTMQPGDDVVSNYFTKGKRGK	
6763 2 760 SGPDFPGRRFRGCCCVRPPAGAGMELGGHV	NDMNSAPRLVSETAE
RKQEQKTGTEAEAADSGAVGARRFLLCLYI	GGFLDLFGVSMVVP
LLSLHVKSLGASPTVAGIVGSSYGILQLFS	STLVGCWSDVVGRR
SSLLACILLSALGYLLLGAATNVFLFVLAY	RVPAGIFKHTLSISR
ALLSDVVPBKERPLVIGHFNTASGVGFILO	PVVGGYLTELEDGF
YLTAFICFLVFILNAGLVWFFPRREAKPGS	
6764 80 438 LKKMDTMMLSVRNLFEQLVRRVEILSEGNE	
KKWQRTDHELGKYKDLLMKAETERSALDVE	
RQRAEADCEKLERQIQLIREMLMCDTSGS	-
6765 3 550 ARYSRVDHFCRRCRAVARAPRFLLQFPSC	
RGSVLVSEALSGSAMDGIVTEVAVGVKRGS	
NMSSMVVTANGNDSKKFKGEDKMDGAPSR\	
VIALGLPFGKVTNILMLKGKNQAFLELATE	EEAAITNGNYYSAVT
PHLRNQ 6766 1 1287 FGGSPKASLTWLWDLGPMKT.HCPVPVTSPL	
2005 Id Dalinani Echinelica Variani	
AVLSLCQQTSRSQPPVRAFLLISTLKDKRC	-
KPVDEGKATVRLKEPPVDICLSKANSSSLI	
VDTPVSTLTPVKTSEFENFKTKMVITSKKI	
QTSYCGLVRVDMRMLCLKSLRKLDLSHNHI ELNLNDNHLESFSVALCHSTLQKSLWSLDI	
LQELKNLKLDDNELIQFPCKIGQLINLRFI	
RNLSLEYLDLFGNTFEQPKVLPVIKLQAPI	
IPYGSHIIPFHLCQDLDTAKICVCGRFCLA	
AHTVVLVDNLGGTEAPIISYFCSLGCYVNS	
6767 336 919 APMICLCSSDLQFRYKEAFLRDRGLQIGYC	
GRLQSDNEYKKDFAKSRSQFHSSTDQPGLI	
RQPLPQPTCDPEQLGLRHAQKAHQLQSDVX	
PPGSYKVEMARRAAELANARGLGLQGAYRG	AEAVEAGDHQSGEV
NPDATEILHVKKKKALLL	
6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEEKHRA	PTMKTLRARFKKTE
LRLSPTDLGSCPPCGPCPIPKPAARGRRQS	QDWGKSDERLLQAV
ENNDAPRVAALIARKGLVPTKLDPEGKSAF	·
6769 284 396 MSTPDFSTAENNQELANEVSCLKAMLTIMI	
6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTE	
ITLNMGVGEAIADKKLLDNAAADLAAISGQ	
KIRQGYPIGCKVTLRGERMWEFFERLITIA	
6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEE	-
WASWNIGVFICIRCAGIHRNLGVHISRVKS	
QEMGNGKANRLYEAYLPETFRRPQIDPYLF	
6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHS	
CLCLTFVSYFGGSG\HKPRWLGWGR\VLMG	
P**GWKLDAGVRTCPANPR\PVCAG\HTSG	~ ~
HGVGATPLYTLGVTYLDENVKSSCSPIYIA	
LIGGALLNIYTEMGRRTELTTESPLWVGAW	
AVPILGYPRQLPGSQRYAVMRAAEMHQLKD	
IRDLPLSIWLLLKNPTFILLCLAGATEATL	
l I	EUNIVI DI DOCAVITE
QFSLSASEAATLFGYLVVPAGGGGTFLGGF	1
QFSLSASEAATLFGYLVVPAGGGGTFLGGF FCLFCTVVSLLGILVFSLHCPSVPMAGVTA	SYGGSLLPEGHLNL
QFSLSASEAATLFGYLVVPAGGGGTFLGGF	SYGGSLLPEGHLNL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 .	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
,	sequence	Bequence	\=possible nucleotide insertion)
6777			
6773	1	630	PWEAPKEHKYKABEHTVVLTVTGEPCHFPFQYHRQLYHKCTHKG
			RPGPQPWCATTPNFDQDQRWGYCLEPKKVKDHCSKHSPCQKGGT
1			CVNMPSGPHCLCPQHLTGNHCQKEKCFEPQLLRFFHKNEIWYRT
			EQAAVARCQCKGPDAHCQRLASQACRTNPCLHGGRCLEVEGHRL
1			CHCPVGYTGPFCDVGE*GSGASRRPAPRWDGLAR
6774	146	389	LTELSDQQYFLFFILSS/WVPTFLSMDVDGRVIKADSFSKIISS
i			GLRIGFLTGPKPLIERVILHIQVSTLHPSTFNQLMISQ
6775	104	614	TCPSQLRVLTARGGRRAPSPOLWTLVLALIEEKWRSHRILRMNS
****	1	021	GRPETMENLPALYTIFQGEVAMVTDYGAFIKIPGCRKOGLVHRT
1			HMSSCRVDKPSEIVDVGDKVWVKLIGREMKNDRIKVSLSMKVVN
			OGTGKDLDPNNV\SLSKKRGGGDPSRITLGRRSPLRLS
-			,
6776	3	1108	HERHERHEGALSQDALLRISIPLDSNMRPEKCRRFVHPQWQLLH
1			LNGTFPNTSDADMEPCVDGWVYDRISFSSTIVTEWDLVCDSQSL
		•	TSVAKFVFMAGMMVGGILGGHLSDRFGRRFVLRWCYLQVAIVGT
	·		CAALAPTFLIYCSLRFLSGIAAMSLITNTIMLIAEWATHRFQAM
			GITLGMCPSGIAFMTLAGLAFAIRDWHILQLVVSVPYFVIFLTS
1			SWLLESARWLIINNKPEEGLKELRKAAHRSGMKNARDTLTLEIL
			KSTMKKELEAAOKKKPFLGERLHMPNICKRISLLPFTKFANFMA
			YFGLNLHG/LKHLGNNVFLLOTLFGAV/TPPGOLVLHLGHWGSG
			RVSSRGRVNCLGLFVLQVW
6777	. 779	63	CFFHGPAWRDCEVRATFAKKQGQSGIISCIAFSPAQPLYACGSY
1. ""	. ,,,,	03	
1			GRSLGLYAWDDGSPLALLGGHQGGITHLCFHPDGNRFFSGARKD
1			AELLCWDLRQSGYPLWSLGREVTTNQRIYFDLDPTGQFLVSGST
•		A.	SGAVSVWDTDGPGNDGKPEPVLSFLPQKDCTNGVSLHPSLPLLG
			HCLPVSVCFLSPTESGGRRRGAGPSLGSPRRHVHLECRLQLWWC
	<u> </u>	i	GGGARLQHP**SPRARKGR
6778	311	805	IQSITDESRGSIRRKNPANTRLRLNVP\EETAGDSE/ERSPEEE
			VQADPRIRSASPKCPTSSPFPKGRSPEGEGET\DPEKVHFHPGP
			KDKSVAEKN\KGP\SPVSSEGIKDFFSMKPEWENLNQSNVRRMH
79			T\AVRLNEVIVKKSRDAKLVLLNMPGPPRNRNGDENY
6779	2	535	RALRROPRLLAANGIEPESMAISEPIKGSRKPCVNKEELALKKP
"""	-	333	MAKCAWKGPREPPODARAEAESPGGASESDODGGHESPPKKKAV
			-
i .	}		AWVSAKNPAPMRKKKKVSLGPVSYVLVDSEDGRKKPVMPKKGPG
1			SRREASDQKAPRGQQPAEATASTSRGPKAKPEGSPRRATNESRK
	,		V
6780	3	403	HEVNDNKPEININIMSPGKEEISYIFEGDPIDTFVALVRVQDKD
1			SGLNGEIVCKLHGHGHFKLQKTYENNYLILTNATLDREKRSEYS
1			LTVIAEDRGTPSLSTVKHFTVQINDINDNPPHFQRSRYEFVISE
I			K
6781	ī	1269	APTRPVFPTLQDLSSSKEPSNSLNLPHSNELCSSLVHPBLSEVS
1			SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT
1			SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI
1			TPVFINSSSIIQVMKGSQPSTIPAAPLTTNSGLMPPSVAVVGPL
1			HIPQNIKFSSAPVPPNALSSSPAPNIQTGRPLVLSSRATPVQLP
Ī			
1'			SPPCTSSPVVPSHPPVQQVKELNPDEASPQVNTSADQNTLPSSQ
I			STTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGQILLTKAC
1			KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEQLSTELDS
1			KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT
			LVPSELISAVPTTKSNHGGIASESLAG
6782	3	1327	RKPTVIRIPAKPGKCLHEDPQSPPPLPAEKPIGNTFSTVSGKLS
1			NVERTRNLESNHPGQTGGFVRVPPRLPPRPVNGKTIPTQQPPTK
1			VPPERPPPPKLSATRRSNKKLPFNRSSSDMDLQKKQSNLATGLS
1			KAKSQVFKNQDPVLPPRPKPGHPLYSKYMLSVPHGIANEDIVSQ
1.			1 ~ ~
1			NPGELSCKRGDVLVMLKQTENNYLECQKGEDTGRVHLSQMKLIT
L		1	PLDEHLRSRPNPFSPPKAPSHAQKPVDSGAPHAVVLHDFPAEQV

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
٧	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
•	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
•	amino acid	sequence	Codon, /=possible nucleotide deletion,
,	sequence	1	\=possible nucleotide insertion)
			DDLNLTSGEIVYLLEKIDTDWYRGNCRNOIGIFPANYVKVIIDI
			PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
	i		LKEYVNEEWARGEVRGRTGIFPLNFVEPVEDYPTSGANVLSTKV
	}		PLKTKKEDSGSNSOVNSLPAEWCEALHSFTAETSDDLSFKRGDR
			I
6783	3	1750	SYHHHHAOOSAAASPNLTASOKTVTTTSMITTKTLPLVLKAATA
0,03		1,30	TMPASVVGORPTIAMVTAINSQKAVLSTDVONTPVNLQTSSKVT
			GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
			LPOVRPKPVAONNIPIAPAPPPMLAAPOLIORPVMLTKFTPTTL
			PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
			QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
			POKLAFMVSLGLVTHDHLEEIQSKRQERKRRTTANPVYSGAVFE
		,	PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
			SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
			RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
			KEEAIPWPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ
			LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
			GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT
			ANCNQGEETK
6784	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
	•		TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKVT
	· · ·		GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
]		LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
			PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
İ			QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
	` ` ` ` ` ` ` ` ` ` ` ` ` ` ` ` ` ` `	'	PQKLAFMVSLGLVTHDHLBEIQSKRQERKRRTTANPVYSGAVFE
	'	•	PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
			SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
			RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
	7		KEEAIPWPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ
	•		LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
	'		GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT
		,	ANCNOGEETK
6785	1	528	LGNTVLHYCSMYSKPECLKLLLRSKPTVDIVNQAGETALDIAKR
			LKATQCEDLLSQAKSGKFNPHVHVEYEWNLRQEEIDESDDDLDD
			KPSPVKKERSPRPQSFCHSSSISPQDKLALPGFSTPRDKQRLSY
			GAFTNQIFVSTSTDSPTSPTTEAPPLPPRNAGKGPTGPPITPHR
6786	1820	1397	RSPKVLVLAPTRELANHVSRDFKDI\TRKLTVARFYGGTSYQSQ
	. 1		INHIRNGIDILVGTPGRIKDHLQSGRLDLSKLRHVVLDEVDQML
			DLGFAEQVEDIIHESYKTDSEDNPQTLLFSATCPQWVYTVA\KK
			YMKSRYEOVDLDGKMTOKAATTVEHLAIQCHWSQRPAVIGDVLQ
			VYSGSEGRAIIFCETKKNVTEMAMNPHIKQNAQCLHGDIAQSQR
			EITLKGFREGSFKVLVATNVAARGLDIPEVDLVIQSSPPQDVES
			YIHRSGRTGRAGRTGICICFYQPRERGQLRYVEQKAGITFKRVG
			VPSTMDLVKSKSMDAIRSLASVSYAAVDFFRPSAQRLIEEKGAV
			DALAAALAHISGASSFEPRSLITSDKGFVTMTLESLEEIQDVSC
			AWKELNRKLSSNAVSQITRMCLLKGNMGVCFDVPTTESERLQAE
ľ	ļ		WHDSDWILSVPAKLPEIEEYYDGNTSSNSRQRSGWSSGRSGRSG
			_ · · · · · · · - · · · · · · · · · · · · · · · · · · ·
			RSGGRSGGRSGRQSRQGSRSGSRQDGRRRSGNRNRSRSGGHKRS
			FD*VFYHLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS
	1		SVWN
			PSSFPKNVPLEELEEPPK*KRSGLGSLTPKSQIONGP*PQTFFF
6787	2646	2270	_ · · · · · · · · · · · · · · · · · · ·
6787	2646	2270	FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI
			FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI LVFLVBMGFHHVGQAGLKLLTL\VIHPPWPPKVLGLQT
6787	2646	936	FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI

070			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			EVILWGS*DS*GYPKGK*LLPKEVPSR/RVLLSGLTPLDATOE\
			FTEDLSK\YVTTMVCVAVNGKPMLGVIHKPFSEYTAWAMVDGGS
			NVKARSSYNEKTPRIVVSRSHSGMVKQVALQTFGNQTTIIPAGG
1			AGYKVLALLDVPDKSQEKADLYIHVTYIKKWDICAGNAILKALG
			GHMTTLSGEEISYTGSDGIEGGLLASIRMNHOALVRKLPDLEKT
		į	GHK
6789	2	<u> </u>	
6789		678	GNGINVLKIAPESAIKFMAYEQIKRLVW**PGDS*GF/YERLVA
		1	GSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARRILARE
			GVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSAD
			PGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVT
	1	ł	MSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLKI
			TLGVQSR
6790	2	4068	APPAGRRRMQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD
	,		EPLVSGLPHVAFSSSSSISGSYSPGYAKINKRGGAGGWSPSDSD
	ĺ		HYQWLQVDFGNRKQISAIATQGRYSSSDWVTQYRMLYSDTGRNW
			KPYHQDGNIWAFPGNINSDGVVRHELQHPIIARYVRIVPLDWNG
			EGRIGLRIEVYGCSYWADVINFDGHVVLPYRFRNKKMKTLKDVI
			ALNFKTSESEGVILHGEGOOGDYITLBLKKAKLVLSLNLGSNOL
			GPIYGHTSVMTGSLLDDHHWHSVVIERQGRSINLTLDRSMQHFR
	ł	ł	TNGEFDYLDLDYEITFGGIPFSGKPSSSSRKNFKGCMESINYNG
		1	VNITDLARRKKLEPSNVGNLSFSCVEPYTVPVFFNATSYLEVPG
			RLNQDLFSVSFQFRTWNPNGLLVFSHFADNLGNVEIDLTESKVG
			VHINITOTKMSQIDISSGSGLNDGQWHEVRFLAKENFAILTIDG
1			DEASAVRTNSPLOVKTGEKYFFGGFLNOMNNSSHSVLOPSFOGC
			MOLIOVDDQLVNLYEVAQRKPGSFANVSIDMCAIIDRCVPNHCE
			HGGKCSQTWDSFKCTCDETGYSGATCHNSIYEPSCEAYKHLGQT
			SNYYWIDPDGSGPLGPLKVYCNMTEDKVWTIVSHDLQMQTPVVG
			YNPEKYSVTQLVYSASMDQISAITDSABYCEQYVSYFCKMSRLL
40.00			NTPDGSPYTWWVGKANEKHYYWGGSGPGIQKCACGIERNCTDPK
	<u> </u>		YYCNCDADYKQWRKDAGFLSYKDHLPVSQVVVGDTDRQGSEAKL
			SVGPLRCQGDRNYWNAASFPNPSSYLHFSTFQGETSADISFYFK
			TLTPWGVFLENMGKEDFIKLELKSATEVSFSFDVGNGPVEIVVR
		1	SPTPLNDDQWHRVTAERNVKQASLQVDRLPQQIRKAPTEGHTRL
	İ		ELYSQLFVGGAGGQQGFLGCIRSLRMNGVTLDLEERAKVTSGFI
	1	ļ	SGCSGHCTSYGTNCENGGKCLERYHGYSCDCSNTAYDGTFCNKD
			VGAFFEEGMWLRYNFQAPATNARDSSSRVDNAPDQQNSHPDLAQ
	ĺ		EEIRFSFSTTKAPCILLYISSFTTDFLAVLVKPTGSLQIRYNLG
•			GTREPYNIDVDHRNMANGQPHSVNITRHEKTIFLKLDHYPSVSY
			HLPSSSDTLFNSPKSLFLGKVIETGKIDQEIHKYNTPGFTGCLS
			RVQFNQIAPLKAALRQTNASAHVHIQGELVESNCGASPLTLSPM
			SSATDPWHLDHLDSASADFPYNPGQGQAIRNGVNRNSAIIGGVI
	,		A\VVIFTPSLCTP\VLP*SR*HVSPHKGTLPIPNEAKGAGSRQK
	,	1	KPGRRPSMNNDPPTSQRPIDESKKEWPHLRGGYLAMG
6791	1801	1193	TGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPEL/PGW
			SAVV*SWLTAASTKVOAILLPOPLE*LGLOIAFMASLATHFSNO
			NSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDV
		}	EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVW
6700	33	1.55	LRMGNGALHGDHQRFSTFAGFLLFETK
6792	33	1073	VRHTNWGVDMYLFSLGSESPKGAIGHIVSTEKTILAVERNKVLL
	}		PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAV
			CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAV
			TCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA
		1	ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC
		[CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG
			APGSASKPKRPQVGEEPGLESRAGR+HCFDREAQQNQP\PVTAL
			AVSRNHTKLLVGDERGRIFCWSADG*EERGSRGSGTTVPG
	 	1	

SEO	T Dwo dd at a d		
. ~	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
:	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6793	2340	805	GRKEANY\YGSLTQAGTVSLGLDAEGQEVFVPFSAVLPMVAPND
		· ·	LVFDGWDISSLNLAEAMRRAKVLDWGLQEQLWPHMEALRPRPSV
			YIPEFIAANQSARADNLIPGSRAQQLEQIRRDIRDFRSSAGLDK
I			VIVLWTANTERFCEVIPGLNDTAENLLRTIBLGLEVSPSTLFAV
	·		ASILEGCAFLNGSPQNTLVPGALELAWQHRVFVGGDDFKSGQTK
ł	•		VKSVLVDFLIGSGLKTMSIVSYNHLGNNDGENLSAPLQFRSKEV
	1		SKSNVVDDMVQSNPVLYTPGEEPDHCVVIKYVPYVGDSKRALDE
			YTSELMLGGTNTLVLHNTCEDSLLAAPIMLDLALLTELCQRVSF
ļ			CTDMDPEPQTFHPVLSLLSFLFKAPLVPPGSPVVNALFRQRSCI
1			ENILRACVGLPPQNHMLLEHKMERPGPSLKRVGPVAATYPMLNK
ļ	j		KGPVPAATNGCTGDANGHLQEEPPMPTT*GPGHTVSRLFLPAAP
			HDPTLKAPTNKGRCHFSPPSTWGSWGL
6794	169	1349	DDVKRKPEASAH*EKPGPPSRPGVRGGRERAGGRGSHGARSCR\
	[EPAPPAPAPPEDHPDEEMGFTIDIKSFLKPGEKTYTQRCRLFVG
1	}		NLPTDITEEDFKRLFERYGEPSEVFINRDRGFGFIRLESRTLAE
1		, ,	IAKAELDGTILKSRPLRIRFATHGAALTVKNLSPVVSNELLEQA
1	· i		FSQFGPVEKAVVVVDDRGRATGKGFVEFAAKPPARKALERCGDG
1			AFLITTPRPVIVEPMEQFDDEDGLPEKLMQKTQQYHKEREQPP
			RFAQPGTFEFEYASRWKALDEMEKQQREQVDRNIREAKEKLEAE
			MEAARHEHQLMLMRQDLMRRQEELRRLEELRNQELQKRKQIQLR
6795	1740		HEEEHRRREEEMIRHREQEELRRQQEGFKPNYMENYVCHFLR -
6/95	1/40	1010	GPRRQTQVRDHELDSF*DWAAQETDCAQNSGERL*KGV/LENFS
-			TMSKSAVKISLDLLSNPLCEQDQDLLNMVTALDTAMKRMDAFNQ
1			EKVNQIQKTVIEPLKKFGSVFPSLNMAVKRREQALQDYRRLQAK
1		•	VEKYEEKEKTGPVLAKLHQAREELRPVREDFEAKNRQLLEEMPR
1	·	<i>.</i>	FYGSRLDYFQPSFESLIRAQVVYYSEMHKIFGDLSHQLDQPGHS
6796			DEQRERENEAKLSELRALSIVADD
6/96	48	683	GKEIQIPTIKLAWLLFGLE*PVGALGKGVVSF**SHVALGQLGW
	and the same and the same and the		LTRAVRSSWRWELCVSAQEVVSQRSA*SSPSPVGACPSLNPPET
	•	•	SVQEGRDCWQR*LPRLFSALVGQPGCWPQGAPPERCV*PGRCKW
		•	HLQSQVLR*ERRRCCRCLPRFA*GWRRRHQRLGLGIHPAPLGST
6797	1620		SPPHPEGNSQQCRR*GWAAELRLPSSVVL*GKLGC*
0,9,	1020	21,1	TERMTPSQPTRGSSCTRPSSMLWTSTWRCLTCHWAGMRMSVVGV
1			TLGPMAQGLLSASGTTTEATWTRPTTHLTLIRWWLLTASRVDPP
	, ,		ERPPPPPSDDLTLLESSSSYKNL/DAQIPQ/DWSMSPSTSG*RP
.] '	.		LTSRASSIMRSRTAIPSAS*SRLTTKHTVGGSPSAWRPRPTSRS
			VSTPVSSSTETTASGSCLTWWSSSPAPCPSSSAPAHSFEASCCK
] .			TSLWGSCGGSGDGSSACGSGWNLSMAGTSCSSPAMCSPSRAPS*
			RSASRPRTWRATTSAASSWAPRRCWCGWA*SAT*PSSTTTISSS
			PHCGWPCPASCASAAAWLSSTWATASVAGSCWGPIM*SSAHSPW
-	1		CLSACSRSSMGTTCL*RSPP\SGASRAAAAWCGSSPSSTFTPSS
	ì		ASSSTWCSASSSRSSPAPTTPSSIPAAQAQRRASCRPTSHSART
6700	2004		APPPASSAAGAARPAAFSAAAEGTPRRSIRCW
6798	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
			ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
	į		VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
	į		ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
			VFDDEBKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
			TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
			ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
1 1			QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
] [PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL
	·		SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
1 1			PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP
		1	APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
L			DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ

			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Degacinee	\=possible nucleotide insertion)
	bequestes		PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
1			RILFHPAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
1		,	MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
			LTFALGEQLSTEVGEVDQFPPVEQWGNL
6799	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
			ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
			VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
			ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
•			VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
l			TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
			ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
1 .			QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
'			PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL
			SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
1			PRPGTAACGASDAPLLOPSAPSSSSSQAPLPPPFPAPVVPASVP
1			APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
1		· .	DOLLERAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFO
<u>.</u>		,	1 . ⁻ 7
1			PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
			RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
· ·	. '		MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
			LTFALGEQLSTEVGEVDQFPPVEQWGNL
6800	404	1646	RRSPSTGLSPVPQPSSPSLSDYSIPWSLLLSGTIAWATPGK*AG
			*PQAW*LGLAPAIAFI/GLTRGRKQNKEKMAEGGSGDVDDAGDC
		,	SGARYNDWSDDDDDSNESKSIVWYPPWARIGTEAGTRARARARA
			RATRARRAVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILE
Į.	,		AALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKAL
	•	·	IVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLL
			TNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLLNLAE
		• • • • • • • • • • • • • • • • • • • •	NPAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN
1 : 5 5 5 7 7		and the second second second second	FKWEENEPTONOFGEGSLFFFLKEFQVCADKVLGIESHHDFLVK
1	•	•	VKVGKFMAKLAEHMFPKSQE
6801	2	1755	SAEEFESQOASVTMHDVDAESFEVLVDYCYTGRVSLSEANVERL
""	~	. 2755	YAASDMLOLEYVREACASFLARRLDLTNCTAILKFADAFGHRKL
'			RSQAQSYIAQNFKQLSHMGSIREETLADLTLAQLLAVLRLDSLD
}		,	VESEQTVCHVAVQWLEAAPKERGPSAAEVFKCVRWMHFTEEDQD
ļ			The state of the s
			YLEGLLTKPIVKKYCLDVIEGALQMRYGDLLYKSLVPVPNSSSS
I			/R*QQQLSCICSRKSTPETGYVCQGDGDLLWTPQRSLS\RYDPY
		• 1	SGDIYTMPSPLTSFAHTKTVTSSAVCVSPDHDIYLAAQPRKDLW
1			VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYILGGRDPITGVK
1			LKEVECYSVQRNQWALVAPVPHSFYSFELIVVQNYLYAVNSKRM
1	İ		LCYDPSHNMWLNCASLKRSDFQEACVFNDEIYCICDIPVMKVYN
	İ		PARGEWRRISNIPLDSETHNYQIVNHDQKLLLITSTTPQWKKNR
]			VTVYEYDTREDQWINIGTMLGLLQFDSGFICLCARVYPSCLEPG
1			QSFITEEDDARSESSTEWDLDGFSELDSESGSSSSFSDDEVWVQ
I .		*	VAPQRNAQDQQGSL
6802	157	1341	ETFPLFFFLLSKTPGKTASMAHFVQGTSRMIAAESSTEHKECAE
1			PSTRKNLMNSLEOKIRCLEKORKELLEVNQQWDQQFRSMKELYE
1]		RKVAELKTKLDAAERFLSTREKDPHORORKDDROREDDRORDLT
1			RDRLQREEKEKERLNEELHELKEENKLLKGKNTLANKEKEHYEC
I	1		EIKRLNKALQDALNIKCSFSEDCLRKSRVEFCHEEMRTEMEVLK
1			
1			QQVQIYEEDFKKERSDRERLNQEKEELQQINETSQSQLNRLNSQ
1	}		IKACQMEKEKLEKQLKQMYCPPCNCGLVFHLQDPWVPTGPGAVQ
1			KQREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPPVCCQAG/PR
}			TPGLK*SSCLWLPKC*NFRFILSKESPSVEVHTNRERQQATRER
			G
6803	11	2203	KLSGRPYRHMGVLGTSKLYDIRKTIFTFTPQFIDQQQFYLALDN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
'	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	-	· · · · · · · · · · · · · · · · · · ·	KMIVEMLRTDLSYLCSRWRMTGQPTITFPISHSMLDEDGTSLNS
;]		SILAALRKMQDGYFGGARVQTGKLSEFLTTSCCTHLSFMDPGPE
]	GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDEVARYLDHLL
	1	,	AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLVTKAKELHVQ
			NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSVRVEIHLPRD
	1		QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKGPDWNTELYN
			ERSATVRELLTELYGKVGEIRHWGLIRYISGILRKKVEALDEAC
			TDLLSHQKHLTVGLPPEPREKTISAPLPYBALTQLIDEASEGDM
			SISILTQEIMVYLAMYMRTQPGLFAEMFRLRIGLIIQVMATELA
			HSLRCSAEEATEGLMNLSPSAMKNLLHHILSGKEFGVERK/SVR
•	l		PTDSNVSPAISIHEIGAVGATKTERTGIMQLKSEIKQVEFRRLS
			ISAESQSPGTSMTPSSGSFPSAYDQQSSKDSRQGQWQRRRRLDG
			ALNRVPVGFYQKVWKVLQKCHGLSVEGFVLPSSTTREMTPGEIK
		,	FSVHVES\VLNVLLRPEYRQLLVEAILVLTMLADIEIHSIGSII
			AVEKIVHIANDLFLQEQKTLGP\DDTMLAKDPASG\ICTLR\YD
1	1		SAPSGRFGTMTYLS\RAA\ATYVQEFLP\HSICAMQ
6804	1	951	GSPGKKEEKAKNKESLCMENSSNSSSDEDEBETKAKMTPTKKYN
			GLEEKRKSLRTTGFYSGFSEVAEKRIKLLNNSDERLQNSRAKDR
			KDVWSSIQGQWPKKTLKELFSDSDTEAAASPPHPAPEEGVAEES
1 .			LQTVAEEESCSPSVBLEKPPPVNVDSKPIEEKTVEVNDRKAEFP
1 .			SSGSNFSA*IPLPYLHLNRLHQSL*QKGSRQQSSVTVSEPLAPN
	·		QEEVRSIKSETDSTIEVDSVAGELQDLQSERE*LASRF*CQCEL
		ļ	KQ**SARTRTS*KSLYRSEKSERCSGRRKFIKKAEKKP*SNSGK
[QQKEGKRHK
6805	1539	206	ROPDLKYFGKSFDVSVSESSSLLSNDLPKFADGIKARNRNQNYL
'		:	VPSPVLRILDHTAFSTEKSADIVICDEECDSPESVNOOTQEESP
			IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLQDQTDEEPPA
	••··		IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLQDQTDEEPPA
		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLQDQTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS
		er y spirit	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI
			IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY
			IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD
			IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV
	•		IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW EYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW EYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP VHETT
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW EYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW EYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERBLISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERBLISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLQDQTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW EYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERBLISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLTVADGANPWSISSCDAFLNVFQSRGLRPEV ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERBLISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD TBEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW EYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP VHLTT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD TBEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYMNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLTVADGANPWSISSCDAFLNVFQSRGLRPEV ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD TEEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD TBEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD TBEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODQTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD TEEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERBLISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD TBEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERBLISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD TEEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD TEEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD TEEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT QAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERBLISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD TBEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT QAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVPRPPSP DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRQ IAICLDPYCGLGFALWCLCSVYSGHQSVLVPPLELESNVSLWLS
6806	272	3794	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW BYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD TEEKLSVITVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT QAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVPRPPSP

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1'	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	sequence	\=possible nucleotide insertion)
<u> </u>	2040000		LQGTAGPDPTTVYVDMRALRHDRVRLVERGSPHSLPLMESGKIL
1			PGVKVIIAHTETKGPLGDSHLGEIWVSSPHNATGYYTVYGEEAL
	i		HADHFSARLSFGDTQTIWARTGYLGFLRRTELTDASGGRHDALY
			VVGSLDETLELRGMRYHPIDIETSVIRAHRSIAECAVFTWTNLL
	İ		VVVVBLDGLEQDALDLVALVTNVVLEEHYLVVGVVVIVDPGVIP
1			INSRGEKQRMHLRDGFLADQLDPIYVAYNM
6807	1444	606	VGHDTVHAMFTCFPKCLGFSPPVNVTVSPRSEESHTTTVSGGNG
		""	SVFQAGPQLQALANLEARRGSIGAALSSRDVSGLPVYAOSGEPR
1			RLTQAQVAAFPGENALEHSSDQDTWDSLRSPGFCSPLSSGGGAE
1			SLPPGGPGHAEAGHLGKVCDFHLNHQQPSPTSVLPTEVAAPPLE
i			KILSVDSVAVDCAYRTVPKPGPQPGPHGSLLTEGCLRSLSGDLN
			RFPCGMEVHSGQRELESVVAVGEAMA\LKFPMGAMSYCLRDRSR
			FLFRLPMGLSCPLQVQ
6808	2063	737	GVGSGAASALARSRPLASRLSSRRRTRAPRSGAMQRLAMDLRML
	2005	'3'	SRELSLYLEHOVRVGFFGSGVGLSLILGFSVAYAFYYLSSIAKK
1	!		PQLVTGGESFSRFLQDHCPVVTETYYPTVWCWEGRGQTLLRPF\
	•		ITSKPPVQYRNELIKTADGGQISLDWFDNDNSTCYMDASTRPTI
Ì]		LLLPGLTGTSKESYILHMIHLSEELGYRCVVFNNRGVAGENLLT
			PRTYCCANTEDLETVIHHVHSLYPSAPFLAAGVSMGGMLLLNYL
		,	GKIGSKTPLMAAATFSVGWNTFACSESLEKPLNWLLFNYYLTTC
			LQSSVNKHRHMFVKQVDMDHVMKAKSIREFDKRFTSVMFGYOTI
·			DDYYTDASPSPRLKSVGIPVLCLNSVDDVFSPSHAIPIETAKON
1	•		PNVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHGH
			RLS
6809	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTOTVPO
1			TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLROMF
			GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV
			EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA
-	i i		VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG
		' '	AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP
,	,	٠.	TRTITPSGPRRPTALEPCETFHRFLLGP
6810	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ
Ì	,		TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF
1 .			GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV
1			EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA
		*	VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG
			AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP
			TRTITPSGPRRPTALEPCETFHRFLLGP
6811	1522	658	DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME
			FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG
1			SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN
1			GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV
1			SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK
1			TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI
<u> </u>			VTACQEGFICTWGRPGKVVSFNP
6812	4001	1682	EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ
			KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL
			SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL
			VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV
			HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE
			ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI
			TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE
[l		EVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT
			VTVTBPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK
			DGLEVEESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA
			FFTVTVTEPPVQFLALETTPSPLCVAPGEPVVLSCELSRAGAPV
			<u> </u>

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
—			VWSHNGRPVQEGEGLELHAEGPRRVLCIQAAGPAHAGLYTCQSG
i			AAPGAPSLSFTVQVAEPPVRVVAPEAAQTRVRSTPGGDLELVVH
i		İ	LSGPGGPVRWYKDGERLASQGRVQLEQAGARQVLRVQGARSGDA
1	ĺ		GEYLCDAPODSRIFLVSVEEPLLVKLVSDLTPLTVHEGDDATFR
1	1		
1	ĺ		CEVSPPDADVTWLRNGAVVTPGPQRQSCCSYGGCRMCGQRKART
1			CVSKWRQAEWVQRGPCAGCEVGSPCPTTLACPWPRMGTSTASSS
			MVSYWPTRAPTAARATTIAPWPGSA
6813	9	836	SSTQQRPGVPAGPRPLDGYLGVADHKPLKMHCRDCALVTSSGHL
			LHSRQGSQIDQTECVIRMNDAPTRGYGRDVGNRTSLRVIAHSSI
i			QRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGKGQVYNNLHLLS
			QVLPRLKAFMITRHKMLQFDELFKQETGQ\NRKISNTWLSTGWF
1			TMTIALELCDRINVYGMGPPDFCRDPNHPSVPYHYYEPFGPDEC
			TMYLSHERGRKGSHHRFITEKRVFKNWARTFNIHFFQPDWKPES
·	`		LAINHPENKPVF
6814	3	737	KFRRQEAN/ARERNRMHGLNDALDNLRKVVPCYSKTQKLSKIET
1			LRLAKNYIWALSEILRIGKRPDLLTFVQNLCKGLSQPTTNLVAG
•			CLQLNARSFLMGQGGEAAHHTRSPYSTFYPPYHSPELTTPPGHG
i			TLDNSKSMKPYNYCSAYESFYESTSPECASPQFEGPLSPPPINY
			NGIFSLKQEETLDYGKNYNYGMHYCAVPPRGPLGQGAMFRLPTD
			SHFPYDLHLRSQSLTMQDELNAVFHN
6815	906	553	QGLDPASQTKVVELLKDGSGRRGDRRSSRDMAGGAGPRSESDLE
		•	DVGPTAEWNGDGSGSLRRSGSFGKLRDALRRSSEMLVKKLOGGT
			PQEPPNPRMKRASSLNFLNKSVEBPTQPGG
6816	1 , .	803	NLLKTHKF\LLGODEDSLHSVPVAOMGNYOEYLKTLASPLREID
9816	. 1.	803	NLLKTHKF\LLGQDEDSLHSVPVAQMGNYQEYLKTLASPLREID PDOPKRLHTFGNPFKODKKGMMIDEADEFVAGPONKVKRPGEPN
9816	1	803	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN
9816	1	803	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN
6816	1 ,	803	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM
9816	1 ,	, 803	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS
6816	.	803	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF
	a de la composición dela composición de la composición de la composición de la composición dela composición de la composición dela composición dela composición de la composición dela composición de la composición de la composición dela composición dela composición dela composición dela composición dela composición dela composición dela composición dela composición dela	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK
6817	172	803 3457	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS
	a de la composición dela composición de la composición de la composición de la composición dela composición de la composición dela composición dela composición de la composición dela composición de la composición de la composición dela composición dela composición dela composición dela composición dela composición dela composición dela composición dela composición dela	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL
	a de la composición dela composición de la composición de la composición de la composición dela composición de la composición dela composición dela composición de la composición dela composición de la composición de la composición dela composición dela composición dela composición dela composición dela composición dela composición dela composición dela composición dela	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA
	a de la composición dela composición de la composición de la composición de la composición dela composición de la composición dela composición dela composición de la composición dela composición de la composición de la composición dela composición dela composición dela composición dela composición dela composición dela composición dela composición dela composición dela	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI
	a de la composición dela composición de la composición de la composición de la composición dela composición de la composición dela composición dela composición de la composición dela composición de la composición de la composición dela composición dela composición dela composición dela composición dela composición dela composición dela composición dela composición dela	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC
	a de la composición dela composición de la IHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE		
	a de la composición dela composición de la IHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET		
	a de la composición dela composición de la IHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVPAFPLLLKLETHIEKL		
	a de la composición dela composición de la IHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVPAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF		
	a de la composición dela composición de la IHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVPAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF		
	a de la composición dela composición de la IHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGFCSERH		
	a de la composición dela composición de la IHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE		
	a de la composición dela composición de la IHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVFAFFLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD		
	a de la composición dela composición de la IHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHWVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVFAFFLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV		
	a de la composición dela composición de la IHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCTYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVPAFFLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHP GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ		
	a de la compansión de l	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVFAFFLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ
	a de la compansión de l	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVFAFFLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ
	a de la compansión de l	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVPAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS
	a de la compansión de l	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVFAFFLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ
	a de la compansión de l	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVFAFFLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS
	a de la compansión de l	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLIRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHP GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDAGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP
	a de la compansión de l	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLIRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH
	a de la compansión de l	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLIRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVPAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHP GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGQIHKLRLKLRKKLKAEKKKLAALMSSPQSRTVRSENLE
	a de la compansión de l	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLIRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVPAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGQIHKLRLKLRKKKKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS
	a de la compansión de l	9 + . 	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVPAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGQIHKLRLKLRKKKKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEEILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS
	a de la composición dela composición de la IHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVPAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGQIHKLRLKLRKKLKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEEILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL		

		·	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
-	sequence		\-possible nucleotide insertion)
			DGGE/LHS/ATTEHKP/VQATPVNLT\TILTSTWQARLPQI
6819	1	961	GIPCTEMGNFDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAY
			GEEKKKKCNPYVKTYLLPDRSSQGKRKTGVQRNTVDPTFOETLK
1			YQVAPAQLVTRQLQVSVWHLGTLARRVFLGEVIIPLATWDFEDS
			TTQSFRWHPLRAKADKYEDSVPQSNGELTVRAKLVLPSRPRKLO
			EAQEGTDQPSLHGQLCLVVLGAKNLPVRPDGTLNSFVKGCLTLP
			DQQKLRLKSPVLRKQACPQWKHSFVFSGVTPAQLRQSSLELTVW
1			DQALFGMNDRLLGGT\RLGSKGDTAVGGDACSQSKLQWQKVLSS
			PNLWTDMTLVLH
6820	1014	340	GDMVYIVGHVPPGFFEKTONKAWFREGFNEKYLKVVRKHHRVIA
]	1	GQFFGHHHTDSFRMLYDDAGVPISAMFITPGVTPWKTTLPGVVN
	J		GANNPAIRVFEYDRATLSLKDMVTYFMNLSQANAQGTPRWELEY
			QLTEAYGVPDASAHSMHTVLDRIAGDQSTLQRYYVYNSVSYSAG
			VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLPLLLMAL
			LGLCT
6821	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTOHGPSPTVHPIOSPON
}			RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
			FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
}			GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
1			GSVIEVLORRQEGLAS
6822	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTOHGPSPTVHPIOSPON
			RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
1			FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
1,		•	GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
			GSVIEVLORRQEGLAS
6823	654	221	PPKLLSRWARMGHGDBIV\LSDLNFPGLLHLPVVGPWRSVOTAC
			GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLOTPVWTE
			YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL
1			ILRKGVLALNPLL
6824	858	104	LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG
			ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV
			NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS
, ,			LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV
		•	WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS
<i> </i>		; '	AALHICHAVILLQLWLGPQPFPKSTQHSKKAH
6825	3	1173	SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL
			PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ
.]	ĺ		NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM
]			KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI
			GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD
			IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF
			VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK
]]		TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF
	1		PFGPLALPMDGYGDSLWBEHEYKFCLALVISTKLYHVRC
6826	2304	954	LKTESFKPW/VNIALAFHLLGERASPNSFWQPYIOTLPREYDTP
1			LYFEEDEVRYLOSTQAIHDVFSQYKNTARQYAYFYKVIQTHPHA
			NKLPLKDSFTYEDYRWAVSSVMTRONOIPTEDGSRVTLALIPLW
]	'		DMCNHTNGLITTGYNLEDDRCECVALQDFRAGEQIYIFYGTRSN
			AEFVIHSGFFFDNNSHDRVKIKLGVSKSDRLYAMKAEVLARAGI
	·		PTSSVFALHFTEPPISAQLLAFLRVFCMTEEELKEHLLGDSAID
			RIFTLGNSEFPVSWDNEVKLWTFLEDRASLLLKTYKTTIEEDKS
			VLKNHDLSVRAKMAIKLRLGEKEILEKAVKSAAVNREYYRQQME
	<u> </u>		EKAPLPKYEESNLGLLESSVGDSRLPLVLRNLEEEAGVQDALNI
			REAISKAKATENGLVNGENSIPNGTRSENESLNQESKRAVEDAK
ļ.			GSSSDSTAGVKE
,			COCOOTAGVIE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1 '	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i i	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion) .
6827	1	779	SSVVEFGLSVLGGLFLLFVLENMLGLLRHRGLRPRCCRRKRRNL
002.	-	,,,,	ETRNLDPENGSGMALOPLOAAPEPGAOGOREKNSOHPPALAPPG
i 1			HOGHSHGHOGGTDITWMVLLGDGLHNLTDGLAIGAAFSDGFSSG
1			LSTTLAVFCHELPHELGDFAMLLQSGLSFRRLLLLSLVSGALGL
1 1			GGAVLGVGLSLGPVPLTPWVFGVTAGVFLYVALVDMLPALFPSS
1 1			
6828		1.654	GAPAYA\HVLLQGLGLLLGGCLMLAITLLEERLLPVTTEG
0828	3	1654	KSQHG/WILQLMHSCKEGYVKDLKGNPGLHRAMLDLDNGTRPSE
1			LGHLSQTASLKRGSSFQSGRDDTWRYKTPHRVAFVEKLTKLVLS
			QLPNFWKLWISYVNGSLFSETAEKSGQIERSKNVRQRQNDFKKM
l i			IQEVMHSLVKLTRGALLPLSIRDGEAKQYGGWEVKCELSGQWLA
			HAIQTVRLTHESLTALEIPNDLLQTIQDLILDLRVRCVMATLQH
			TAEEIKRLAEKEDWIVDNEGLTSLPCQFEQCIVCSLQSLKGVLE
1 1		,	CKPGEASVFQQPKTQEEVCQLSINIMQVFIYCLEQLSTKPDADI
.]]			DTTHLSVDVSSPDLFGSIHEDFSLTSEQRLLIVLSNCCYLERHT
1			FLNIAEHFEKHNFQGIEKITQVSMASLKELDQRLFENYIELKAD
			PIVGSLEPGIYAGYFDWKDCLPPTGVRNYLKEALVNIIAVHAEV
1 1	,	•	FTISKELVPRVLSKVIEAVSEELSRLMQCVSSFSKNGALQARLE
1			ICALRDTVAVYLTPESKSSFKQALEALPQLSSGADKKLLEELLN
]			KFKSSMHLQLTCFQAASSTMMKT
6829	1	782	MRMEAGEAAPPAGAGGRAAGGWGKWVRLNVGGTVFLTTRQTLCR
1 1		•	EQKSFLSRLCQGEELQSDRDETGAYLIDRDPTYFGPILNFLRHG
1			KLVLDKDMAEEGVLBEAEFYNIGPLIRIIKDRMEEKDYTVTOVP
1 1			PKHVYRVLQCQEEELTQMVSTMSDGWRFEQLVNIGSSYNYGSED
1 1			QAEFLCVVSKELHSTPNGLSSESSRKTKSTEEQLEEQQQQEEEV
		1	EBVEVEQVQVEADAQEK/CCYKPEAPGCEAPDHLQGLGVPI
6830	1.	939	MEPGSVENLSIVYRSRDFLVVNKHWDVRIDSKAWRETLTLOKOL
'''			RYRFPELADPDTCYGFRFCHOLDFSTSGALCVALNKAAAGSAYR
1		6	CFKERRVTKAYLALLRGHIQESRVTISHAIGRNSTEGRAHTMCI
1		•	EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHOL
1 1			RV\HCSALGHPVVGDLTYGEVSGREDRPFRMMLHAFYLRIPTDT
1 1		i.	ECVEVCTPDPFLPSLDACWSPHTLLQSLDQLVQALRATPDPDPE
		:	
1 1			DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT LEPDS
6831		1007	SLFFGSSTPDNKVAEOEDLETOPSPSVEKAVTVIDPEGTIPTNF
0031	: 3	1087	· · · · · · · · · · · · · · · · · · ·
	· · · · · · · · · · · · · · · · · · ·	•	NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGQNVKEKSMILSN
1 1	,		VEDLQQPKF1SEVSREDYGKKE1SGDSEEMNINSVVTSADGENL
	,	•	EIQSYSLIGBKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI
]			SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE
[SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEEETK
			LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS
]]			
			NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG
			NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG SEKEKDEKKKK
6832	1809	412	· · · · · · · · · · · · · · · · · · ·
6832	1809	412	SEKEKDEKKKK
6832	1809	412	SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFPEYLLV
6832	1809	412	SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF
6832	1809	412	SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG
6832	1809	412	SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL
6832	1809	412	SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY
6832	1809	412	SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME
6832	1809	412	SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT
6832	1809	412	SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK
6832	1809	412	SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE
			SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YEEQKKQ/TETKGKNCEIRAVVNKND
6832	1809	1129	SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YEEQKKQ/TETKGKNCEIRAVVNKND PLMTLSQCGGIPGHGHSHGGHGHGHFKGPRVKSTRPGSSDIN
			SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE YEEQKKQ/TETKGKNCEIRAVVNKND

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			NALVFYFSWKGCSEGDFCVNPCFPDPCKAFVEIINSTHASVYEA
Ì			GPCWVLYLDPTLCVVMVCILLYTTYPLLKESALILLQTVPKQID
			IRNLIKELRNVEGVEEVHELHVWQLAGSRIIATAHIKCEDPTSY
		ļ	MEVAKTIKDVFHNHGIHATTIQPEFASVGSKSSVVPCELACRTQ
		•	CALKQCCGTLPQAPSGKDAEKTPAVSISCLELSNNLEKKPRRTK
			AENIPA\VVIEIKN\IPNK\QPESSL
6834	78	1151	AGQERPAPIWRLLWLPTPSVSRKAEPAHIPINR*GA*E*RGGLP
1			LCGSSASAYGWH*RLTPWSPGGS*HM*SSKAPVTQAREVLVAGP
			CSKLVLSGARGIVGTTVQVLVEAQQPLLLLFTGVWGLNLRAGER
1			SRAL*LIBEVTQVRDAHLGNAVVGCAQCLSQGQVGSALAKALLE
			AAAAVRDCKEVLTVSGDKQQAEVSVRL*VRDVCVEEAGCVEFGQ
			AHGRPGLALAKGRGGTNEVEEQVQVDGVQKLVLSAHECHELVAG QQDGEDQAARTRLLQAGAHSVAHGRRQGQAPCRPHOEAGVSCHE
		*	LQQVVGDAL*ARE*APQIIVLLLLEDVAQLRTGKKA*DLVVDVE
	'		OLLROL
6835	1	834	GIPAADR\EASLELIKLDISRTFPNLCIFQQGGPYHDMLHSILG
1			AYTCYRPDVGYVQGMSFIAAVLILNLDTADAFIAFSNLLNKPCQ
			MAFFRVDHGLMLTYFAAFEVFFEENLPKLFAHFKKNNLTPDIYL
1)		IDWIFTLYSKSLPLDLACRIWDVFCRDGEEFLFRTALGILKLFE
1			DILTKMDFIHMAQFLTRLPEDLPAEELFASIATIQMQSRNKKWA
1			QVLTALQKDSREMREGKSVPPTLRLQREFALGTNQSPMPRPLCC
			FRLTPGQPRRTDAL
6836	1 ,	850	MSCGRPPPDVDGMITLKV\DNLTYRTSPDSLRRVFEKYGRVGDV
			YIPREPHTKAPRGFAFVRFHDRRDAQDAEAAMDGAELDGRELRV
	1		QVARYGRRDLPRSRQGRRHAAGPEAA/RYGRRSRSYGRRSRSPR
1		,	RRHRSRSRGPSCSRSRSRSRYRGSRYSRSPYSRSPYSRSRYSRS
			PYSRSRYRESRYGGSHYSSSGYSNSRYSRYHSSRSHSKSGSSTS
		$I \leftarrow I$	SRSASTSKSSSARRSKSSSVSRSRSRSRSSSMTRSPPRVSKRKS KSRSRSKRPPKSPEEEGOMSS
6837	1	1369	TDGAAVAGNPGSDYFPGGTAP/GGPRTRRP\SGTSSSGSKASGP
		. 1303	PNPPAQGDGTSLSPNYTLESTSGNDGKPVSGGGGRGRGRRKRDS
	·		GHVSPGTFFDKYSAAPDSGGAPGVSPGQQQASGAAVGGSSAGET
1 .		· · · · · · · · · · · · · · · · · · ·	RGAPTPHEKALTSPSWGKGAELLLGDQPDLIGSLDGGAKSDSSS
,			PNVGEFASDEVSTSYANEDEVSSSSDNPQALVKASRSPLVTGSP
,			KLPPRGVGAGEHGPKAPPPALGLGIMSNSTSTPDSYGGGGGPGH
			PGTPGLEQVRTPTSSSGAPPPDEIHPLEILQAQIQLQRQQFSIS
			EDQPLGLKGGKKGECAVGASGAQNGDSELGSCCSEAVKSAMSTI
	i		DLDSLMAEHSAAWYMPADKALVDSADDDKTLAPWEKAKPQNPNS
			KEAHDLPANKASASQPGSHLQCLSVHCTDDVGDAKARASVPTWR
			SLHSDISNRFGTFVAALT
6838	16	499	LTDTPPPKTHMIHHSISDYKATLRCWALGFYPMEITLTWQQDEE
			DQTRDMELVETRPAGDGTFQKWAAVVVPSGEE/Q/RYMCHVQHE
			GLPEPLTLRWEQSSQPTIPIVGIVAGLVLLGAVVTGAVVSAVMC
6839		1105	RKKNSDRVSYSEAASSDHAQGSDVSLTACKV
0039	1	1195	AAPAGGGPDPEALSAFPGRHLSGLSWPQVKRLDALLSEPIPIHG
			RGNFPTLSVQPRQIRAGGPQHPGGAG\IHVHRVRLHGSAASHVL
			HPESGLGYKDLDLVFRMDLRSEASFQLTKAVVLACLLDFLPAGV SRAKITPLTLKEAYVOKLVKVCTDSDRWSLISLSNKSGKNVELK
			FVDSVRRQFEFSIDSFQIILDSLLLFGQCSSTPMSEAFHPTVTG
			ESLYGDFTEALEHLRHRVIATRSPEEIRGGGLLKYCHLLVRGFR
			PRPSTDVRALQRYMCSRFFIDFPDLVEQRRTLERYLEAHFGGAD
			AARRYACLVTLHRVVNESTVCLMNHERROTLDLIAALALQALAE
			QGPAATAALAWRPPGTDGVVPATVNYYVTPVQPLLAHAYPTWLP
			CN
6840	4254	2061	ELQGDFSVPDVPKSMAWCENSICVGFKRDYYLIRVDGKGSIKEL
			FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALNW
			· · · · · · · · · · · · · · · · · · ·

C 656	(5 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 		
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1 :	residue of	amino acid	
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
,	sequence	sequence	Codon, /=possible nucleotide deletion, ()=possible nucleotide insertion)
 -	Dequence		TDIPVAMEHQPPYIIAVLPRYVEIRTFEPRLLVQSIELQRPRFI
			TSGGSNIIYVASNHFVWRLIPVPMATQIQQLLQDKQFELALQLA
			EMKDDSDSEKQQQIHHIKNLYAFNLFCOKRFDESMOVFAKLGTD
			PTHVMGLYPDLLPTDYRKQLQYPNPLPVLSGAELEKAHLALIDY
			LTQKRSQLVKKLNDSDHQSSTSPLMEGTPTIKSKKKLLQIIDTT
.		ĺ	LLKCYLHTNVALVAPLLRLENNHCHIEESEHVLKKAHKYSELII
		ļ	LYEKKGLHEKALQVLVDQSKKANSPLKGHERTVQYLQHLGTENL
			HLIFSYSVWVLRDFPEDGLKIFTEDLPEVESLPRDRVLGFLIEN
			FKGLAIPYLEHIIHVWEETGSRFHNCLIQLYCEKVQGLMKEYLL
	1	ĺ	SFPAGKTPVPAGEEEGELGEYRQKLLMFLEISSYYDPGRLICDF
			PFDGLLEBRALLLGRMGKHEQALFIYVHILKDTRMABEYCHKHY
			DRNKDGNKDVYLSLLRMYLSPPSIHCLGPIKLELLEPKANLQAA
			LQVLELHHSKLDTTKALNLLPANTQINDIRIFLEKVLEENAQKK
* . ·	4 4 4		RFNQVLKNLLHAEFLRV\QEERILHQQVKCIITEEKVCMVCKKK
			IGNSAFARYPNGVVVHYFCS\KEVNPADT
6841	1	3206	TPSTTGTKSNTPTSSVPSAAVTPLNESLQPLGDYGVGSKNSKRA
	-		REKRDSRNMEVQVTQEMRNVSIGMGSSDEWSDVQDIIDSTPELD
			MCPETRLDRTGSSPTQGIVNKAFGINTDSLYHELSTAGSEVIGD
}			VDEGADLLGEFSGMGKEVGNLLLENSQLLETKNALNVVKNDLIA
			KVDQLSGEQEVLRGELEAAKQAKVKLENRIKELEEELKRVKSEA
j			IIARREPKEEAEDVSSYLCTESDKIPMAQRRRFTRVEMARVLME
	•		RNQYKERLMELQEAVRWTEMIRASREHPSVQEKKKSTIWQFFSR
			LFSSSSSPPPAKRPYPSGNIHYKSPTTAGFSQRRNHAMCPISAG
	,		SRPLEFFPDDDCTSSARREQKREQYRQVREHVRNDDGRLQACGW
			SLPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKLWCA
		;	AGVNLSGWRPNEDDAGNGVKPAPGRDPLTCDREGDGEPKSAHTS
	• •		PEKKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANQPGTVVD
	\$		QFTVCNAHVLCISSIPAASDSDYPPGEMFLDSDVNPEDPGADGV
	man (4)		LAGITLVGCATRCNVPRSNCSSRGDTPVLDKGQGEVATIANGKV
	age or a management of the court		NPSQSTEEATEATEVPDPGPSEPETATLRPGPLTEHVFTDPAPT
, ,			PSSGPQPGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAPTMWLG
7	·		AQNGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRVLVALAD
1 .			GTLAIFHRGEDGQWDLSNYHLMDLGHPHHSIRCMAVVYDRVWCG
			YKNKVHVIQPKTMQIEKSFDAHPRRESQVRQLAWIGDGVWVSIR
			LDSTLRLYHAHTHQHLQDVDIEPYVSKMLGTGKLGFSFVRITAL
	· • • • • • • • • • • • • • • • • • • •		LVAGSRLWVGTGNGVVISIPLTETVVLHRGQ\LLG\LRANKTSP
' :			TSGEG\ARPGG\IIHVYG\DDSSDRAARSFIPYCSMAQAQLCFH
٠. ا			GHRDAVKFFVSVPGNVLATLNGSVLDSPAEGPGPAAPASEVEGQ
	•		KLRNVLVLSGGEGYIDFRIGDGEDDETEEGAGDMSQVKPVLSKA
	 		ERSHIIVWQVSYTPE
6842	3	926	RCQQLSATILTDHQYLERTPLCAILKQKAPQQYRIRAKLRSYKP
. [İ	RRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPDVKLQN
ļ	·		TSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLSNECLLLIEGGT
}			LSEICKLSNKFNSVIPVRSGHEDLELLDLSAPFLIQGTVHHYGC
j			KQWST*RSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFVMTFT
		}	LDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMDMFC
6942			PPGIKIDAYPWLECFIKSYNVTNGTDNQICYQIFDTTVAEDVI
6843	2	851	NHRKVLSGAKRYECNECGKSFAYTSSLIKHRRIHTGERPYECSE
			CGRSFAENSSLIKHLRVHTGERPYECVECGKSFRRSSSLLQHQR
-			VHTRERPYECSECGKSFSLRSNLIHHQRVHTGERHECGQCGKSF
1			SRKSSLIIHLRVHTGERPYECSDCGKSFAENSSLIKHLRVHTGE
.			RPYECIDCGKSFRHSSSFRRHQRVHTGMRPYK*SKFWKFSCPGF
			LLLQGQRVHTGSRCYECDKWGIFFS*NASFFT*KSAPTEEVPFE
			CNECEKAFSPLSLVTTIFT
CC44.			
6844	244	642	EHQLAGFELRKTQTSMSLGTTREKTDRVKSTAYLSPQELEDVFY QYDVKSEIYSFGIVLWEIATGDIPFQGCNSEKIRKLVAVKRQQE

Deginning No: Ucation Corresponding Coation Corresponding Coffice Common Corresponding Coffice	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Notication Corresponding to first amino acid residue of amino acid residue of amino acid sequence Solitanian Solit	ID			(A=Alanine C=Cvateine D=Aenartic Acid R=
Cocation Corresponding Cofirst Contrasponding Cofirst	NO:		1 -	Glutamic Acid. F=Phenylalanina G=Glucina
LeLeucine	1		1	H-Wistiding T-Trolouging & Toroing
Confirst amino acid residue of amino acid anino acid anino acid amino acid anino acid anino acid anino acid sequence Sestine, T-Mirenoine, V-Voline, M-Tryptophan, Y=Tyrosine, X-Unknown, *=stop Codon, /=possible nucleotide deletion) PLGSDCFSELREIDECRHDPSVPFDVSDLIKKLSTFSK*CIK	-			Indicated Management Associated Asociated Associated Associated Associated Associated Associated As
amino acid residue of amino acid sequence anno acid sequence (anno acid sequence) anno acid sequence (anno acid sequence) (anno acid se	ĺ			Debeddine, Memethionine, Neasparagine,
residue of anino acid sequence	1		a contract of the contract of	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence Codon	1.		I -	S=Serine, T=Threonine, V=Valine,
Apposaible nucleotide insertion	1.		l .	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
PLGEDCESELREITDECRAHDESVRENUETIEKKLSTESK-CIK	1		sequence	Codon, /=possible nucleotide deletion,
6845 3 1519 VAVERDECYMENTYMODIAMILIFILMCHEFTARARLEYFIRTLD GALRINAQUILGYCGARFANESADSGLEVCEDITGVQSVHYNDEG GLERNAQUILGYCGARFANESADSGLEVCEDITGVQSVHYNDEG GLERNAQUILGYCGARFANESADSGLEVCEDITGVQSVHYNDEG GARRIVANTIOLOLGPERGGUNDVVPANAPFECRSVENSPERE KYHLRGUMSPDEVISGVNNSVYTHVLVQMSLRFAAALAQDLGLP IPSOMLAVADKIKVPPDVEDNEHPEFDGYFRESVVNGADVULG YPVPPSLSPDVRKNLEITEAVTSPQGPAHTMSMFAVGMMELKD AVRARGLLDASFANNABPFKVWTENADISGAVSFLTGMGGFUG VVGCCGFRYTRAGTSPDVDELGGSTVNSUGSTYCOMKINESS SEDSUTVENYTARAGSMAPHLERELMFSQSRISLLEGHKVSFSRS AGRICMSSPPLRPSSSSSEPFGRISTSVDELGGSTUMTLGSSSS TESSLTUDBASE*SGTGASSTSLGPSLWFLHPPLLGTLLACHES AGRICMSSPPLRPSSSSSEPFGRISTSVDELGGSTUMTLGSSSS TESSLTUDBASE*SGTGASSTSLGPSLWFRLHPPLLGTLLACHES PARALGGKUPALAGGMTENERFSVVNGLAGGHSPATHAGHTSPK AGRICMSSPPLRPSSSSSEPFGRISTSVDELGGSTUMTLGSSSSP TESSLTUDBASE*SGTGASSTSLGPSLWFRLHPPLLGTLLACHES AGRICWSPPLRPSSSSSEPFGRISTSVDELGGSTUMTLGGRISSPRG TESSLTUDBASE*SGTGASSTSLGPSLWFLHPPLLGTLLACHES AGRICWSPPLRPSSSSSEPFGRISTSVNGLGGSLWFLHPPLLGTLLACHES AGRICWSPRLAGGMET SENGENGVARHLITGGRISSPRG TESSLTUDBASE*SGTGASSTSLGPSLWFLHPPLLGTLLACHESSPRG TESSLTUDBASE*SGTGASSTSLGPSLWFLHPPLLGTLLACHESSPRG TESSLTUDBASE*SGTGASSTSLGPSLWFLHPPLLGTLLACHESSPRG TESSLTVTRAGAGATATATAGEGGLAGGAGSTWTLACHESSPRG TESSLTVTRAGAGATATAGEGGLAGGAGAGATAGAGAGAACAA NOTHER AGRICUSTATAGAGAGAACAA NOTHER AGRICUSTAGAGAGAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		sequence		\=possible nucleotide insertion)
Sept	1	1.		PLGEDCPSELREIIDECRAHDPSVRPSVDEILKKLSTFSK*CIK
GALENAQNIOSYQAKPAMESADSGLEVCEPITYSTYSPEVELVIKADV GLAPELYYHTTOLOLIPEAGGGWIVENVANAENSEREE KYHLRISWIN PEPHISSYNNISYYNVILVONIALERAAALAQDIGJE I PSQWLAVADKIKVPPDVEQNEPPEFOYEPGEVYKQADVYLLG YPVPFSLSSPVYRKINLETYEAVTSOQGANTHARAGMELIAD AVRARGILDRSFANMABPFKVWTENADGSGAVNFLITGMGGFLQA VVFCCTGFEVYTRGVYFDYVLSGISRWYSGISPLUTGMSSEPTQA AGRIQMSPPKKINLETYEAFTSOVROHEVGONIANSPPK SEDSYLVEVTARAGWAAHLEAELMPSGSELSLLEGHKVSPPRS AGRIQMSPPKLYBGSSSSEPFGFTSDURDLGSEPLWTIGSSSEP SEDSYLVEVTARAGWAAHLEAELMPSGSELSLLEGHKVSPPRS AGRIQMSPPKLYBGSSSSEPFGFTSDURDLGSEPLWTIGSSSEP TESLTUDPASE*SGTGASETSLOPSLMFRHHPPLLGTLLACHPS PAARLSGKUHAAMPEFKAPCL 6846 213 1258 1176KTGGASVALSOW ITEREKTSTUDPASIBFRHHPPLLGTLLACHPS PAARLSGKUHAAMPEFKAPCL WITCHLACHPSEPLATION OF THE STANDARD OF THE S				I
GALENAQNIGYCGAKFANESADSGLEVCPBDITYGYGSVYNNANY GLAFELYNTITOOLOLOFERAGOMOVANAVBWCGRVENSPREE KWHLRGWMSPDEYHSGVANSYYTNYLVONSLERPAALAOJOLDE I ESOMLAVADKIKVP PDVENSHPERCOMPEGVYKOADVYLLG YPVPFSLS PDVRRKILE LYBAYTS POGENTHISMRAVGHMELKD AVRARGLIDESSAMMAEPFKVWTENADSGANTLTORGOFLOA VVPCCTGFRVTRAGVTFDVCLSGISRUSVSGI FYGONKLMFSF SEDSUTVEVRARAGFWAPHLERELMPSGSELSLIDEGKVSPFRR AGRICHSPF KLANGSSSSESFRAFTSDVEDLOSPLAWTIGSSSS AGRICHSPF KLANGSSSSESFRAFTSDVEDLOSPLAWTIGSSSS TESLTUDPASE*SGTGASETSJOPSLMPRLHPPLLGTLLACHPS PAARLSGKVHAAMFEKAPLT TESLTUDPASE*SGTGASETSJOPSLMPRLHPPLLGTLLACHPS PAARLSGKVHAAMFEKAPLT TESLTUDPASE*SGTGASETSJOPSLMPRLHPPLLGTLLACHPS PAARLSGKVHAAMFEKAPLTVLAHGSGGVYTTTESSAMG IIFTKTRGSAVALSOM ITEMEKRATURTIMEGYTTESSAMG IIFTKTRGSAVALSOM ITEMEKRATURTIMEGYTTTESGAMG IIFTKTRGSAVALSOM ITEMEKRATURTIMEGYTTTESGAMG IIFTKTRGSAVALSOM ITEMEKRATURTIMEGYTTTESGAMG IIFTKTRGSAVALSOM ITEMEKRATURTIMEGYTTTESGAMG IIFTKTRGSAVALSOM ITEMEKRATURTIMEGYTTTESGAMG IIFTKTRGSAVALSOM ITEMEKRATURTIMEGYTTTESGAMG IIFTKTRGSAVALSOM ITEMEKRATURTIMEGYTTTESGAMG IIFTKTRGSAVALSOM ITEMEKRATURTIMEGYTTTESGAMG IIFTKTRGSAVALSOM ITEMELLATIVASEGLDI KERCHIVITYRGL VINNELAMVALSARRATURTURATURTIMEGYTTESAMG IIFTKTRGAVALSOM INTEMELLATIVASEGLDI KERCHIVITYRGL VINNELAMVALSARRATURTURATURTURATURTURA MYKAIRLOKAKOANGARATURTURATURTURATURANGARATURTURATURTURA MYKAIRLOKAKOANGARATURTURATURTURATURTURA MYKAIRLOKAKOANGARATURTURATURTURATURTURATURTURATURTURA MYEALANGAVALARAURKAULTITYROKARATURTURATURTURA MYEALANGAVALARAURKAULTURTURGSASPALDAKURTURGARAURTURA MYEALANGAVALARAURKAULTURGSASPALDAKURTURGARAURAURAURA MYEALANGAVANGALARAURKAULTURGASSPALDAKURTURGARAURAURAURAURAURAURAURAURAURAURAURAURAU	6845	3	1519	VAVRDECYWRHVFWDODLWMLLFILMCHPETARARLEYRIRTLD
GLAPELYYHTTODLOLFREAGGMDVYRNVAEWGREWESPEE KYHLRGUMSP DEVHSGVMSVATYNTUVGNICHERAALAQDIGLE 1 FSGMLAVADKIKUP BUPENGYPGGEVYKQADVULG YPVPFSLS PDVPRKNIELTYEAVTSOGGANTHARGUMBLKUC AVRARGILDRSFANMAEPFKVHTEMALGSGAVNFLTGMGGFLQA VVFGCTGFRVTRAGVTFDVCLSGISRVSVSGIFYGGMIKNSFS SEDSUTVEWTARAGWAPHLEAELMPSGSSLSLIGHGHKVSFPRS AGRIGMSPFKLDGSSSSSFFGRTFSDVRDPLGSELMGHKVSFPRS AGRIGMSPFKLDGSSSSSFFGRTFSDVRDPLGSELMGHKVSFPRS AGRIGMSPFKLDGSSSSFFGRTFSDVRDPLGSENDHULGSSSS TESSLTUPDASS-SGTGASESTLDGSLWRFHLPLLGTLLGGHSS TESSLTUPDASS-SGTGASESTLDGSLWRFHLPLLGTLLAGGHSS AGRIGMSPFKLDGSSSSFFGRTFSDVRDPLGSENDHULGSSSS TESSLTUPARS-SSFFGRTFSDVRDPLGSFRLDGSSSFFKP TYPVERSPS-SGTGASESTLDGSLWRFHLPLLGSSSSFFKD TESSLTUPARS-SGTGASESTLDGSLWRFHLPLLGSSSSFFKD TESSLTUPARS-SGTGASESTLDGSLWRFHLPLLGSSSSFFKD TESSLTUPARS-SGTGASESTLDGSLWRFHLPLLGGSSSFFKD TYPVERNSSTRAGVHAWAGSGAVLGSGEDHVIERGHVAMTPEFKELYIV RENKTLQKKCADVQINGEI ICKGGAWGTMWHKGLLIGLGKIR NFVVVERNSTKKQVKAWALDFITPSDUSSKRYUTT WEFDALNGVI-RAEAIQHCVANGGMEKRGAVKWNKLQTURQQ PFAYGTLTVSLLDTREGCLNESPPPDYSKVKQRRGWARGLGSDP PFAYGTLTVSLLDTREGCLNESPPPDYSKVKQRRGWARGLGCF GVVVSLDALAGMSERGLLLVKVNGGMSKEWGKANGVARGLGSDP PFAYGTLTVSLLDTREGCLNESPPPDYSKVKQRRGWARGLGCF GVVVSLDALAGMSERGLLJKVANGGMSKAVSAVLESDP PFAYGTLTVSLLDTREGCLNESPPPDYSKVKQRRGWARGLGCF GVVTSLDALAGMSERGLLJKVANGGMSKAVSAVLESDP PFAYGTLTVSLLDTREGCLNESPPPDYSKVKQRRGWARGLGCF GVVTSLDALAGMSERGLLJKVANGGMSKAVSAVLESDP PFAYGTLTVSLLDTREGCLNESPPTDYSKVKVRRENGVARGLGCF GRUTSLIFKYRVDAS GRLSSVIFKYRVDAS ARMWINSLOGINIVLSNFKKRNTLSLAMLKSLGSDLLKGLAALVR REGADLVU EGGRGAVHTVADAGACKAVSAVLESDP PFAYGTLTVSLLAGRGFAVHTVADAGACKAVSAVLESDP PFAYGTLTVSLLAGRGFAVHTVADAGACKAVSAVLESDP PFAYGTLTVSLLAGRGFAVHTVADAGACKAVSAVLESDP PFAYGTLTVSLAGRGFAVHTVADAGACKAVSAVLESDP PFAYGTLTVSLAGRGFAVHTVADAGACKAVSAVLESDP PFAYGTLTVSLAGRGFAVHTVADAGACKAVSAVLESDP PFAYGTLTVSLAGRGFAVHTVADAGACKAVSAVLESDP PFAYGTLTVSLAGRGFAVHTVADAGACKAVSAVLESDP PFAYGTLTVSLAGRGFAVHTVADAGACKAVSAVLESDP PFAYGTLTVSLAGRGFAVHTVADAGACKAVSAVLESDP PFAYGTLTVSLAGRGFAVHTVADAGACKAVSAVLESDP PFAYGTLTVSLAGRGFAVHTVADAGACKAVSAVLESDP PFAYGTLTVSLAGRGFAVHTVATHAGACCCATAGACCA PFAYGLGSCAGACCATAGACCACCA				GALENAONLGYOGAKFAWESADSGLEVCPEDTYGVORVHVNGAV
KYHLRGWASPDEVHSGVNNSYTNYLUQNSLERPAALADJGLLE I ISSOMLAVADKIKVPPDWSDHPEPGNYERGADVULG I FYSVESLSPDWRRKILETYRAVTSPOGPANTHSMRAVGMELKD AVRARGILDRSFANMAEPFKWYTERADGSGAVTHATMGGFLOA VVFGCTGFEVTRAGVTFDVCLSGISRVSVSGIFYGGNKINSSF SEDSVTWEVTRAGPWAPHLERALBPSGSILEGHKVSPRSG AGRIOMSPPKLPGSSSSSEPGRFFBDVRDPLQSPLWVTLGSSSP TESLTVDPASE*SGTGASETSLGPSLWFRIHPPLLGTLLAGCHFS AARLOGKVRAAWPEFKAFC 1		İ		GLAFELYYHTTODLOLFREAGGWDVVPAVAEFWCSPVFWSDDFF
IPSQMLAVADKIKVPFDVSQNFHPEFGGEPGEVVKQADVILLG YPVFPSIS-DPURRENLEIT-LEAVTSPQGFMINSFPAGWINELKE AVRARGILDESFANNAEPFKVMTENANGSGAVNFILLGMGGFLQA VVPGCTGFFPVTRAGVTFDVCLSGIGRSVSVGIFVQGNKLINGSF SEDSVTVEVTARAGPWAPHLEARLINPSQGRLSLIPGHKVSFPRS AGRIQMSPPKLPGSSSSEPFGTFSDVRDPLQSILWTLGSSSS AGRICMSPPKLPGSSSSEPFGTFSDVRDPLQSILWTLGSSSS AGRICMSPPKLPGSSSSEPFGTFSDVRDPLQSILWTLGSSSS AGRICMSPPKLPGSSSSEPFGTFSDVRDPLQSILWTLGSSSS AGRICMSPPKLPGSSSSEPFGTFSDVRDPLQSILWTLGSSSS AGRICMSPPKLPGSSSSEPFGTFSDVRDPLQSILWTLGCHSSPKSPKS AGRICMSPPKLPGSSYSEPFGTFSDVRDPLQSILWTLGCHSSPKSPKS ARRICHART SERVEL SER		1		KYHLRGVMS PDEVHSGVNNSVYTNULVONSL PENNALAODLGL P
AVRARGILDERSFANNAR PERVETENATS-POGEPAMTWSMFAUGMMELKU AVRARGILDERSFANNAR PERVETENATS-VENTLICHMEGH V VPGCTGFRVTRAGVTFDVCLSG ISRVSVSGI PYQGNKLNPSF SEDSVTVEVTARAGVMAPHLERELWFSQSRISLILPGHVSFPRR AGRIQMSP PKLPGSSSSEP PCRTFSDVRDPLGSELWTIGSSSS TESLTVDPASE*SGTGASSTSIGPSLWPDLGSELWTIGSSSS TESLTVDPASE*SGTGASSTSIGPSLWPDLGSELWTIGSSSS TESLTVDPASE*SGTGASSTSIGPSLWPDLGSELWTIGSSSS TESLTVDPASE*SGTGASSTSIGPSLWPDLGSELWTIGSSSS TESLTVDPASE*SGTGASSTSIGPSLWPDLGSELWTIGSSSS TESLTVDPASE*SGTGASSTSIGPSLWPDLGSELWTIGSSSS TESLTVDPASE*SGTGASSTSIGPSLWPDLGSELWTIGSSSS TESLTVDPASE*SGTGASSTSIGPSLWPDLGSELSTUPLAHSESGLDI KECKTUPLKYGE ARABISSAVALSQWITENSER*CL IFFKKTGASVALSQWITENSER*CL IFFKKTGASVALSQWITENSER*CL WYKARACHOVAGARGRARADESTVULVAHSEGLDI KECKTUPLKYGE VINEIAWOAGARGRARADESTVULVAHSEGUDI KECKTUPLKYGE VINEIAWOAGARGRARADESTVULVAHSEGUDI KECKTUPLKYGE WYKARACHOVAGRARATSCHALLIATTVAERGUDI KECKTUPLKYGE WYKARACHOVAGRARATSCHALLIATTVAERGUDI KECKTUPLKYGE WYKARACHOVAGRARATSCHALLIATTVAERGUDI KECKTUPLKYGE WYKARACHOVAGRARATSCHALLIATTVAERGUDI KECKTUPLKYGE WYKARACHOVAGRARATSCHALLIATTVAERGUDI KECKTUPLKYGE WYKARACHOVAGARGAANTATAGACHOVAGACHASTAGAALKACHOVAGACHOVA	1			
AVRARGILDRSFANMAEPEKWHTENJAGSAVNITLINGGELQA VVPGCTGFEVPTRAGVTPDVCLSGISRUSVSGIFYGGNILNESF SEDSVTVEVTARAGPWAPILRAELINPSGSRLSLIPGHKVSPPRS AGRIOMSPPKLPGSSSSEPGRTFSDVRDPLGSFLIPGHKVSPPRS AGRIOMSPPKLPGSSSSEPGRTFSDVRDPLGSFLIPGHKVSPPRS TESLTVDPASE*SGTGASETSLGPSLWPFLEPFLIGTLLACHESP PAARLSGKVHAAWEFKAFCL LYFLKTIK*INLAEHEF*VENEKLTKLRNTIMEGYTRTEESARG IIFFKTRGSAVALSGWITTENEKFAEVGVKAHHLIGAGHSSEFKP MYONEGKEVISKFFRGKINLLATATVAEGHSSEFKP MYONEGKEVISKFFRGKINLLATATVAEGHSSEFKP MYNEGKEVISKFFRGKINLLATATVAEGHSSEFKP MYNEGKEVISKFFRGKINLLATATVAEGHSSEFKP MYNEGKEVISKFFRGKINLLATATVAEGHSSEFKP MYNEGKEVISKFFRGKINLLATATVAEGHSSEFKP MYNEGKEVISKFFRGKINLLATATVAEGHSSEFKP MYNEGKEVISKFFRGKINLLATATVAEGHSSEFKP MYNEGKEVISKFFRGKINLLATATVAEGHSSEFKPTINDFREM MYKAIHCVQRMKPEEVAHKILLATATVAEGHSSEFKTINFREM MYKAIHCVQRMKPEEVAHKILLATATVAEGHSSEFKTINFREM MYKAIHCVQRMKPEEVAHKILLATATVAEGUSINESSERVCIT RENOVERSHELLACGGSEDIHVIEKMETKINIAHHK NNFSLITFLCKNCSVLACGGSDIHVIEKMETKINIAHHK NNFSLITFLCKNCSVLACGGSDIHVIEKMETKINIAHHK NNFSLITFLCKNCSVLACGGSDIHVIEKMETKINIAHHK NNFSLITFLCKNCSVLACGGSBCHWILDTSCCLISBEB MYVVFRSLDALGCUNAGDMERGKYMMKLOTIRQQ PPAYGTLTVRSLLDTREHCLMERM PPDPYSKVKQRENGVALRCF PGVVRSLDALGWERGQLALVKGLLAGNVFPUKGRENGVALRCF PGVVRSLDALGWERGQLALVKGLLAGNVFPUKGPENAVLESBLYVAE RIAGMDPVVHSALREERLLLVOGTGSSPCTLDLSKELDKGLAALVR ERGADLVVIEGMGRAVHTNYHAARCGSIKLAVIKNAWLARRLG GRLESVIFKSVPAE RIAGMDPVVHSALREERLLLVOGTGSSPCTLDLSKELDKGLAALVR ERGADLVVIEGMGRAVHTNYHAARCGSIKLAVIKNAWLARRLG GRLESVIFKSVPAE RIAGMDPVVHSALREERLLLVOGTGSSPCTLOLSKELDKGLAALVR ERGADLVVIEGMGRAVHTNYHAARCGSIKLAVIKNAWLARRLG GRLESVIFKSVPAE RIAGMDPVVHSALREERLLAGTGSTLAVAEDKASSLAVIKNAWLARRLG GRLESVIFKSVPAE 19 16 AMWINSLCGIRNIVLSNPKRRNTISLAMKSLOGDILHADASN VUPPASLLGEFMTARKLASLSRPVVSLGKATFYKOLPODLGTA YJLTSQAWVDHLAALRGGGGTAFFLOKRAFPVYGLODLGTA YJLTSQAWVDHLAALRGGGGTAFFLOKRAFPVYGLODLGTA YJLTSQAWVDHLAALRGGGGGTAFFLOKRAFPVYGLODLGTA YJLTSQAWVDHLAALRGGGGGSPAPFPCDTSFFFVAHTGOEDLTVGSYEC VUVKAGKGGCGSPAPRFTGTDSFFFVAHTGOEDLTVGSYEC VUNGETTAVALSKLUDVINGHSTNNTFTLERGFLATCH UPPAYALLSSKLUDVINGHSTONFTGLTGCHATTVTDFDFLATCH VERAVALSSKLUDVINGHSTONFTGLTGCHATTVTDFDFLAT	1			
VVFGCTGFRVTRAGFWEDVCLSGISWSVSGIFYGGMKLNFSS SEDSVTVEVTRAAGFWEDVLREARLEWPSGRSILDFGHKVSPPRS AGRIOMSPKLPGSSSSEPGRTTSDVRDPLQSPLWVTLGSSSP TESLTVDPASE*SGTGASETSLØPSLWFRLHPELVTLGSSSP TESLTVDPASE*SGTGASETSLØPSLWFRLHPELVTLGSSSP TESLTVDPASE*SGTGASETSLØPSLWFRLHPELVTLTGSSSP TESLTVDPASE*SGTGASETSLØPSLWFRLHPELVTLLACHFS PARALSGKVHAAMPEFKAPCG VFFLKTIK* INRILAEHF*YENEKLTKLRNTIMEQYTRTESARG LYFIKKTIK* INRILAEHF*YENEKLTKLRNTIMEGYTRTESARG VTNEIAWLOARGRARADESTVULVAHISGSLØBSPKE MTGNEGKEVISKFRTGKINLLIATTVAEEGLDIKEGNIVIRYGL VTNEIAWLOARGRARADESTVULVAHISGSLÜKERVITIVRYGL VTNEIAWLOARGRARADESTVULVAHISGSLÜKERVITIVRYGL VTNEIAWLOARGRARADESTVULVAHISGSLÜKERVITIVRYGL VRENATLOKKCADVQINGEIICKCOQAMGTMWVHKGLDLPCLKIR NFVVVERNNSTKRYKKWELPIITPRILDTSECLESDED SEKCHNSTRILLEMPFLTDLALILLEPPSTVPTYTHGHSDDSLSSKTUTI WFEDALNGUL*RABAIQPHCVNAGDBMEKFRQKVWHNTTPERKELYTIK WFEDALNGUL*RABAIQPHCVNAGDBMEKFRQKVWHKLQTTLRQQ PPAYGTITTVSILDTERELLLEPPSTVPTYTHGHSDDSLSSKTUTI WFEDALNGUL*RABAIQPHCVNAGDBMEKFRQKVWHKLQTTLRQQ PPAYGTLTVTSILDTERELLLEPPSTYPTYTHGHSDDSLSSKTUTI WFEDALNGUL*RABAIQPHCVNAGDBMEKFRQKVWHKLQTTLRQQ PPAYGTLTVTSILDTERELLLEPPSTYPTYTHGHSDSLIADS TOTAL SLUCTURE SITURGATUR STANDVTHSSSLIAVE REGADLVVIEGHGRQVITTNTHAADRCCSLLAVIKRAHLABRIG GRLFSVIFKYSVPAR RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRILDVIKRAHLABRIG GRLFSVIFKYSVPAR RIAGMDPVVHSALREERLLLVQTGSSSPCLDLASRIKSSAPATFGVN VGLFGSTPGVALARAVPRKVALEMLITGEPISADGALHGLIAN VVFRASLLGEFTHTARKTALSSRPVVSLGAKTFYKQLPODIGTA YYLTSQAMVDNLALARDCOGGTTARLOKRTFYKQLPODIGTA YYLTSQAMVDNLALARDCOGGTTARLOKRTFYKQLPODIGTA YYLTSQAMVDNLALARDCOGGTTARLOKRTFYKQLPODIGTA YYLTSQAMVDNLALARDCOGGTTARLOKRTFYKQLPODIGTA YYLTSQAMVDNLALARDCOGGTTARLOKRTFYKQLPODIGTA YYLTSQAMVDNLALARDCOGGTTARLOKRTFYKOLPODIGTA YYLTSQAMVDNLALARDCOGGTTARLOKRTFYKOLPODIGTA YYLTSQAMVDNLALARDCOGGTTARLOKRTFYKOLPODIGTA YYLTSQAMVDNLALARDCOGGTTARLOKRTFYKOLPODIGTA YYLTSQAMVDNLALARDCOGGTTARLOKRTFYKOLPODIGTA YYLTSQAMVDNLALARDCOGGTTARLOKRTFYKOLPODIGTA YYLTSQAMVSTARLOKRTFYTTARLOKRTFYTTARLOKRTFYTTARLOKRTFYTTARLOKRTFYTTARLOKRTFYTTARLOKRTFYTT	1			
SEDSYTYEVTARAGFMAPHLEBALMPSQSRISLIGHKYSPPRR AGRICMSPPKIPGGSSESPPGMTFSDVRDPLQG PLAVTLIGSSP TESLTVDPASE*SGTGASETSLOPSLWPRLHPPLLGTLLACHPS PAARLSGKVHAAMPEFKAFCI 6846 213 1258 LYFLKTIK*LINIKLAEHP*YENDEKLTKLRINTIMEQYTRTEESARG IIFTKTRQSAYALSQWITEMBEKFAFVGVKARHHLIGAGHSSFFKE WTQNEQKEVISKFRTGKINLILATTVEGLIJKGKENSFFKE WTQNEQKEVISKFRTGKINLILATTVEGLIJKGKENSFFKE WTQNEQKEVISKFRTGKINLILATTVEGLIJKGKENSFKEV WYKAIHLVONMKPEELYAKILLELQMOSIMEKKHKTKRINTAKHYK NPPSLITFLCKNCSVLACSGEDIHVIEKMHVNMTPEFKELYIV RENNTLQKKCADYQINGEIICKKOGAMGTMWUKKGIDLPCLKIR NPFVVFKNNSTKKQYKKWEDLEITFNJSECLIFSBED 6847 1450 348 SMCWNSDRLEMBLIDLALLLYPSSVPPYTGHLSDDSLSRKYCLT WFEDALMGVL*PRABIOPHCVNAGDRWFOKGAKAVSAVLESDD YPGAVGTLTVRSLLDTREHCLNEPNPPDPYSKVKORENGVALRC; PPAYGTLTVRSLLDTREHCLNEPNPPDPYSKVKORENGVALRC; PPAYGTLTVRSLLDTREHCLNEPNPPDPYSKVKORENGVALRC; PPAYGTLTVRSLLDTREHCLNEPNPPDPYSKVKORENGVALRC; PPAYGTLTVRSLLDTREHCLNEPNPPDPYSKVKORENGVALRC; PPAYGTLTVRSLLDTREHCLNEPNPPDPYSKVKORENGVALRC; PPAYGTLTVRSLLDTREHCLNEPNPPDPYSKVKORENGVALRC; PPAYGTLTVRSLLDTREHCLNEPNPPDPYSKVKORENGVALRC; PPAYGTLTVRSLLDTREHCLNESPNPPDYSKVKORENGVALRC; PPAYGTLTVRSLLDTREHCLNESPNPPDYSKVKORENGVALRC; PPAYGTLAVKSLLDTREHCLNESPNPPDYSKVKORENGVALRC; PPAYGTLAVKSLLDTREHCLNESPNPPDYSKVKORENGVALRC; PPAYGTLAVKSLLDTREHCLNESPNPPDYSKVKORENGVALRC; PPAYGTLAVKSLLDTREHCLNESPNPPDYSKVKORENGVALRC; PPAYGTLAVKSLLDTREHCLNESPNPPDYSKVKORENGVALRC; PRAYGTLAVKTYSTYPTCHE 6848 19 16 AMWINSLDGTRNIVLSSPKKRNTLSLANLKSLQSDLLHGHADSSNL VVPEALLGETHTLARKHASLSFRVVSLGKATTYKQLDGLGTL VVPEALLGETHTLARKHASLSFRVVSLGKATTYKQLDGLGTL VVPEALLGETHTLARKHASLSFRVVSLGKATTYKQLDGJKT VVPEALLGETHTLARKHASLSFRVVSLGKATTYKQLDGJKT VVPEALLGETHTLARKHASLSFRVSLGKATTYKQLDGJKT VVPEALLGETHTLARKHASLSFRVSLGKATTYKQLDGJKT VVPEALLGETHTLARKHASLSFRVVSLGKATTYKQLDGJKT VVPEALLGETHTLARKHASLSFRVVSLGKATTYKQLDGJKT VVPEALLGETHTLARKHASLSFRVVSLGKATTYKQLDGJKT VVPEALLGETHTLARKHASLSFRVSLGKATTYKQLDGJKT VVPEALLGETHTLARKHASLSFRVSLGKATTYKQLDGJKT VVPEALLGETHTLARKHASLSFRVSLGKATTYKQLDGJKT VVPEALLGETHTLARKHASLSFRVSLGKATTYKQLDGJKT VVPEALLGETHTARAGT VVPANAGRENCH VVPEALLGGETHTLARKHASLSFRVSLGKATTSVHTHO				
AGRICMSPPKLIPGSSSSEFFGRITFSDVEDPLGSPLAVTLGSSSS TESLITVOPASET SCITGASTRISLOPSLWFRLHPPLIGTLLACHPS PAARLSGKVHAAWPEFKAFCL LYFLKTIK*LINKLAEHF*PENEKLTKLRNTIMEQYTRTEESARG 11FFKTRGSAYALSGWITSMEKKHKKLRNTIMEQYTRTEESARG 11FFKTRGSAYALSGWITSMEKKHKKLRNTIMEQYTRTEESARG 11FFKTRGSAYALSGWITSMEKKHKKTRNIAKHYK 11FFKTRGSAYALSGWITSMEKKHKKTRNIAKHYK 11FFKTRGSAYALSGWITSMEKKHKTRNIAKHYK 11FFKTRGSAYALSGWITSMEKKHKTRNIAKHYK 11FKTRGSAYALSGWITSMEKKHKTRNIAKHYK 11FKTRGSAYALSGWITSMEKKHKTRNIAKHYK 11FKTRGSAYALSGWITSMEKHKKTRNIAKHYK 11FKTRGSAYALSGWITSMEKHKKTRNIAKHYK 11FKTRGSAYALSGWITSMEKHKKTRNIAKHYK 11FKTRGSAYALSGWITSMEKHKTRNIAKHYK 11FKTRGSAYALSGWITSMEKHKTRNIAKHYK 11FKTRGSAYLSGWITSMEKHKTRNIAKHYK 11FKTRGSAYLSGWITSMEKHKTRNIAKHYK 11FKTRGSAYLSGWITSMEKHKTRNIAKHYK 11FKTRGSAYLSGWITSMEKHKTRNIAKHYK 11FKTRGSAYLSGWITSMEKHTRNIAKHYK 11FKTRGSAYLSGWITSMEKHTRNIAKHYKTRNIAKHYK 11FKTRGSAYLSGWITSMEKHTRNIAKHYKTRNIAKHYK 11FKTRGSAYLSGWITSMEKHTRNIAKHTRGSGVITSMEKHTRNIAKHTRG 11FKTRGSAYLSGWITSMEKHTRNIAKHTRGSGVITSMEKHTRNIAKHTRG 11FKTRGSAYLSGWITSMEKHTRNIAKHTRGSAYLNOHTHSSILVAE 11FKTRGSAYLSGWITSMEKHTRNIAKHTRGSAYLNOHTHSSILVAE 11FKTRGSAYLSGWITSMEKHTRNIAKHTRGSAYLNOHTHSSILVAE 11FKTRGSAYLSGWITSMEKHTRNIAKHTRGSAYLNOHTHSSILVAE 11FKTRGSAYLSGWITSMEKHTRNIAKHTRGSAYLNOHTHSSILVAE 11FKTRGSAYLSGWITSMEKHTRNIAKHTRGSAYLTAHATGAATGCOBLIKATHYKOLPOOLGT 11FKTRGSAYLSGWITSMEKHTRNIAKHTRGATAGAGGUTHABATGCATAGAGGWITSMEKHTRGTAYAAGGGGTATAGAGGWITSMEKHTRGTAYAAGGGGTATAGAGGWITSMEKHTRGTAYAAGGGGTATAGAGGAGAGAGAGAGAGAGAGAGAGAG	1		!	
TESLTVDPASE*SGTGASETSLOPSLWFRLHPPLLGTLLACHPS PAALLSGKVHAAWBE FKAPCT LYFLKTIK*LNRLAEHP*YENEKLTKLRNTIMEQYTRTEESARG LIFTKTRGSAYALSGWITEMERKAEVGWKAHHLIGGHISSEFKR WTQMEQGEVISKFRTGKINLLLATTVABEGLDI KECNIVIRYGL VTNEIAWOQARGRARADESTYUVAHSGSGVI EHETVNDPREKM MYKAIHCVONMKPEETVAHKILELQMOSIMEKKMKTKRNIAKHYK NNPSLITFLCKNCSVLACSGEDIHVIERMHVMMTPEFKELYIV RENNTLQKKCAVQINGEI ICKCQQAWGTMWUKKGLDLPCLKIR RENNTLQKKCAVQINGEI ICKCQQAWGTMWUKKGLDLPCLKIR RENNTLQKKCAVQINGEI ICKCQQAWGTMWUKKGLDLPCLKIR RENNTLQKKCAVQINGEI ICKCQQAWGTMWUKKGLDLPCLKIR RENNTLQKKCAVQINGEI ICKCQQAWGTMWUKKGLDLPCLKIR RENVENDRALLEVALESELDIVERCHOPSVEKVQERNOVALRCP BGVVRSILDALGWERQLALIVKGVELEITPNJSECLEFSDED NFVVFENNSTKKQVKKWVELPITPNJSECLEFSDED VRFGEBAKRLQERPWLODPSSEMLOPSECLEFOR PAYGTLTVRSLLDTREHCLNEPNPPDPYSKVKQRENOVALRCP BGVVRSILDALGWERQLALIVKGILAGNVFVOKAKVQAVLESDP YFGFEBAKRLQERPWLDVSYSEMLQRIKKGPPHKCALIFADNSG IDIILGYFPFVBELLLEGTSVILACNSGPALNOVTHSSSLIVAR RIAGMDPVHSALRERELLLVOTGSSSPCLUSKELDKAVLASNLESDI ZERGADLVVIEGMGRAVHTNYHAABCESLKLAVIKNAMLARRIG GRLFSVIFKYEVPAE AMMINISLDGIRNIVLSNPKKRNILSLAMLKSLQSDILHDADSND LKVIITSABGPVFSSGIDLKELIFBEQGRDHABVFOTGSKWMH IRNIPPVUATAMOGLARAAGCOLVAS COLNASBVFOTGSKWMH IRNIPPVUATAMOGLARAAGCOLVAS COLNASBVFOTGSKWMH IRNIPPVUATAMOGLARAAGCOLVAS COLNASBVFOTGSKWMH IRNIPPVUATAMOGLARAAGCOLVAS COLNASBVFOTGSKWMH IRNIPPVUATAMOGLARAAGCOLVAS COLNASBVFOTGSKWMH VVEPAVALGSKLDVINKHSFNNFTLSGGDADAGDDAGDAGRESCHLGTM VVEPAVALGSKLDVINKHSFNNFTLRVGLINGI LADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQDABRSCSHLGTM VEPAVALGSKLDVINKHSFNNFTLRVGLINGI LADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQDABRSCSHLGTM VEPAVALGSKLDVINKHSFNNFTLRVGLINGI LADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQDABRSCSHLGTM VEPAVALGSKLDVINKHSFNNFTLRVGLINGI LADFDELLSK PKFSGVEKIKTIGSTYMATGLINGI LADFDELLSK PKFSGVEKIKTIGSTYMATGLINGI LADFDELLSK PKFSGVEKIKTIGSTYMATGLINGI LADFDELLSK PKFSGVEKIKTIGSTYMATGLINGI LADFDELLSK PKFSGVEKIKTIGSTYMATGLINGI LADFDELLSK PKFSGVEKIKTIGSTYMATGLINGI LADFDELLSK PKFSGVEKIKTIGSTYMATGLINGI LADFDELLSK PKFSGVEKIKTIGSTORGRENGUMAGGLINKPUTSPSTTHVKNLES LTULFRUKGCOLDLPAGLGCCMIKKSKSGLVVEDHLFDTLIPLEVK EALN	1	1		
BAAKLSGKVHAAMPEFKAFCL				
1258	1.		1	
TIFKKTRGSAYALSGWITEMEKRAEVGVKAHHLIGAGRISSETKR MTQNEGGKEVISKERTGKINLIATTVAEBGLDIKEGNIVIRYGL VTNEIAWQAGRERAEDESTYULAHSGGGVIEHTVADFPEKM MYKAIHCVQMMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYK NNPSLITFLCKNCSVLACSGEDIHVIEKGHHVMMTPEFKELJYIV RENKTLQKKCADYQINGBIICKCQAWGTMYHKGLDLPCLKIR RENKTLQKKCADYQINGBIICKCQAWGTMYHKGLDLPCLKIR RENKTLQKKCADYQINGBIICKCQAWGTMYHKGLDLPCLKIR RENKTLQKKCADYQINGBIICKCQAWGTMYHKGLDLPCLKIR NFVVVPKNNSTKKQVKKWPLPITFPNLDYSECCLFSDED GRAGTITVESLLDTREHCLNEFNFPDPYSECCLFSDED PGVVRSIDALIHEREGRIALIVKGLLAGNVFDMCAKAYSAVLESDD YFGEEAKRKLQERPWLUDSYSEMLQRLKGPPHKCALIFADNGG IDIILGYPPVRSLLLIRGTEVILACNSGPALNDVTHSESLIVAE RIAGMDPVVHSALRERELLLVQTGSSSPCLDLSRLDKSLAALWR ERGADLVVISGMGRAYNTNYHAALRCESKKLAVIKNAWLAERIG GRLFSVIFKKEVPAE 6848 19 16 AMWINSLDGIRRIVLSNPKKRNTLSLAMLKSLQSDILIDADSND LKVIIISAEGPVFSSGNDLKELTERGGRYHAEVPQTCSKVMH IRNHPVPVIAMNGLATAAGCQLVASCDIAVASDKSSFATTGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQBALLHGLIKK VVPERALEQESTMRIARKIASLSRVJKKAPTYVEQDOLGTA YYLTSQAMVDNLALRDGGGITAFLOKRKPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEGGSPAPRPQTDTSF*PVGWNSTQGDDLYNGSYEC VCVLFASVPDFKEFFYSESNINHBGLECLRLIMEIIADPBELLSK PKFSGVEKIKTIGSTYMAATGLANTSGODAQDAERSCSHLGTM VGFAVALGSKLDVIKHSFYNNFRLUSHIGDVAGVGAGATYKQUTGAGAKPQ VDIWGNTVNVASRMESTGVLGKIQVTEETAMALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLITRTGPFSATIG RDFBLLKCHLWFFTDVAEIFSANTIG GLESLARLKHLKILHVKSNITKVPSNITDVAPHITKLVIINDGT KLLVINSLKKMNVAELELQNCSLERIPHAIFSLSNLQELDLKS NINTTEREIISPGNLKRUTCLKLKHVITPPSITTHVKLESL VFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDLIPANGI CLESLARLKHLKLILKKRNITKVPSNITVAPHITKLVIINDGT KLLVINSLKKMNVAELELQNCSLERIPHAIFSLSNLQELDLKS NINTTEREIISPGNLKRICTLKLKHVITPPSITTHVKNLESL VFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDLIPANGI CLESLARELKHLKLILKKRINTICKUSHLVTIPPSEVGGOLSQ LTQLELKGRACLDRIPADAGLGCCRMIKKSGLVVEDHLFPTLTPLEVK EALNODINTPFANGI CLESLARELKHLKLILKKRNITKVPSNITTVAPHTTERVKLESL VFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ EALNODINTPFANGI CLESLARELKHLKLILLKKGRUCTLTSLPEKVGGUSQ LTQLELKGRACLORPADAGLGGGEVYFSLLTLD LTDLELKGRACLORPADAGLGGGEVYFSLLTLD LTDLELKGRACLORPADAGLGGGEVYFSLLTLD	<u> </u>			
### ITFIKTROSAYALSQWITENBERFAEVGVKAHHLIGAGHSSEFKE #### MYONEQREVISKRITGKINLLIATTVAEGGUIKECNIVIRYGL VTNEIAMVQARGRARADESTYUVAHSGSGVIEHETVINDTREKK MYKAIHCVQNMKPEEVAHKILELQMQSIMEKKKYKKRITAKHYK NPSLITTFLCKKCSVLACSGEDINVIEKKMYKKKKRITAKHYK NPSLITTFLCKKCSVLACSGEDINVIEKKMYKKKKRITAKHYK NPSLITTFLCKKCSVLACSGEDINVIEKKMYKKKURLADLPCLKIR ###################################	6846	213	1258	LYFLKTIK*LNRLAEHP*YENEKLTKLRNTIMEQYTRTEESARG
UTNEIAMVQARGRARADESTYULVAHSGSGVIEHETVNDPREKM MYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYK NNPSLITTLCKNCSVLACGEDIHVIEKMHVNTPEPEKELYIV RENKTLQKKCADYQINGEIICKCGQAWGTMWHKGLDLPCLKIR NFVVYFKNNSTKKQYKKWUELIPPINLDYSECCLFSDED 6847 1450 348 SMCWNSDRLEMPLIDLALILYPPSYVPYTCHLSDDSLSRKYCLT WFEDALMSVL*RABAIQPHCVMAGDRMEKRQKYWNKLQTLRQQ PFAYGTITVRSLIDTEHCLINEPPPDPYSKVKQRENGVALRCF PGVVRSLDALGWERQLALVKGLLAGNVPDKGAKAVSAVLESDP YFGFEAKRKLQERPWLVDBYSEWLQRIKGPPHKCALIFADNSG IDIIIGWFPVRSLLLRGTEVULACNSGPALNDVTHSESLIVAE RIAGMDEVVHSALREERLLLVCTGSSSFCLDLSRIDKGLAALVR ERGADLVVISGMGRAVHTSTHAADARCESLKLLAVIKNAWLAERIG GRLFSVIFKYEVPAE 6848 19 16 AMWINSLDGTRNIVLSNPKKRNTLSLAMKSIQSDILHDADSND LKVII SAEGPYSSSCHDLKELTBEQGRDYHAEVFGTCSSKYMH IRNHPVPVIAMVGLATAAGCQLVASCDIAVASDKSSFAPTGVN VGLFCSTPGVALRAAVPRKVALEMIFTGEPISAQBALHGLINK VVPEAELQEETMRIARKIASISRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGGGTTAFIQKRKPWSHEPV*VBH 6849 70 821 SLGUDGSCLEGGSFAPPTGTUSPPISAQBALHGLINK VVPEACHQESCHEKGSFAPPTGTUSPPISAQBALHGLINK VVPEAVALGSKLDVINHFSNIPFTRVGLENDEDLYHGSYE VCVLFASVPDFKEFYSESNINHBGLECLRLLNEIIADFDELLSK PKRSGVSKIKTIGSTYMAATGLNATSGQDAQDABRSCSHIGTM VEFAVALGSKLDVINHFSNIPFLRVGLNHGPVVAGVTGAQKPQ YDIKGNTVNVASRMESTGVLGKIQUTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGINHEWTEKLRGHISRNAQDKGEHLIFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCCPAKVEQTAFSIL RDHLRCHHVFPTDVASIPAWVYLLKNIR.RELVLIGNINSENNKIL GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVHNDGT KLLVLNISLKRMMVYABLBLQNCELERI PHAIFSLSNLQEIDLKS NNIKTIEBIISFGHLKRITCLKLHNINK IVTIPPSITHVKNLESL YFSNNKLESLPVAVPSLQKLRCLDVSYNNISMIPIEIGLLONLQ HLHITGNKVDILPKQLFKCIKLRINKINKIVTPIPSITHVKNLESL YFSNNKLESLPVAVPSLQKLRCLDVSYNNISMIPIEIGLLONLQ HLHITGNKVDILPKQLFKCIKLRINKINKIVTPIPSITHVKNLESL YFSNNKLESLPVAVPSLQKLRCLDVSYNNISMIPIEIGLLONLQ HLHITGNKVDILPKQLFKCIKLRINKINKIVTPIPSITHVKNLESL YFSNNKLESLPVAVPSLQKLRCLDVSYNNISMIPIEIGLLONLQ HLHITGNKVDILPKQLFKCIKLRINKINKIVTPIPSITHVKNLESL YFSNNKLESLPVAVPSLQKLRCLDVSYNNISMIPIPITGLEVK EALMQDINTIPANGI UXAQVSAREGGENCLGWILADSSQESYKSLEEAEDCYPPSILTIDD LRDLFMQVEGGFLLSKRGTDLSWRARGUMBAGLMIGAGA				IIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKP
UTNEIAMVQARGRARADESTYULVAHSGSGVIEHETVNDPREKM MYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYK NNPSLITTLCKNCSVLACGEDIHVIEKMHVNTPEPEKELYIV RENKTLQKKCADYQINGEIICKCGQAWGTMWHKGLDLPCLKIR NFVVYFKNNSTKKQYKKWUELIPPINLDYSECCLFSDED 6847 1450 348 SMCWNSDRLEMPLIDLALILYPPSYVPYTCHLSDDSLSRKYCLT WFEDALMSVL*RABAIQPHCVMAGDRMEKRQKYWNKLQTLRQQ PFAYGTITVRSLIDTEHCLINEPPPDPYSKVKQRENGVALRCF PGVVRSLDALGWERQLALVKGLLAGNVPDKGAKAVSAVLESDP YFGFEAKRKLQERPWLVDBYSEWLQRIKGPPHKCALIFADNSG IDIIIGWFPVRSLLLRGTEVULACNSGPALNDVTHSESLIVAE RIAGMDEVVHSALREERLLLVCTGSSSFCLDLSRIDKGLAALVR ERGADLVVISGMGRAVHTSTHAADARCESLKLLAVIKNAWLAERIG GRLFSVIFKYEVPAE 6848 19 16 AMWINSLDGTRNIVLSNPKKRNTLSLAMKSIQSDILHDADSND LKVII SAEGPYSSSCHDLKELTBEQGRDYHAEVFGTCSSKYMH IRNHPVPVIAMVGLATAAGCQLVASCDIAVASDKSSFAPTGVN VGLFCSTPGVALRAAVPRKVALEMIFTGEPISAQBALHGLINK VVPEAELQEETMRIARKIASISRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGGGTTAFIQKRKPWSHEPV*VBH 6849 70 821 SLGUDGSCLEGGSFAPPTGTUSPPISAQBALHGLINK VVPEACHQESCHEKGSFAPPTGTUSPPISAQBALHGLINK VVPEAVALGSKLDVINHFSNIPFTRVGLENDEDLYHGSYE VCVLFASVPDFKEFYSESNINHBGLECLRLLNEIIADFDELLSK PKRSGVSKIKTIGSTYMAATGLNATSGQDAQDABRSCSHIGTM VEFAVALGSKLDVINHFSNIPFLRVGLNHGPVVAGVTGAQKPQ YDIKGNTVNVASRMESTGVLGKIQUTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGINHEWTEKLRGHISRNAQDKGEHLIFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCCPAKVEQTAFSIL RDHLRCHHVFPTDVASIPAWVYLLKNIR.RELVLIGNINSENNKIL GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVHNDGT KLLVLNISLKRMMVYABLBLQNCELERI PHAIFSLSNLQEIDLKS NNIKTIEBIISFGHLKRITCLKLHNINK IVTIPPSITHVKNLESL YFSNNKLESLPVAVPSLQKLRCLDVSYNNISMIPIEIGLLONLQ HLHITGNKVDILPKQLFKCIKLRINKINKIVTPIPSITHVKNLESL YFSNNKLESLPVAVPSLQKLRCLDVSYNNISMIPIEIGLLONLQ HLHITGNKVDILPKQLFKCIKLRINKINKIVTPIPSITHVKNLESL YFSNNKLESLPVAVPSLQKLRCLDVSYNNISMIPIEIGLLONLQ HLHITGNKVDILPKQLFKCIKLRINKINKIVTPIPSITHVKNLESL YFSNNKLESLPVAVPSLQKLRCLDVSYNNISMIPIEIGLLONLQ HLHITGNKVDILPKQLFKCIKLRINKINKIVTPIPSITHVKNLESL YFSNNKLESLPVAVPSLQKLRCLDVSYNNISMIPIPITGLEVK EALMQDINTIPANGI UXAQVSAREGGENCLGWILADSSQESYKSLEEAEDCYPPSILTIDD LRDLFMQVEGGFLLSKRGTDLSWRARGUMBAGLMIGAGA	1.			MTQNEQKEVISKFRTGKINLLIATTVAEEGLDIKECNIVIRYGL
MYKATHCVOMKPEEYAHKILELQMGSIMEKMKTKKNIAKHYK NNPSLITFLCKNCSVLACSGEDIHVIEKMHYNNTPEFKELYIV RENKTLÇKKCADVQINGBIICKCGQAWGTMYHKGLDLPCLKTR NFVVVFKNNSTKKQYKKWUELPITFPNLDYSECCLFSDED SMCKNSDRLEMPLIDLALILYPFSYVPYTGHLSDBLSRKYCLT WFEDALMGUL*RAEAIQPHCVNAGDRMEKPRQKYWNLQTIRQQ PFAYGTLTVUSLLDTREHCLNEENPPDPSKVKQRENGVALRCF PGVVVSLDALGWBERQLALVKGLAGNVPDMGAKAVSAVLESDP YFGFEAKRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSSSLIVAE RIAGMPPVVHSALREERLLLVGSSSPCTLDISLDKGLAALVR ERGADLVVI IEGMGRAVHTNYHAADRCESIKLAVIKNAWLAERIG GRLFSVIFKYEVPAE GRAFEVYIFKYEVPAE LKVIIISAEGPVFSSCHDLKELTERQGRDYHAEVPOTCSKYMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATFGVN VGLFCSTFGVALARAVPRKVALEMFTEEPISAQEALLHGLINK VVPEAELQESTMRIARKIASLSRFVVSLGKATFYKQDPODLGTA YYLTSQAWVDNLALRROGGEGITAPLQKKRPVWSEPP*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSF*PVGNWATQQEDLYHGSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLINEIIADFBLLSK PKFSGVEKIKTIGSTYMAATGLATGQDAQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLINGPVVAGVIGAQKPQ YDIMGNTVNVASRMESTGVLGKGLVTESTAWALQSLGYTCYSRG VIKVKGRGQLCTTFLNTDLTTRTPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQEHLHCCPAKVEQTAFSFL RDHLRCCHVKFTDVAEITAWVLLKNLRELYLIGNINSENNKMI GLESLRELRHIKLHVKSNLTKVPSNITDVAPHLTKLVIINDGT KLLVLNSLKKMMNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRITCLKLMHNKIVTIPPSITTWKNLESL YFSNNKLESLPVAVFSLGKLRCLDVSYNNISMIPBIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTINLGQNCITSLPEKVGQLSQ LTQUEKKGNCLDRLPRQLGCGMKKKSGLVVEDHLFPTUPLEVK EALNQDINIPFANGI VSAQVSAREGENCLGWILADSSQESYKSLEEAEDCYPPSLLTLD LRDLFHQVEGGFLLSCPKRGTDLSMGRAREVGMWAAGLMIGAGA	1			VTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREKM
NNPSLITECKNCSVLACSGEDIHVIEKMHHVMMTPEFKELYIV RENKTLQKKCADVQINGEIICKCQQAWGTMMVHKGLDLPCLKIR NFVVVFKNNSYKKQYKKWSLPITFPNLDVSECCLFSDED		1		MYKAIHCVONMKPEEYAHKILELOMOSIMEKKMKTKENTAKHYK
RENKTICKCADYQINGEI ICKCQQAGTIMWYHKGLDLPCLKIR NFVVVFKNNSTKKQYKKWELBITFPNIDYSECCLFSDED 6847 1450 348 SMCWNSDRLEMPLIDLALILYPPSYVPYTCHLSDDSLSRKYCLT WFEDALNGVL*RABAIQPHCVNAGDRMEKRQKYWNKLQTLRQQ PRAYGTLTVRSLLDTREHCLNEPNFPDPYSKVKQRENGVALRCF PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP YFGFESARKLQERPWLVDSYSENLQRKGPFHKCALIFADNSG IDIIIGVPF FYREILLRGTSVILACNSGPALNDVTHSESLIVAE RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEMGRAVVHTNTHAAIRCESLKLAVIKNAWLAERIG GRLFSVIFKYEVPAE 6848 19 16 AMWINSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTBEGGRDVHARDVFDTCSKVMHH IRNHPVPIJANVNCLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLINK VVPEAELGETMRIAGSLRFVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGGGGITAFLOKRKYWSHEPV*VEH 6849 70 821 SLGVDGSCLEGGSSPAPRQTDTSF*PYGNNATQCDLYHQSYEC VCVLFASVPPKFFYSESNINHBGLECLRILNSIIADFDELLSK PKFSGVEKIKTIGSTYMAAFGLNATSGQDAQQABERSCHIGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VEFAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VEFAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VEFAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VEFAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VEFAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VERAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VERAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VERAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VERAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VERAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VERAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VERAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VERAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VERAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VERAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFDLTG VERAVALGSKLDVINKHSFNNFRLRVGLNEGVPAVFSIL RDHHRCLHVKFTDVAEIPAMVYLLKNLRELYLIGNLNSENNKMI GLESLREILRHLKILHVKSNLTKVPSNITDVAPHLTKLVINNGT KLLVLNSLKKMMNVABELELQNCELERI PHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLCLLVSYNNISMTPISIGLLQNLQ HLHTTGNKVILESLLYAFSLQACCCOVSYNNISMTPISIGLLQNLQ HLHTTGNKVILESLLYAFSLQACCCRMLKKSGLVVEDHLFDTLFVK EALNQDINIPFANGI CASCI				
NFVVVFRNNSTKKQYKKWVELP1TPPNLDVSECCLFSDED				
6847 1450 348 SMCWNSDRLEMBILDIAJILYPPSYVPYTGHLSDDSLSRKYCIT WFEDALNGVL*RAEAIQHCVNAGDRMEKFRGKYWNKLQTLRQQ PFAYGTLTVRSLLDTREHCLNEFNPFDDFSKVVQRRGWALRCF PGUVRSLDALGWEERQLALUKGLLAGNVFDWGAKAVSAVLESDP YFGFEAKRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG IDIILGVPFFVREILLROSGSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERIG GRLFSVIFKYSVPAE 6848 19 16 AMWWNSLGGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTBEQGRDYHAEVFQTCSKVMH IRNHPVPVIAWUNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTFGVALARAVPRKVALEMLFTGEPISAGEALLHGLINK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAWVDNLALRDGGGITAFLQKRKPWSHEFV*VEH 6849 70 821 SLGVDGSCLEGGSPAPRPQTTTSP*PVGNWATQGEDLYHGSYBC VCVLFASVPDPKEFYSESNINHEGLECLRLLNEILADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDINGNTUNASRMESTGUKKJQTTEFETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGINHEMTFEKLRGHISRNAQDKGELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPALFSNAQDKGELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPALFSNAQDKGELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPALFORGLENTLICHCPAKVEQTAFSFL RDHLRCHVKFTDVAE IPAWFVLKINLEELYLIGKLNSENNKMI GLESLREIRHLKILHVKSNLTKVPSNITDVAPHLTKLVYHNDGT KLLVANSLKKMNVAELBLQNEGLERFIPHAIFSLSNLQBLDLKS NNIRTIEEILSFQHLKRILTCKKLWHNKVTTIPPSITHVKNLESL YFSNNKLESLEVAVFSLQKLRCLDVSYNNISNIPIEIGLLQNLQ HLHTGRKVDILPRQLEKCIKLRTLNLGQNCTTSLPEKVGQLSQ LTQLEKGNCLDRLPRQLGCCRMLKKSGLVVEDHLPDTLPLEVK EALNQDINIPPANGI VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				NEVVVEKNNSTKKOVKKWVELDITEDNI DVSECCI.ESDED
WFEDALNGVL*RAEAIQPHCVNAGDRMEKPRQKYMNKLQTLRQQ PPAYGTLTVRSLLDTREHCLNEFNPPDPYSKVKQRENGVALRCF PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAYSAVLESDP YFGFESARRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTRSSSLIVAE RIAGMDPVVHSALREERLLLVGTGSSSPCLDDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAADRCESLKLAVIKNAWLAERIG GRLFSVIFKYBVPAE 6848 19 16 AMWINSLOSIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIANVNGLATRAVGLVASCDIAVASDKSSFATFGVN VGLFCSTFGVALRARVPKALEMDFTGEPISAQRALHGLINK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLISQAWVDNLALRDGGGTTAFLQKRKPVWSHEPV*VEH 6849 70 821 SLGVDSGCLEGGSPAPAPOTDFSP*PVGMATQGEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLINE ILDFFDELLSK PKFSGVERIKTIGSTYMAATGLANATGQDAQQDAERSCCHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTESTAMALQSLGYTCYSRG VIKVKGKQQLCTYFINTDLTRTGPPSATLG 6850 2 1235 ARGINHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPBAKTPAKLSQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAETPAWTLQLHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAETPAWTLQLEHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAETPAWTLXVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLGNLQBLDLKS NNIRTIEEIISFQHLKRLTCLKLMHNKIVTIPPSITHVKNLESL YFSNNKLESLBVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHTTGNKVDILPRQLFKCIKLRTLNLGQNCTISSBFKGVGGLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPPANGI CHANGOUTH PROMICE EALNQDINIPPANGI LRQLFYPSLLTRICLERAGEDCYPPSLLTID LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	6847	1450	348	SMCWNSDDI.FMDI.TDI.ALTI.VDDCVVDVTCUI CDDCI CDVVCI III
PPAYGTLTUTSLLDTREHCLMEMPPDPYSKVKQRENGVALRCP PGVVRSLDALGWEERQLALWKGLLAGNVFDWGAKAVSAVLESDP YPGTEEARKKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE RIAGMDPVVHSALREERLLLVGTGSSSPCLDLSRLDKGLAALVR ERGADLVVHEGMGRAVUTIGMSSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTYHAALRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVPAE 19 16 AMWWISLOGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATFGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLINK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLFQDLGTA YYLTSQAMVDNLALRIGQEGITAFIQKRKPVWSHERPV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFIDELLSK PKFGSVEKKKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFFLRVGLNHIGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKTQVTEETAWALQSLGYTCYSRG VIKVKKGKQLCTYFINTDLTTTGPPSATLG ARGINHEWTFEKLRGHISRNAQDKGELHLFWLSGYPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKALRELYLIGNLNSENNKMI GLESLREILRHLIHLFWLNTLTVPSHITTDVAPHLTKLVLHNNDGT KLLVLNSLKKMMNVAELBLQNCELERIPHAIFSUSNLQELDLKS NNIKTIEBIISFQHLKRITCLKLWHNKIVTIPPSTTHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNXVDILPFAQLGCCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTID LRDLFNQVEQPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA		2.50	340	WEEDAL NOW + DATA TODUCTANA ODDWENTED ON THE DOC
PGVVRSLDALGMEERQLALVKGILAGNVPDMGAKAVSAVLESDP YPGFEAKRKLQERPMLVDSYSEMLQRLKGPPHKCALIFADNSG IDIILGVFFVRELLLRGTEVILACNSGPALNDVTHSSSLIVAE RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAADRCESLKLAVIKNAMLAERIG GRLFSVIFKYEVPAE 6848 19 16 AMWINSLDGIRNIVLSNPKKRNYTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSCHDLKELTEEQCRDYHAEVPQTCSKVMHH IRNHEVPUYLAMVNGLAHAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLEPQLGTA YYLTSQAMVDNLALRDGGEGITAFLQKRKPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEGGSPAERPQTDTSF*PVGNWATQGEDLYHQSYEC VCVLFASVVDFKEFYSESNINHEGLECLRLLINEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQDAERSCSHLGTM VEFAVALGSKLDVINKHSPNNFRLRVGLINHGPVVAGVTGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGINHEWTPERLRCHISRAQDKGELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLREIYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRITCLKLMHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNXVDILPKQLFKCIKLRTINLGQNCITSLPEKYGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPRANGI 6851 1765 660 VSAQVSARGERNCLGWILADSSQESYKSLEBAEDCYPPSLLTID LRDLFNQVEQPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				WFEDALINGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTDRQQ
YPGFEEAKRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG IDIILGVFFPVELLLRGTEVILACNSGPALNDVTHSSLIVAE RIAGMDPVVHSALREERLLLVQTGSSPCLDLSKLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAADRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVPAE 19 16 AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTERGGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMMFTGEPISAQEALHGLINK VVPEEAELQEETHRIARKIASLSRPVVSLGKATFYKQLEPOLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEGGSPAPRPOTDTSP*PVGWNATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLINEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFWLSGVPDAVFDLTD LDVLKLELIPEAKIPANISQMTNLQELHLCHCPAKVEGTAFSFL RDHLRCLHVKFTDVAEIIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIKTIEEIISFQHLKRLTCLKLWINKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHHTGNKVDILPKQLFKCIKLKHINKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHHTGNKVDILPKQLFKCIKLKRILNGGNCITSLPBKVGQLSQ LTQLEKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				PRAYGILIVESLLDTREHCLNEFNFPDPYSKVKQRENGVALRCF
IDIIIJSVFPYVREILLRGTEVILACNSGPALNDVTHSESLIVAE RIAGMDPVVHSALREBELLLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVI EGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVPAE 6848 19 16 AMWWNSLDGIRNIVLSNPKKRNILSLAMLKSLQSDILHDADSND LKVIIISAGPVFSSGHDLKELITBQGRYNHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSRATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEAILHGLINK VVPEAELQEETHRIARKIASISRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEQGSPARPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQODAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIMGNTUNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGINHEWFFEKLRQHISRNAQDKGELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVINSLKKMNNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEBIISPQHLKRTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMTPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLEKGNCLDRLPRQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGMNLADBSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	1			PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP
RIAGMDPVVHSALREERLILVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTTYHAADRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVPAE 19 16 AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALAARAVPRKVALEMLFTGEPISAQEALLHGLINK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIJADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGEVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKTQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTMLQEHLCHCPAKVEQTAFSFL RDHLRCHHVKFTDVAEIPAWVILKNLEELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLITKLVINNDGT KLLVLNSLKKMMNVAELELQNCSLERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLITCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAYFSLQKLCCLDVSYNNISMIPPIBIGLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSARREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	1 .			
ERGADLVVIEGMGRAVHTNYHAADRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVPAE AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELITERGGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMETGEPISAQEALLHGILINK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKEVWSHBEV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLINEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSPNNFRLRVGLNHSPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFINTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWFFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPBAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVINSLKKMMNVABLELQNCELEERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPRQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWILADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE
GRLFSVIFKYEVPAE AMMWISLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTERQGRDYHAEVFQTCSKVMMH IRNHPVPVIANVNGLATAAGCQLVASCDIAVASDKSSFATFGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLINK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGGEGITAFLQKRKEVWSHEPV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDPKEFYSESNINHEGLECLRLINE I IADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNIVNVASRNESTGVIGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGINHEWTFEKLRQHISRNAQDKGELHLFWLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVVINNDGT KLLVLNSLKKMMNVABLBELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWINKIVTIPPSTTHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHHTGNKVDILPKQLFKCIKLRTINLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRIPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSARBGENCLGWNLADSSQESYKSLEEAEDCYPPSILITLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA			الارواد المستقد الاراد المستقد الاراد المستقد الاراد المستقد الاراد المستقد المستقد المستقد المستقد المستقد ا	RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR
6848 19 16 AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTBEQGRDYHAEVFQTCSKVMMH IRNHPVPVIANVNGLATAAGCQLVASCDIAVASDKSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEGGSPAPRPOTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKKTIGSTVMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMYNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTXVPSNITDVAPHLTKLVUHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCCMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGMNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG
LKVIIISAEGPVFSSGHDLKELITEEQGRDYHAEVFOTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMIARKIASLSSFVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKKKPVWSHEPV*VEH SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGFVVAGVICAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTTTGPPSATLG VKVKKGKQLCTYFLNTDLTTTGPPSATLG RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVHNDGT KLLVUNSLKKMNNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISPQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLEKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	<u> </u>	· · · · · · · · · · · · · · · · · · ·		(, , , , , , , , , , , , , , , , , , ,
LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVLARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGOEGITAFLQKRKPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHIGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVIGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPBEKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRITCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLEKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	6848	19	16	AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND
IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMIFTGEPISAQEALLHGILINK VVPEAELQEETMRIARKIASLSRFVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVTGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKQQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVHNDGT KLLVLNSLKKMMNVAELBLQNCCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHHITGNKVDILDFQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA		•		LKVIIISAEGPVFSSGHDLKELTERQGRDYHAEVFOTCSKVMMH
VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMNNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	ľ		:	
VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMNNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				
YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 8850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNIKHESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA			•	VVPEAELOEETMRIARKIASLSRPVVSLGKATFYKOLPODIGTA
6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNE!IADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWIFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	1	•	•	YYLTSOAMVDNLALRDGOEGITARI.OKRKDUWSHEDU*VEU
VCVLFASVPDFKEFYSESNINHEGLECLRLLNE I IADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHS FNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAXIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLERHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLFLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	6849	70	821	
PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTTFLNTDLTRTGPPSATLG ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	1 - 1	. •		
VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLREHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				
YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				
VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				
ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				
LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMNNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	1-6050			
RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	0030	2	1235	
GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	1 1	į		~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~
KLLVLNSLKKMMNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	1 1			RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	1 1			GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT
YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA			,	KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS
YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	į į			NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL
HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				
LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				
EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				
6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				
LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	6851	1765	660	
	-		000	
CICVIALITICKUDSEKLEREGEEEMUDDQEDDEBEPDIWFDFET	1			
	<u> </u>			CICAINDIIGKUDSEKDEREGEERMUDUĞEDBEEAUIMADAEL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequence	\=possible nucleotide insertion)
<u> </u>	, boquonec 1		MARPWIEDGDWIEPGAPGGTEDRPSGGGKANRAHPIKQRPFPYE
			HKNTWSAQNCKNGSCVLDLSKCLFIQGKLLFAEPKDAGFPFSOD
ļ			INSHLASLSMARNTSPTPDPTVREALCAPDNLNASIESQGQIKM
j			YINEVCRETVSRCCNSFLOOAGLNLLISMTVINNMLAKSASDLK
l			FPLISEGSGCAKVQVLKPLMGLSEKPVLAGELVGAQMLFSFMSL
			FIRNGNREILLETPAP
6852	1	407	RTRGEETYANFIKHNDGKNIFYAARTPATLFAVMFAMYIISGLT
6652	1 -	407	
1			GFIGLNSIAVLCNLVMGLALIFLCTWAYVKYSGEFREIGTVIDQ
i			IAETLWEQVLKPLGDNLMEENIRQSVTNSIKAGLTDQVSHHARL
6853	ļ	460	KTD CDCCAVCTEL VYDNDY VDTI WCANTTENVECUDDWY Y BUDWCDWO
0003	3	469	GDSCAVCIELYKPNDLVRILTCNHIFHKTCVDPWLLEHRTCPMC
•			KCDILKALGIEVDVEDGSVSLQVPVSNEIFNSASSHEEDNRSET
		: .	ASSGYASVQGTYEPPLEEHVQSTNESLQLVNHEANSVAVDVIPH
6854	1740	F0F	VDNPTFEEDETPNQETAVREIKS
0054	1148	585	HESYIGTFDPGELCVCAAIQWLQDNSASYFLNRKLVYEPSTQAK
1	* .		PVKNTFLRMWIYSHHIYQQDLRKKILDVGKRLDVTGFCMTGKPG
			IICVEGFKEHCEEFWHTIRYPNWKHISCKHAESVETEGNGEDLR
	ł		LFHSFEELLLEAHGDYGLRNDYHMNLGQFLEFLKKHKSEHVFQI
6855	1012	1140	LFGIESKSSDS
6855	1913	1148	GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDQTDDLAK
-			EEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALASRF
			YIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHI
			QLTYFSRWSEVEDSCDSDAIERMYCAPEVGAITEETEACDWWSL
			GAVLFELLTGKTLVECHPAGINTHTTLNMPEWVSEEARSLIQQL
6856	7.7.9		LQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR
6836	1617	997	VTQLYVSVDASTKDSLKKIDRPLFKDFWQQFLDSLKALAVKQQR
	Í		TVYRLTLVKAWNVDELQAYAQLVSLGNPDFIEVKGVTYCGESSA
			SSLTMAHVPWHEEVVQFVRELVDLIPEYEIACEHEHSNCLLIAH
			RKFKIGGEWWTWINYNFFQELIQEYEDSGGSKTFSAKDYMARTP
6857	1	617	HWALFGASERGFDPKDTRHQRKNKSKAISGC
6051		911	KGPEATAMVCVCSHPNCRQNHIKPSHSAAQTWCGSPTPASAPNH
	;		KLMAMEQGKTLPSATEDAKEEGLEAQISRLABLIGRLESKALWF
		•	DLQQRLSDEDGTNMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF
	:		
6858	.2	669	RHVKVDTLSQPEALSRILVPAAWCTVGRD RSRGIKDFENDPPLSSCGIFOSRIAGDALLDSGIRISSVFASPA
5030		200	1
	:		LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ
	·	•	IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR
			KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS
6859	└─ ─ ─┤	2150	GETWERKAYERA KKKEDAN CDCCCOAN CDTTOCH COMOTT KCC
0037	1	1150	GETMFKKAKTKAKKKPRKRSDSSGGYNLSDITQSPSSTGLLKSG
	•		KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE
			AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT
			SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT
			VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN
1			AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN
1	i i		SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM
	1	•	VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF
			I
			YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC
6860	1889	1515	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
6860	1889	1515	
			DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
6860	1889	1515	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
6862	2	471	EEIDREFHNKLKLKEDKLEKQEKPVNGEDKGDSGVDTQNSEGNA
	1		DEEDPLGPNCYYDKTKSFFDNISCDDNRERRPTWAEERRLNAET
ĺ			FGIPLRPNRGRGGYRGRGGLGFRGGRGGGRGGTFTAPRGFRG
L			GFRGGRGGREFADFEYRKTTAFGP
6863	2216	487	PQEPALKSEFSQVASNTIPLPLPQPNTCKDNGPCKQVCSTVGGS
	1		AICSCFPGYAIMADGVSCEDQDECLMGAHDCSRRQFCVNTLGSF
	}		YCVNHTVLCADGYILNAHRKCVDINECVTDLHTCSRGEHCVNTL
ļ	<u>}</u>		GSFHCYKALTCEPGYALKDGECEDVDECAMGTHTCQPGFLCQNT
			KGSFYCQARQRCMDGFLQDPEGNCVDINECTSLSEPCRPGFSCI
	1		NTVGSYTCQRNPLICARGYHASDDGTKCVDVNECETGVHRCGEG
			QVCHNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHT
			CENTLGSYRCSCASGFLLAADGKRCEDVNECEAQRCSQECANIY
•			GSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILCTFRCLNVPGS
			YQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGS
1	1	·	FRCLRFECPPNYVQVSKTKCERTTCHDFLECQNSPARITHYQLN
			FQTGLLVPAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRRLN
			AYTGVVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT
			TFAL
6864	2	2933	LADSSPSNLQIIIKELLSMHHQPDPALTKEFDYLPPVDSRSSSG
			FVGLRNGGATCYMNAVFQQLYMQPGLPESLLSVDDDTDNPDDSV
			FYQVQSLFGHLMESKLQYYVPENFWKIFKMWNKELYVREQQDAY
			EFFTSLIDQMDEYLKKMGRDQIFKNTFQGIYSDQKICKDCPHRY
			EREEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK
			EKRITVKRTCIKSLPSVLVIHLMRFGFDWESGRSIKYDEQIRFP
·		· · ·	WMLNMEPYTVSGMARQDSSSEVGENGRSVDQGGGGSPRKKVALT
			ENYELVGVIVHSGQAHAGHYYSFIKDRRGCGKGKWYKFNDTVIE
		1	EFDLNDETLEYECFGGEYRPKVYDQTNPYTDVRRRYWNAYMLFY
		,; ;	QRVSDQNSPVLPKKSRVSVVRQEAEDLSLSAPSSPEISPQSSPR
			PHRPNNDRLSILTKLVKKGEKKGLFVEKMPARIYQMVRDENLKF
			MKNRDVYSSDYFSFVLSLASLNATKLKHPYYPCMAKVSLQLAIQ
	,	•	FLFQTYLRTKKKLRVDTEEWIATIEALLSKSFDACQWLVEYFIS
	÷	'	SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL
		4	HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL
	,		LRHSALRHMISFLLGASRONNQIRRWSSAQAREFGNLHNTVALL
			VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM
	* '1		SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH
			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN
	·		GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH
			WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA
		l	YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL
6865	1000	10.0	RSDLDDVDP
C000	1820	1242	DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS
			CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV
			LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ
ſ	1		DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS
6866			PFGQSSVQTIQPKRDS
D 856	1571	495	DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF
0000	l l		IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISORKP
			11EGMERAGS VALLED V EXERDIT F 5G VD 11 V 15 DN LW 15 QR RP
			AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG
			AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG
			AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR
			AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV
			AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEFMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
-	sequence		\=possible nucleotide insertion)
6867	2833	1704	GTRIMSQPKQKELAGFVRQKMLLDYSVYMGRCVPQESRSPQRSP
			LQSAESSPTAGKKLPEVPPSEEBEQEAWVNALLGRIFWDFLGEK
]			YWSDLVSKKIQMKLSKIKLPYFMNELTLTELDMGVAVPKILQAP
			KPYVDHQGLWIDLEMSYNGSFLMTLETKMNLTKLGKEPLVEALK
			VGEIGKEGCRPRAFCLADSDEESSSAGSSEEDDAPEPSGGDKOL
			LPGAEGYVGGHRTSKIMRFVDKITKSKYFQKATETEFIKKKIEE,
			VSNTPLLLTVEVQECRGTLAVNIPPPPTDRVWYGFRKPPHVELK
			ARPKLGEREVTLVHVTDWIEKKLEQEFQKVFVMPNMDDVYITIM
			HSAMDPRSTSCLLKDPPVEAADQP
6868	1	346	RPTRPPTRPEEIKNLILPYISDMNFVQDLCEDFYELFKTDKGFD
	·		KATFESQMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQG
			GSQGRIVHLSNSFTQTVNCRKPFFSSW
6869	3	1619	MYMERMDKRALISFWESVEHLKNANKNEIPQLVGEIYQNFFVES
1 1	1, 5, 5,	·	KEISVEKSLYKEIQQCLVGNKGIEVFYKIQEDVYETLKDRYYPS
			FIVSDLYEKLLIKEEEKHASQMISNKDEMGPRDEAGEEAVDDGT
	•		NQINEQASFAVNKLRELNEKLEYKRQALNSIQNAPKPDKKIVSK
	,		LKDEIILIEKERTDLOLHMARTDWWCENLGMWKASITSGEVTEE
1			NGEQLPCYFVMVSLQEVGGVETKNWTVPKRLSEFHNLHRKLSEC
			VPSLKKDQLPSLSKLPFKSIDHTFMEKFENQLNKFLQNLLSDER.
			LCQSEALYAFLSPSPDYLKVIDVQGKKNSFSLSSFLERLPRDFF
] !			SHQEEETEEDSDLSDYGDDVDGRKDALAEPCFMLIGEIFELRGM
		,	FKWVRRTLIALVQVTFGRTINKQIRDTVSWIFSEQMLVYYINIF-
1			RDAFWPNGKLAPPTTIRSKEQSQETKQRAQQKLLENIPDMLQSL
			VGQQNARHGIIKIFNALQETRANKHLLYALMELLLIELCPELRV
6070			HLDQLKAGQV
6870	1	1566	MAAVVAATRWWQLLLVLSAAGMGASGAPQPPNILLLLMDDMGWG
		,	DLGVYGEPSRETPNLDRMAAEGLLFPNFYSANPLCSPSRAALLT
			GRLPIRNGFYTTNAHARNAYTPQEIVGGIPDSEQLLPELLKKAG
1			YVSKIVGKWHLGHRPQFHPLKHGFDEWFGSPNCHFGPYDNKARP NIPVYRDWEMVGRYYEEFPINLKTGEANLTQIYLQEALDFIKRQ
]		•	ARHHPFFLYWAVDATHAPVYASKPFLGTSQRGRYGDAVREIDDS
		•	IGKILELLQDLHVADNTFVFFTSDNGAALISAPEQGGSNGPFLC
:			GKQTTFEGGMREPALAWWPGHVTAGQVSHQLGSIMDLFTTSLAL
			AGLTPPSDRAIDGLNLLPTLLQGRLMDRPIFYYRGDTLMAATLG
	,		QHKAHFWTWTNSWENFRQGIDFCPGQNVSGVTTHNLEDHTKLPL
][•	•	IFHLGRDPGERFPLSFASAEYQEALSRITSVVOOHOEALVPAOP
] .]			QLNVCNWAVMNWAPPGCEKLGKCLTPPESIPKKCLWSH
6871	209	1126	RMSLNPPIFLKRSEENSSKFVETKQSQTTSIASEDPLQNLCLAS
	•		QEVLQKAQQSGRSKCLKCGGSRMFYCYTCYVPVENVPIEQIPLV
			KLPLKIDIIKHPNETDGKSTAIHAKLLAPEFVNIYTYPCIPEYE
			EKDHEVALIFPGPQSISIKDISFHLQKRIQNNVRGKNDDPDKPS
			FKRKRTEEQEFCDLNDSKCKGTTLKKIIFIDSTWNQTNKIFTDE
			RLQGLLQVELKTRKTCFWRHQKGKPDTFLSTIEAIYYFLVDYHT
			DILKEKYRGQYDNLLFFYSFMYQLIKNAKCSGDKETGKLTH
6872	880	459	FGLLMVVLSLIFMKGNCVREDLIFNFLFKLGLDVRETNGLFGNT
į ł			KKLITEVFVRQKYLEYRRIPYTEPAEYEFLWGPRAFLETSKMLV
			LRFLAKLHKKDPQSWPFHYLEALAECEWEDTDEDEPDTGDSAHG
		•	PTSRPPPR
6873	1929	955	DEQAVLCSKDKTYDLKIADTSNMLLFIPGCKTPDQLKKEDSHCN
			IIHTEIFGFSNNYWELRRRRPKLKKLKKLLMENPYEGPDSQKEK
			DSNSSKYTTEDLLDQIQASEEEIMTQLQVLNACKIGGYWRILEF
}		i	DYEMKLLNHVTQLVDSESWSFGKVPLNTCLQELGPLEPEEMIEH
			CLKCYGKKYVDEGEVYFELDADKI CRAAARMLLQNAVKFNLAEF
			QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDDLPE
			DNQERFNSLFSLREKWTEEDIAPYIQDLCGEKQTIGALLTKYSH
	[SSMQNGVKVYNSRRPIS
			·

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
110.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	
1.	amino acid	1 .	P=Proline, Q=Glutamine, R=Arginine,
1		residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6874	1	307	DSIADHVNSAAVNVEEGTKNLGKAAKYKLAALPVAGALIGGMVG
	·		GPIGLLAGFKVAGIAAALGGGVLGFTGGKLIQRKKQKMMEKLTS
			SCPDLPSQTDKKCS
6875	1688	349	VIGTGERGNSASEKWEIMFNEELGDPFIIIHSISLLNAEEHSIA
j			TLLLRIEKEELDMKGSGFYVSLEWVTISKKNQDNKKYEIIKRDI
			LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEENMDEDI
			SEKIKEPLYYWQQTEDDLTVTIRLPEDNTKEDIQIQFLPDHINI
1	ĺ		VLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTW
	ļ		PELVIGDKQGELIRDSAQCAAIAERLMHLTSEELNPNPDKEKPP
	[CNAQELEECDIFFEESSSLCRFDGNTLKTTHVVNLGSNQYLFSV
			IVDPKEMPCFCLRHDVDALLWQPHSSKQDDMWEHIATFNALGYV
			QASKRDKKFFACAPNYSYAALCBCLRRVFIYRQPAPMSTVLYNR
		· ,	KEGRQVGQVAKQQVASLETNDPILGFQATNERLFVLTTKNLFLI
			KVNTEN
6876	41	1285	VGEMTLIWRHLLRPLCLVTSAPRILEMHPFLSLGTSRTSVTKLS
			LHTKPRMPPCDFMPERYQVIFLVNSGSEANELAMLMARAHSNNI
			DIISFRGAYHGCSPYTLGLTNVGIYKMELPGGTGCQPTMCPDVF
			RGPWGGSHCRDSPVQTIRKCSCAPDCCQAKDQYIEQFKDTLSTS
į			VAKSIAGFFAEPIQGVNGVVQYPKGFLKEAFELVRARGGVCIAN
	ľ		EVQTGFGRLGSHFWGFQTHDVLPDIVTMAKGIGNGFPMAAVITT
1			PEIAKSLAKCLQHFNTFGGNPMACAIGSAVLEVIKEENLQENSQ
ł			EVGTYMLLKFAKLRDEFEIVGDVRGKGLMIGIEMVQDKISCRPL
			PREEVNQIHEDCKHMGLLVGRGSIFSQTFRIAPSMCITKPEVDF
			AVEVFRSALTQHMERRAK
6877	1	778	GTSPSPARAYAPPTERKRFYQNVSITQGEGGFEINLDHRKLKTP
, .	ì	,	QAKLFTVPSEALAIAVATEWDSQQDTIKYYTMHLTTLCNTSLDN
			PTQRNKDQLIRAAVKFLDTDTICYRVEEPETLVELQRNEWDPII
		7 F	EWAEKRYGVEISSSTSIMGPSIPAKTREVLVSHLASYNTWALQG IEFVAAQLKSMVLTLGLIDLRLTVEQAVLLSRLEEEYQIQKWGN
		and the second second	IEWAHDYELOELRARTAAGTLFIHLCSESTTVKHKLLKE
6878	931	263	OTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGON
1 0078	, 931	203	LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAP
			EYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLD
		:	TGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVIS
i	1 :,		VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSF
			II
6879	3	845	IRVIGESDIMQEFLSESDENYNGVSDVELRVALPDGTTVTVRVK
		045	KNSTTDOVYOAIAAKVGMDSTTVNYFALFEVISHSFVRKLAPNE
			FPHKLYIONYTSAVPGTCLTIRKWLFTTEEEILLNDNDLAVTYF
1	l .		FHQAVDDVKKGYIKAEEKSYOLQKLYEQRKMVMYLNMLRTCEGY
	ľ		NEIIFPHCACDSRRKGHVITAISITHFKLHACTEEGQLENQVIA
İ		1	FEWDEMORWDTDEEGMAFCFEYARGEKKPRWVKIFTPYFNYMHE
			CFERVFCELKWRKEEY
6880	2110	1437	RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVOCFISS
			MANIYNEKILKEGNOLTESIFIONSKLYFFGILFNGLTLGLORS
	1		NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH
			VLMAOVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS
		•	KPOVPEYAPROERIRDLSGNLWERSSGDGEELERLTKPKSDESD
			EDTF
6881	2638	2244	NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR
			ORVAAVKDLIROLPKPNODTMOILFRHLRRVIENGEKNRMTYQS
	1		IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR
6882	1	850	GIPEAOLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN
] -		QEGNMVTARQEPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT
		,	TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSQPYRLVHFEPH
			MRPRRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK
	l	<u> </u>	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
:	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 :	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
· ·	} .		KVKATNFRPNIVISGCDVYAEDSWDELLIGDVELKRVMACSRCI
			LTTVDPDTGVMSRKEPLETLKSYRQCDPSERKLYGKSPLFGQYF
ļ			VLENPGTIKVGDPVYLLGQ
6883	2794	2256	NSKLKLNQNLKLFITLTYQVLSLHGWGPGIHLQKEGAFPVTQNR
1	l		ALQLLYDLRYLNIVLTAKGDEVKSGRSKPDSRIEKVTDHLEALI
1 .			DPFDLDVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPRSSTF
			NSQEPHNILPLASSQIRFGLLPLSMTSTRKAKSTRNIETKAQYD
L			ANC
6884	2	99	BFERVTAEAVKPRETSEPRAAAQRFCEKFPFL
6885	297	1554	STGQFWHVTDLHLDPTYHITDDHTKVCASSKGANASNPGPFGDV
			LCDSPYQLILSAFDFIKNSGQEASFMIWTGDSPPHVPVPELSTD
1	1		TVINVITNMTTTIQSLFPNLQVFPALGNHDYWPQDQLSVVTSKV
1			YNAVANLWKPWLDEEAISTLRKGGFYSQKVTTNPNLRIISLNTN
1 .	. ,		LYYGPNIMTLNKTDPANQFEWLESTLNNSQQNKEKVYIIAHVPV
]			GYLPSSQNITAMREYYNEKLIDIFQKYSDVIAGQFYGHTHRDSI
·			MVLSDKKGSPVNSLFVAPAVTPVKSVLEKQTNNPGIRLFQYDPR
1			DYKLLDMLQYYLNLTEANLKGESIWKLEYILTQTYDIEDLQPES
,			LYGLAKQFTILDSKQFIKYYNYFFVSYDSSVTCDKTCKAFQICA
			IMNLDNISYADCLKQLYIKHNY
6886	2	1341	QCGGIPGREGGSSRPLEEGTGSSPACVRGAAPGSEDAFYPTRAK
			QARVSQELKKAAKRTVSISEGPDTLGDGMRERRETLALAPEPEP
			LEKEACEKWKRPFRSASATSLTLSHCVDVVKGLLDFKKRRGHSI
]			GGAPEQRYQIIPVCVAARLPTRAQDVLDAHLSEVNAVRFGPNSS
		•	LLATGGADRLIHLWNVVGSRLEANQTLEGAGGSITSVDFDPSGY
l i	'		QVLAATYNQAAQLWKVGBAQSKETLSGHKDKVTAAKFKLTRHOA
j . [VTGSRDRTVKEWDLGRAYCSRTINVLSYCNDVVCGDHIIISGHN
	·		DQKIRFWDSRGPHCTQVIPVQGRVTSLSLSHDQLHLLSCSRDNT
ł			LWIDI DUNUDANG PACTO POQUE AND AND AND AND AND AND AND AND AND AND
			LKVIDLRVSNIRQVFRADGFKCGSDWTKAVFSPDRSYALAGSCD
]			GALYIWDVDTGKLESRLQGPHCAAVNAVAWCYSGSHMVSVDQGR KVVLWQ
6887	1047	116	l
""	101/	110	WTARPSQKPFWEAGAVPGDPLSTGCSQAQLGGCCPRGPWGPQHG
,			GOORAAGPTLPRGERGGPQQSGPGLAAQTPPTSKQVAWRAFLTG
			TYRSQSPRSPAGPFRGGTGWWPEPAVCLCVAVGPQRLSSPGLVY
			NASGSEHCYDIYRLYHSCADPTGCGTGPDARAWDYQACTEINLT
			FASNNVTDMFPDLPFTDELRQRYCLDTWGVWPRPDWLLTSFWGG
:			DLRAASNIIFSNGNLDPWAGGGIRRNLSASVIAVTIQGGAHHLD
.			LRASHPEDPASVVEARKLEATIIGEWVKAARREQQPALRGGPRL
6888			SL ,
0000	1	992	FVAYVKKEIPHIVVTHCLLNPHALVIKTLPTKLRDALFTVVRVI
	ł		NFIKGRAPNHRLFQAFFEEIGIEYSVLLFHTEMRWLSRGQILTH
1		İ	IFEMYEEINQFLHHKSSNLVDGFENKEFKIHLAYLADLFKHLNE
l			LSASMQRTGMNTVSAREKLSAFVRKFPFWQKRIEKRNFTNFPFL
ı			EEIIVSDNEGIFIAAEITLHLQQLSNFFHGYFSIGDLNEASKWI
'	1		LDPFLFNIDFVDDSYLMKNDLAELRASGQILMEFETMKLEDFWC
ļ			AQFTAFPNLAKTALEILMPFATTYLCELGFSITFTFQNKVPEAA
		_ <u></u>	LILSDDIRVAISKKVPSFLGHH
6889	1	1534	LTLENQIKEEREQDNSESPNGRTSPLVSQNNEQGSTLRDLLTTT
.]	}		AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDDIIASVV
Ì			ENKIPPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW
i	1		ICEKHILWLKDYKNSSNWKLFKECWKQGQPAVVSGVHKKMNISL
	ł	ľ	WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRQ
			KNKSGETVVLKLKDWPSGEDFKTMMPARYEDLLKSLPLPEYCNP
ſ			EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI
1	ļ		EVSDVVNILVYVGIAKGNGILSKAGILKKFEEEDLDDILRKRLK
- 1	1		DSSEIPGALWHIYAGKDVDKIREFLQKISKEQGLEVLPEHDPIR
		1	DQSWYVNKKLRQRLLEEYGVRTWTLIQFLGDAIVLPAGALHQVQ
	·	L	- Z ANTONIA CONTROL TO A KIN I DI TOL TODATA DE MONDIO A O

SEQ	Predicted	Predicted end	Amino agid cognosts acceptable
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	 		NFHSCIQVTEDFVSPEHLVESFHLTQELRLLKEEINYDDKLQVK
1			NILYHAVKEMVRALKIHEDEVDDMEEN
6890	3	667	THACGMWIPLYLHRALVVHKTAETCNSPPCGAKDSLIFGAITCF
1			TGFLGVDTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFV
1			AAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAV
			ALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA
Í	İ		LMLCPFVVVLGGMFFLATALFFVSDRARAEQQVNQLAMPPASVK
			A A STATE A ST
6891	1980	1262	LRIHQELLSKELKLLRGITIESIIHIGLAAGKEQFMQDASNVMQ
	[LLLKTQSHLYNMEDNNPEVRQAAAYGLGVMAQFGGDDYRSLCSE
			AVPLLVKVIKRAHSKTKKNVIATENCISAIGKILKFKPNCVNVD
			EVLPHWLSWLPLHEDKEEAIQTLSFLCDLIESNHPVVIGPNNSN
	[LPKIISIIAEGKINETINYEDPCAKRLANVVRQVQTSEDLWLEC
			VSQLDDEQQEALQELLNFA
6892	3	876	RSVAAASGPGAWGTDHYCLELLRKRDYEGYLCSLLLPAESRSSV
			FALRAFNVELAQVKDSVSEKTIGLMRMQFWKKTVEDIYCDNPPH
			QPVAIELWKAVKRHNLTKRWLMKIVDEREKNLDDKAYRNIKELE
			NYAENTQSSLLYLTLEILGIKDLHADHAASHIGKAQGIVTCLRA
			TPYHGSRRKVFLPMDICMLHGVSQEDFLRRNQDKNVRDVIYDIA
			SQAHLHLKHARSFHKTVPVKAFPAFLQTVSLEDFLKKIORVDFD
			IFHPSLQQKNTLLPLYLYIQSWRKTY
6893	1	842	DGERKSMSVERTFSEINKAEEQYSLCQELCSELAQDLQKERLKG
1			RTVTIKLKNVNFEVKTRASTVSSVVSTAEEIFAIAKELLKTEID
1			ADFPHPLRLRLMGVRISSFPNEEDRKHQQRSIIGFLQAGNQALS
1	• .		ATECTLEKTDKDKFVKPLEMSHKKSFFDKKRSERKWSHQDTFKC
			EAVNKQSFQTSQPFQVLKKKMNENLEISENSDDCQILTCPVCFR
			AQGCISLEALNKHVDECLDGPSISENFKMFSCSHVSATKVNKKE
6894	1745		NVPASSLCEKQDYEAH
0034	1742	1463	TTLCKPLVPREHQFYETLPAEMRKFTPQYKGKSQLLEGLPHWRG
			DVRDRGHGRPWQPSLEPSLPPTLCFPSLSSFSSSWPSAQHLTPS
6895	2379	470	VFNPW
0055	2313	478	VTYVELCOLASPTALLIMRTVLDLIVEDLQSTSEDKEQQYTSQT
			TRLLALLYALASHKACKLAILHLINGTIKGDERYAEIFQDLLAL
	.		VRSPGDSVIRQQCVEYVTSILQSLCDQDIALILPSSSEGSISEL
			EQLSNSLPNKELMTSICDCLLATLANSESSYNCLLTCVRTMMFL
	•		AEHDYGLFHLKSSLRKNSSALHSLLKRVVSTFSKDTGELASSFL
}	•		EFMRQILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELKQLL QSKEESPENLFLELEKLVLEHSKDDDNLDSLLDSVVGLKQMLES
ļ }	j		SGDPLPLSDQDVEPVLSAPESLQNLFNNRTAYVLADVMDDQLKS
	ļ		MWFTPFQAEEIDTDLDLVKVDLIELSEKCCSDFDLHSELERSFL
	İ		SEPSSPGRTKTTKGFKLGKHKHETFITSSGKSEYIEPAKRAHVV
	J		PPPRGRGGGGGGGGIRPHDIFRQRKQNTSRPPSMHVDDFVAAES
			KEVVPQDGIPPPKRPLKVSQKISSRGGFSGNRGGRGAFHSQNRF
			FTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGQSNFNRG
]]			PLPPLRPLSSTGYRPSPRDRASRGRGGLGPSWASANSGSGGSRG
		•	KFVSGGSGRGRHVRSFTR
6896	1	. 555	GNIVIQKKKYNKQHIIPLENVTIDSIKDEGDLRNGWLIKTPTKS
]	FAVYAATATEKSEWMNHINKCVTDLLSKSGKTPSNEHAAVWVPD
	Ì	.	SEATVCMRCQKAKFTPVNRRHHCRKCGFVVCGPCSEKRFLLPSQ
		l	SSKPVRICDFCYDLLSAGDMATCQPARSDSYSQSLKSPLNDMSD
			DDDDDDSSD
6897	3	920	GDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY
	1		AGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVL
			SLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLA
			YLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDE
			DFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML
			They of Armit of the Committee of the Co

Description President end President end President end Coacion Co	SEO	Predicted	1 1000 23 01 23 00 2	
Moclectide Coration Corresponding to first Education Editatidine, I = Isoleucine, Kelysine, Lebeucine, M=Methionine, N=Asparagine, Lebeucine, M=Methionine, N=Asparagine, Lebeucine, M=Methionine, N=Asparagine, Lebeucine, M=Methionine, N=Asparagine, Lebeucine, M=Methionine, N=Asparagine, Lebeucine, M=Methionine, N=Asparagine, Lebeucine, M=Methionine, N=Asparagine, Lebeucine, M=Methionine, N=Asparagine, Lebeucine, M=Methionine, N=Asparagine, Lebeucine, M=Methionine, N=Asparagine, Lebeucine, M=Methionine, N=Asparagine, Lebeucine, M=Methionine, N=Asparagine, Lebeucine, M=Methionine, N=Asparagine, Lebeucine, M=Methionine, N=Asparagine, Lebeucine, M=Methionine, N=Methionine, N=Lebeucine, Lebeucine, M=Methionine, N=Lebeucine, Lebeucine, M=Methionine, N=Lebeucine, Lebeucine, M=Methionine, N=Lebeucine, Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, N=Lebeucine, M=Methionine, M=Methionine, M=Methionine, N=Lebeucine,				
Cocation Corresponding Coffree				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence	140:		1	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid amino acid sequence 8-PPTOLINE, Q=Glutamine, R=ARQImine, amino acid sequence 8-TYPLOSHAR, Y=TYPCOSHAR, X=Unknown, *=Stop coden, /=possible nucleotide deletion, V=possible nucleot				H=H1stidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence shallow of amino acid sequence shallow of amino acid sequence shallows of the possible nucleotide deletion, 'possible nucleotide deletion,' 'possible nucleotide deletion,' 'possible nucleotide insertion' 'possibl				Debeucine, Memethionine, NeAsparagine,
residue of amino acid sequence		1	B	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence Codon, /=possible nuclectide inertion	}			S=Serine, T=Threonine, V=Valine,
Sequence Neposeible nucleotide insertion				W=Tryptopnan, Y=Tyrosine, X=Unknown, *=Stop
LELELAMSKORDHEVECPULVVEVVALEDE PEDKKVYPAUGG LWSEAVGGQVHPNYFWMVSGCVEPP PSKKYQQMPPPEPPL G898 919 346 OKTVTAVASILKORGGTYTEMERRIMGAVTIKIPP KERMITUTITUW LSNI INRSILFYLEMQYDI INGSELREVETARATTWE INGILING GGELSLAFYGTTGSELROVETARATTWE INGILING GGELSLAFYGTGSELTGSELTGVETARATTWE INGILING MPHENPASGKVSQVGCQTSDEALSMLSBGSDASTTERTTASESC KKNEGOPALPTIGDL MPHENPASGKVSQVGCQTSDEALSMLSBGSDASTTERTTASESC KKNEGOPALPTIGDL MPHENPASGKVSQVGCQTSDEALSMLSBGSDASTTERTTASESC KKNEGOPALPTIGDL MPHENPASGKVSQVGCQTSDEALSMLSBGSDASTTERTTASESC KKNEKOPALPTIGDL MPHENPASGKVSQVGCQTSDEALSMLSBGSDASTTERTTASESC KKNEKOPALPTIGDL MPHENPASGKVSQVGCATSDEALSMLSBGSDASTTERTTASESC KKNEKOPALPTIGDL MPHENPASGKVSQVGCQTSDEALSMLSBGSDASTTERTTASESC KKNEKOPALPTIGDL MPHENPASGKVSQVGCQTSDEALSMLSBGSGASTERTATASESC KKNEKOPALPTIGDL MPHENPASGKVSQVGCQTSDEALSMLSBGSGASGASIS TFHTKPFYGGKLHKVTAFVKKRVPLEKKOPPESRLKHTSSERS MENTATERKTYLERKOLTERSENSTVALHKALPESASLLTMFNRAALDSTRITE MENTATERKTYLERKOLTERSENSTVALHKALPESASLLTMFNRAALDSTRITE MPHENDALDSTRITE LADAVGKGSTERSHLBERTVKYSQCDALGSTTERHANDQKSS MEDETIVODLICATION MENTATER			sequence	Codon, /=possible nucleotide deletion,
LIMSBAVGGOMENTERMOSTERMOST ITERPETMUTITICS	 	sequence		
See	1		<u> </u>	
LSNIINESLLFYLEMQTDINGGSLKPURTARKTYWFIMGILNAA QGFLISLAFIGWTGCSLGFQSFREEIQWSSLTTEARGGAHPSIL MPHENPAGSKYGVGGTGSBLEMSLEGGSDASTIEIHTAGBES RKWEGDPALPTHODL 827 MKWEKNDATLLDKKKINMDCFISCFFKKMLTTLMFSHSGILSL LEHGESTFSLPCAYARSILTVPWWELGKVSVMCAKTYSASI TFHTKFFTGGKHRVTAEVKHNIINTTVCCHOGGWNSVLEFTTY MGSTKYVDLYKLAVTKKYVPLEKQDPFSSRLWKWVTDSLRSS EIDKATEKKHTLEERQRTESHTATTWKTKYPTKEGDWYY HKPLWKIIPTTQPAE 6900 3 451 FEVLGSKGITELBERSTSALHHALBESASILIMFØRRANLFSTHIP VLPGKVGESTERELBLETKVSQQEQLLQSTTEHLKNANQQKSS MEQFIVSQLTRTHDVLKKARTYLEVRKLHQSEAPSLSPTHHP LADLVGSWSTERELBLETKVSQQEQLLQSTTEHLKNANQQKSS MEQFIVSQLTRTHDVLKKARTYLEVRKLHQSEAPSLSPTHHP LADLVGSWSTERELBLETKVSQQEQLLQSTTEHLKNANQQKSS MEQFIVSQLTRTHDVLKKARTYLEVRKLHQSEAPSLSPTHHP LADLVGSWSPLAKFQSK 6902 2 267 GAPPFPFSQPFRQPQAAFSSHPISDLTFNPSSALEGGAGAGA SDMPBFSUDLIBELTNPBELLSYLDPPDLPSNSDDLLSLFENN. 6903 1 149 RINGVYRGGFTGHTLUTDGWVGNFQDESCFLFSTVKAESSDGT HILK 6904 464 2092 MEASLEVSLCACGDVECKFDLFFRWQAIGKKSGNFDLLLC VGWPRGSTOLDABESEYKTGIKKAPIQTYVLGANNGSFVKYFQDA DGCELAENITYLGRKGIPTGSSGLQIVILGSTBINEFVPQTSF SPRUVSSIRMMLCTTSQFKGVDILLTSTPPKCVSGNFGKSSEVD TKKCSSALVSSLATGALFRYFHAALEKTYTERKFGYGNTSKGKPPD VTENPYRKSGQASAIGGALAHVLSGTSTPBNKCVSHFGNSSEVD TKKCSSALVSSLATGALFRYFHAALEKTYTERKFGYRNSHILIGEN AQHARFIALANVGNPEKKKYLYAFSIVMKLMDAAELVKQPPD VTENPYRKSGGASAIGGALAHVLSSTEDLEKGGRASS TGBDSKSSHPRQPRKPPOPPOPPOCWCLASPEVEKKKATLUTGH CYLALAKGGISDAVLLDIGTGYSSVELASPEVEKKKULVVIIGTH CYLALAKGGISDAVLLDIGTGYSSVELASPEVEKKKATLUTGH CYLALAKGGISDAVLLDIGTGYSSVELASPEVEKKKATLUTGH RFFKSRGKWCVVFRNYKSHHLOLQVIPVISCSTTDDIKGDF TIGNGKSSPHIPKOPKPYLYTYVLVKKKKLSLPA 6905 1 226 VSKTGBAFTITSHVLFALGVYRTLVLFKNINKRLYRFGFFDLTAT VAGLVQVVVLVCDPFYLYTTVLVKKKKLLSLPA TTATATVSGLVALEMI KVTGGYPFEAYKNWELMLAIP LVVPTET TEVRTKIKRIGSTFTINDKTVHKKDFTTLKKKYDDUDQSS SSSSALSSASTATSSSTIFKDEFTLKKRSSNIKKLSPAPOLGDPS SSGSSAVAGSSTIFKDSFTTLKKRSSNIKKLSPAPOLGPS SSGSSAVAGSSTIFKDSFTTLKKRSSNIKKLSPAPOLGPS SSGSSAVAGSSTIFKDSFTTLKKRSSNIKKLSPAPOLGPS SSRLESSAVSRAGSLLHMVATSPGRLFFRLLYMMGTTWYRLTTA SLLDVFUTURASGESERITURGKRAPDSFOGGSGGGGGISHED TLALLEGLVSRREARALEEDTFRATARTGESSGTSHED DAHTGYTGRAFTFYPGLQ TFHP	6898	919	246	DMVSEAVQGQVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL
GGFLISLAFYGWTGCSLEFGSPRKEIGWESITTSAAGGAHSPEN MPHENDAGGKVSQVGGGTOSDELSMLEGGDASTITHTASSES NKNEGDPALPTHODL LEHGESYTPSLPCHVARSILTUPWELLGGKVSVMCAKTGYSASI TFHTKPYGGKLHRVITASVKHNITTTVUCWGGKMSVLHSTIS NGSTKYVDLTKLAVTKRVYAPLEKQDPFSSRRLMKNVTDSLRSS EIDKATHKHTLERQRTESRHTETGTTWKTKYFIKEGDWYY HKVEMKIDPTJOGAB 451 TEVLGSKGHELRSSTSALHHALESSASLLIMFWRAALPSTHIP VLORKVGSTBERELBERTKVSQCGCOLLGSTTELKNANQCKSS MEGPTVSQLTRTHDVLKKARTHLEVRCHLHGSEAPSLSFTHHB LADLVGSWPALRFQEK MEGPTVSQLTRTHDVLKKARTHLEVRCHLHGSEAPSLSFTHHB LADLVGSWPALRFQEK 6901 1 201 DDNNVQRLETDFMITLOQGSTLEGMAAMLDNVMQALRFYEGRP SFPKAARGFLIKNSFYNYHLGFS 6902 2 267 GAPPPPSGPPROPDAAFSSIPHSDLTFNDSSALEGAGGG SDMPRESUDLIBELTMPDBLLSVLDPPDLYRDSMDDLLSLFENN 6903 1 149 RINGVYRGGFTGHHLVIDQMVQNFQDESCFLFSTVKAESSDGI HILK 6904 464 2092 MEASLEVSLCVLACGDVESKFDLIFNVQAIQKKSGNFDLLLC VGMFFGSTQDABWERYKTGIKARFICTYVLGANNQSTVKYFQOA DGCELAENTITJERKGTFTGSSGLJVVLSGTSLMBEVPQYSF SPKOVSSLRMMLCTTSGPKOVDILLTSPMPKCVGNFGSSSEVD TKKCGSALVSSLATGLRFFYHAALERTYTER/HHILLGR AQHATFIJALANVGNPSKKKYLYAFSIVMKIMDAAELVKOPPD VTENPYRKSGGASIGKGULAPVESSCATFWHILIGER TGRBKSSPHPRQPRKPPOPPOPPCWFCLASPEVKKHLVNIGH CYLALAKGGISGASIGKGULAPQAAAYFVHNIILGRA TRAFFKSRGKWCVVFRNYKSHHLDLGVIVVDSCSSTTDDIKGAP 1TQAGQQIGLIKEPTBAASNLARKNYSSIEPADFKTKRTAGKTPAI RRFFKSRGKWCVVFRNYKSHHLDLGVIVVDVESCSTTDDIKGAP 1TQAGQQIGLIKEPTBAASNLARKNYSSIEPADFKTKRTAGKTIPAT ATTTATVSGLVALEPTBAASNLARKNYSSIEPADFKTKRTAGKTIPAT ATTTATVSGLVALENIKVTGGYPFEAYKNWFLAILAPIVVTTT TEVRKTKIKRISTITMBRWTYSSIEPADFKTKRTAGKTIPAT ATTTATVSGLVALENIKVTGGYPFEAYKNWFLAILAPIVVTTT TEVRKTKIKRISTITMBRWTYSEEPADFKTKRTAGKTIPAT ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLAILAPIVVTTT TEVRKTKIKRISTITMBRWTYSEEPADFKTKRTAGKTIPAT ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLAILAPIVTTTT TEVRKTKIKRISTITMBRWTYSEEPADFKTKRTAGKTIPAT ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLAILAPIVVTTT TEVRKTKIKRISTITMBRWTYSEEPADFTKRTAGGGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1 0050) 11	340	QXIVIAVASBBAGRQGITTENERRMGAVIKIRFFKIMBVLIICW
MPHENPASCKYSQUGQTSDEALSMLSEGSDASTIEIHTASESC NKNEGDPALPHGDL 6899 120 827 MKVRKINDANYLLDKINKINNDCFISCFFKKMLTTHEWSHIGILSL, LEHGESYTFSLPCAYARSILTVPHVELGGKVYSMCAKTGYSASI TFHTKPPYGKLKRVTASVKINITMTVVCRVQGEMNSVLETTS NGETKVULITILAVTKEVRPLEKQDPFESRRLWKNVTDSLRSS EIDKATERKHTLERGRTEERHTETTGYBKTFYFKEGDGWY HKPLWKIIPTTQPAE 6900 3 451 TEVLGSKGIBLERSSTSALHHALBESASLLTMFWRAALPSTHIP VLPGKVGBSTERELLELBKTKVSQGCOLLQSTTEHLKNNAQCKSS MEGPIVSQITTHTUVLKKARTNLEVKELHQSEAPSLSPTHHHP LADLVGDSWPALRFQEK 6901 1 201 DDNNVQRIEDTFONTLQGGSTLEQWAAWLONVMQALKYEGRP SPEKAARQFLLKNSPYRVHLOFS 6902 2 267 GAPPFPFSQPFRQPPQAAPSSHPHSDLTFNSSALEGQAGAQGA SPPREARQFLLKNSPYRVHLOFS 6903 1 149 RINGVYRGSTGTHILVIDQMVCNRGDESCFLESTVKARSSDGI HILL 6904 464 2092 MEASLEVSLSCVLACGDVEGKFDLIFNRVQAIGKKGNPPDLLSFENN CKSPFSKSTODAEEBEVKGIKKAPLOTVYJGANGBTVKYTQA DGCELAENITYLGRKGIFTGSSGLOTVLSGTESINBEVPGYSF SPRUNSLRMMLCTTGGFROYDTLITSSFWCGNFGNSGSGWD TKKCGSALVSSLATGLKPTYTFARLEKTYTERLPYNNHILLEN AGHATFIALANVGNPEKKKYLYAPSIV PMKLMDAAELVKQPPD VTENFYRKSGGRASIGKGULTAPVESACGYFFDLEEKGGRKRS TGRDSKSSPHPKQPKKKYLYAPSIV PMKLMDAAELVKQPPD VTENFYRKSGGRASIGKGULTAPVESACGYFFDLEEKGGRKRS TGRDSKSSPHPKQPKKKYLYAPSIV PMLADAELUKQPPD VTENFYRKSGGRASIGKGULTAPVESACGYFFDLEEKGGRKRS TGRDSKSSPHPKQPKKPPQPPGGCOFFTDLEEKGGRKRS TGRDSKSSPHPKQPKKPQDPFGCLASPEVERHVKATL RRFFKSGKKMCVVFFRNYKSHHLQUVI PVFLSCTTDIKDAF ITAGEGGIELLEIEBHSIN KOLTOGYPFDLAETVYLDTGTELLFFR IKNIPPLOFGRBVLASEALINVPDRSDWRCQISKEDEFILARR FRODEPYDTULD THATTATVSGLVALERHUNDINGTHYVFTET TEVRKTKIK RIGSISFTINGRAVTHURGEDFILTUVPTET TEVRKTKIK RIGSISFTINGRAVTHURGETTILDIFINAVKEKYGIE PTHVVQGVKMLVYPWMGHAKRLKLUTHKLVKPTTEKKYDLTV SYRDENGSSFTINGLSFTINGRESGRITISTYLGRGKSCLUTDIFINAVKEKYGIE PTHVVQGVKMLVYPWRGHAKRLKLUTHKLVKPTEKKYDLTV TEVRKTKIK RIGSISFTINGLFGASGGSGGGGGGISHED DAHTSYYSESLVHESWPPPSSLEELHGDANNGEDLEVRRIGT TEVRKTKIK RIGSISFTINGLFGASGGVSTENGLEPAPOGGGGGGISHED DAHTSYYSESLVHESWPPPSSLEELHGLANNGEDLEVRRIGT GGSSSRASCLUVARATEDELGERGASSGSGGLIKHED THALLEGUNGRAALLKONGENTOESPOSSUKELRRLE DALAALFSSLNWKAARREELLERGGAFGGGGGGISHED DALALOGUNGRAALALKGSSATGLESGSTSSULGRAEGOUNGDSED DALFKUV	1			
NKMEROPALPHOGIL	1			
6899 120 827	ł			
LEHGESYTFSLPCAYARSILTVPUVELGGKUSVNCAKTGYSASI TFHTKRPYGGKLRRVTASVKHNITHTVVCRVQGEMBYSLEFTYS MGSTKYVDITKADVTKKRVPLEKOPPTESRRLWKNVTDSLRSS BIDKATEHKHTLEERGRTEERHTTGTPWKTKYFIKEGDGWVY HKPLMKII PTTOPAE 6900 3 451 TEVLGSKGIHSLKSSTSALHHALESASLLTMFWRAALPSTHIP VLPOKVGBSTSFREILLERIKVSQGCOLLGGSTTEHLKNANQQKSS MEOPIVSQLTRTHOVLKKARTNLEVRKLLHQSEAPSLSPTHHHP LADLVODSWPAPLROPK 6901 1 201 DDNNVQRLETDFWHTLGVGSTLEQWAAWLDNVMMQALKPYEGRP SPRAARGFLLKMSYVRYHLGPS 6902 2 267 GAPPPPFSGPPGPPGAPSSSHHSDLTFNESSALEGQAGAQA SDMFBPSLDLIPELINTPDELLSXLDPPDLPSNSNDDLLSLFENN 6903 1 149 RINQVYRGGPFROPPGAPSSHHSDLTFNESSALEGQAGAQA SDMFBPSLDLIPELINTPDELLSXLDPPDLPSNSNDDLLSLFENN 6904 464 2092 MEASLDVSLSCVLACCDUFGKFPILENVQAIQKKGGMPDLLLC VGNFFGSTQDAEWESYKTGIKAPIQTYVLGANNQBTVKYFQDA DGCELAENITYLGRKGIFTGSSGLGIVYLSSTTSLMBEVPGYSF SPRUVSSLRWMLCTTGGFKGVDLLTLSFWERCVGMFGMSSGEVD TKKCGSALVSSLATGLKPRTHFABLEKTYTERLFYRANILLIQN AQARTEFILALANNGMPEKKKYLVARSI VYBERLFYRANILLIQN AQARTEFILALANNGMPEKKYLVARSI VYBERLFYRANILLIQN AQARTEFILALANNGMPEKKYLVARSI VYBERLFYRANILLIQN CYLALAKGGISDDHVLLIPJGHYQSVVELGAEVUEEVEKYKATL REPFKSGKGWCVYFERNYKSHLOLQUI PELGSTTDDIKDAP 1TQAQQQIELLEI PEHSDIKQIAQPGAAYFYVELDTGELLFHR IKNNFPLQFGREVLYLDSFULSCHLILDINGTSCSTTDLINGETHAR FRYSGKGKVVYFERNYKSHLOLQUI PELGSTTDDIKDAP 6905 1 226 VSKTGEAETITSHYLFALGVYRTLLYFNWIMRYHFEGFFDLIAI VAGLWQTVLUCOFFYLLYTKVLKGKKLSLAP 6906 3 611 SYDDINGHIDFITAASNIRAKWYSIEPADFFKTKRIAKITPAT TEVERTKIRNGISFTIMORTVYHGREDFFLAKKTYDLTV TEVETKKIRNGISFTIMORTVYHGREDFFLAKKTYDLTV TEVETKKIRNGISFTIMORTVYHGREDFFLAKKTYDLTV TEVETKKIRNGISFTIMORTVYHGREDFFTLARIPTYPGTGP 6907 2 2228 LRGVPWMAAGAFFFSSGEETSHLIMMERSGRLTFYSQGDDGG SSGLSSAUSAGSTLFKOSLDASSGNYKGLSPAPQGGSISHED 6908 SASLESAVSRAGSLLWMAATSPGRFFILLVWAAGTTWYRLTTAA SLLDWFVLTRFSSLKTFHAPLLPILLITCHYAGWYFYPYGLQ TFHPALVSWAAAGSRFABGGLWARDSSPHPQAEQRWMSRVHSL ERRLEALAAEFSSMWQKAARILERLEUGGAPGQCGGGGISHED 1 TALLEGLUSVAREAALLEKGRAPGLJORSFRILATENGTYBYPGLQ TFHPALVSWAAAGSRFABGGLWEARDSSPHPQAEQRWMSVKISL ERRLEALAAEFSSMWQKAARILERLEUGGAPGGCGGGLSHED 1 DLJALGGUEZGLAALLKGSSATEVGLEGGGGGSLHED 1 DLJALGGUEZGLAALLKGSSATEVGLEGGGGGGSH	6899	120	927	, · · · · · · · · · · · · · · · · · · ·
TFHTKPFYGGKLHRVTAEVKHNITTTVTVCKVQGENNSVLEFTYS MGETKYVDLTKLAUTKKKRYPDLEKQDPFSERRLWKNYTOLLRS ELDKATEHKHTLEERQRTEERHRTETGTPWKTKYFIKEGDGWVY HKPLWKIIPTTQPAB 451 TEVLGSKGIHELRSSTSALHHALBESASLLTMFWRAALPSTHIP VLPGKVGESTERELLELRTKVSQGEOLLGSTTEHLKNANQKES MEGFIVSGLITHHDVLKKARTTLEBYLGSEAPSLSFTHHPH LADLVGDSWPALRFORK 6901 1 201 DDNNVQRETDFKMTLQGGSTLEQMAAWLDNVMMQALKPYEGRP SFPKAARQFLLKWSFYRYHLGFS 6902 2 2667 GAPPFPFSGPFROPGAARSSHPISDLTFPSSSALEGQAGAGA SSPPKSALDLLPELTMPDELLSYLDPPDLPSNSNDDLLSLFRNN. 6903 1 149 RINGVYRGGFTGHHILVIDQWQNFQDESCFLFSTVKAESSDGI HILK 6904 464 2092 MEASLEVELSCYLLACGDVEGKEDILPRIVQLAGKKGSMFDLLLC VGNFFGSTQDAEWEEYKTOLKKAPIGTYVLGANNGETVKFFGA DGCELAENITYLGRKGIFTGSSGLGIVYLGGTVKTGMSTVKFTGA DGCELAENITYLGRKGIFTGSSGLGIVYLGGTVKGFWSSGEVD TKKCGSALVSSLATGLKRYHFALALFYVLLTSHEVPGTVSFF SPRUVSSLRMHLCTTSGPKGVDILLITSPWKCVGNFGNSSGEVD TKKCGSALVSSLATGLKRYHFALALFYVLLTSHELVFRHILLGEN AGHATRFTALANVGNPEKKKTLAFSIVPMKUNGTVKFTGA TKRCGSALVSSLATGLKGULAPVEESAFVELPYRMVILLGEN AGHATRFTALANVGNPEKKKTLAFSIVPMKUNGTWKFGD TERMYKSGGBASIGKULAPVEESAFVELPYBLDTGELHFR GROEDSTELLFIRENDIKGILAQPGAAYFYVELDTGEKLFR TKROPPLOFGRBVLASEALIAVPDKSDWRQCGISKEDESTLARR FREGEPVDFTLIDD 40810450450450450450450450450450450450450450	1 0000	120	027	TENCERARE DONARD INTERPRETATION OF THE PROPERTY OF THE PROPERT
NGETKYULITKLAUTKKRURPLEKODPFESRILMKNUTDSLIRES SIDKATERIKHTLESGROFTERHRETGTPWKTKYPIKEGDGWVY HKPLWKIIPTTOPAE				
BIDKATEHKHTLEERQRTEERIRTETGTPMKTKYFIKEGDGWVY KKPLMKI IPTTQPAB				
HKPLMKI IPTTOPABE 6900 3 451 TEVEGSEGIHELESSTSALHHALBESASLITMFREAALPSTHIP VLPGKVGESTERELLELRTKVSQQEQLLQSTTEHLKRANQQKES MEGFIVSQLTRTHOVIKKARINLEVRKLLHGSEAPSLSFTHHHP LADLVGDSNPALRFQEK 6901 1 201 DDNNVQRLETDFKMTLQQGSTLEQMAMUDNVMQALKPYEGRP SPFKARAPQPLLKMSPYNYHLGFS 6902 2 267 GAPPPPPSQPPQAPAPSSHPHSDLTFNPSSALEGQAGAGA SDMPBPSLDLLPELTNPDELLSYLDPPDLPSSNDDLLSLFRNN. 6903 1 149 RINQVYRQGPTGHHLVDLDWLQNFQDESCFLFSTVKARSSDGI HILLK 6904 464 2092 MEASLEVSLSCVLACGDVECKFDLLFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTTVLGANNQETVKYFQDA DGCELAENITTIGRKGJTFTGSGLGIVVLSGTSLBNSPVPGSFF SPKDVSSLRMHLCTTSQFKVOPILLTSPWPKCVGNFFGNSGEVD TKKCGSALVSSLATGLKPRYHFPALEKTYTKELPYRNHILLGEN AGHATFIALANVGNPEKKKYLYRSIVPMKLMDABALVKQPDD VTENPYRKSGGEASIGKOILAPVEBSACQFFFDLNEKQGKKRSS TGRDKSKSPHPKQPKKPPQPPGFGFFCLASPEWKHLVVNICTH CYLALAKGGLSDDBVLLLPIGHYGSVVLSLSAEVVEEWEKYKATL RRFFKSRCKMCVVFERNYKSHHLQQVIPVPISCSTTDDIKDAF ITQAGCQIELLEIPBEBDIKQIQAAYFYVELDTGEKLFHR IKKNPFLOFGREVLASEAILNVPDKSDWRQCQISKEDESTLARR FRKDPPPTDFTLDD 6905 1 226 VSKTGEASTITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAT VAGLVQTVLYCOFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDINGHIDPITAASHLKANYISEPADRFKKTGTAGKITPAT ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLKLATPIVPTET TEVRKTKINGISFTIWDRWTVHGKEDFYKKTGTAGKITPAT ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLKLATPIVPTET TEVRKTKINGISFTIWDRWTVHGKEDFYKKTTEKKVVDLTV SFAPDIDGDEDLFGPPVRTYTSHDTD 6907 2 2228 LRGVPWVAAGAFFRSSCESSTSHLIMSRRSQRLTRYSQGDDGS SSSGSSVAGSGSTLFKDSGLETLLKMSSSMKKLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSLEELIGDANWGGDLRVRRRCGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDVVGSDVDQQSS SSRLSANVSRAGSLLMWVATSFGRLFRLLWMAGTTWYRLTTAA SLLDVYLTRFFSLKTFHWFILLFILLTTGAMPYPYYGLQ THPFALVSWMAAKDSKRADEGWEARDSSPHFQAGQRVMSRVHISL ERRLEALAAFFSSNWOKAMRLERLEELGQAPQAGQGGGGLISHED DLFKLVARAGGSEARIQQLKSEWGSVMSRVHISL ERRLEALAAFFSSNWOKAMRLERLEELGQAPGOGGGGLISHED DLFKLVARAGGSEARIQQELAAPGGPGVORGPGSVKELRRLE DQLAALQGELAAALAKQSSVAREVGLLPQQQTQAPGOVGDVGSUFS		1		
451 TEVLGSKCIHELRSSTSALHHALBESASLLTMFWRAALPSTHIP VLPGKVGBSTERELLEURTKVSQGSQLLGSTTEHLKNANQQKSS MEGF IVSQLTRTHDVLKKANTNQLKESPTHKHEN LADLVGDSWPALRFQEK 6901 1 201 DDNNVQRETDFRWTUQQSTLEQWAAWLDNVMMQALKPYEGRP SFPKAARQFLLKWSFYRYHLGFS 6902 2 267 GAPPPPFSQPPRQPPQAAPSSHHSDLTFNPSSALEGQAGAGGA SMPREPSDLLPELTINPBELLSYLDPPDLPSNSMDDLLSLFKNN. 6903 1 149 RINGVYRQGPTGIHLVIDQMVQNFQDESCFLFSTVKAESSDGI HILL 6904 464 2092 MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGMFFGSTQDABWEEYKTGIKKAPJQTTVLGAMNQETVKYFQDA DGCELAENITTIGRKGIFTGSSGGIVTUSTGSTESLNEPVFGYSF SPKOVSSLRMMLCTTSQPKGVDILLTSPWRACVGNFGNSSGSVD TKKCGSALVSSLATGLKFRYHFAALEKTYYERLPYRNHILQEN AGHATRFTALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGGASIGKQILAPVEESACQFFFDLNECQGRKRSS TGRDSKSSPHKQRFKPPPPAGPAGFAVLVNIGTH CYLALAKGGLSDDHVLILDJGHYQSVVELSAENVEEVEKYKATL RRFFKSRGWCVVFFRRYKSHHLQLQVIPVPISCSTTDDIKDAF IKQMPEDPFTLDD FINAKFGREENITH IKQMPPQPGFGFFAYSMVSHHLQLQVIPVPISCSTTDDIKDAF IKQMPPQPPPGFFAYSMVSHLQLQVIPVPISCSTTDDIKDAF IKQMPPQPPFTDFTLDD SAKTYTT IKQMPPQPFTDFTLDD SAKTYTT IKGMPPJGFGRRVLASEAILNVPDKSDWRQCQISKBDESTLARR FRKDPEPDFTLDD 6905 1 226 VSKTGRASTISHYLFALGVYRTLVLFFNIHRYHFEGFFDLTAI VAGLVQTVLYCDFFYLYTIKVLGKKKLSLPA ATTTATVSGLVALEMIKVTGGYPFSAYXMWFLAILAPIVPTET TEVRTKYKRNGISFT INDRWTHGEGTPTLLDFINAVEKKYGIE PTMVVQGVMLXYPVWBGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVTYYFSHDTD 6906 3 611 SYDDINGHIPPITAASNLRAKMYSIEFADRFKTKRIAGKITPAI ATTTATVSGLVALEMIKVTGYPFEAVXMWFLAILAPIVVPTET TEVRTKYKRNGISFT INDRWTHGEGTPTLLDFINAVEKKYGIE PTMVVQGVMLXYPVWBGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVTYYFSHDTD 6907 2 2228 LRGVPVWAAGAFFRSSGEESTSHLTMSRRSQRLTRYSQGDDGS SSSGSSVASSGSTLFKDSGVLTKRSGNKKKLSPAPQLGPSS DAHTSYYSELVILFMINGTTWYRLTTAA SLLDVYLTRFSSLKTFFWFLILDLILTCLTTGAMYFPYYCLQ THPHALVSWMAANGSRRADEGWARDSSPHFQAGQRVWBRVHSIL ERREALAAFFSSMVCKAMLEREGGADAGOGGGLSHED DLFKKIVRASGEBARIQQLSEARALKLEPGGADAGOGGGLSHED DLFKKIVRASGEBARIQQLSEARALKLEPGGADAGOGGUSHED DLFKKIVRASGEBARIQQLSEARALKLEPGGADAGOGGUSHED DLFKKIVRASGEBARIQQLSEARALKLEPGGAOAQAGVOGGALSHELD DLFKKIVRASGEBARIQDLSEARAEHQDDSE DLFKKIVRASGEBARIQDLSEARAEHQDAGAAVSLERGESTAGG	,	1		
VLPGKVGESTERELLEURTKVSQGSQLLQSTTEHLKNAMQQKSS MEGFIVSQLITTHDVLKKARTNLEVRKLLHQSEAPSLSPTHHHP LADLVGDSMPALRFQEK 6901 1 201 DDMNVQRLETDFKMTLQQGSTLEQMAMLDNVMMQALKPYEGRF 6902 2 2667 GAPPPPSQPPRQPAPSSHHSDLTFNFSSALEGQAGAQGA SDMPEPSLDLLPELTNPDELLSYLDPPDLPSNSDDLLSLFRNN. 6903 1 149 RINGVYRQFTGIHILVIDQMVQNFQDESCFLFSTVKAESSDGI HILLK 6904 464 2092 MEASLEVSLSCULACGDVEKKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTDDAEMESYKTGIKKRPJQTYULGANNQETVKYFQDA DGCELAENITYLGRKGIPTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQFKGVDILLTSPWRKVCNNFGNSSGVD TKKGGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAPSIVPMKHDAABLUKQPPD VTRPYRKSGGASIGKQILAPVERSACQFFFDLINKGQRKBSS TGRDSKSSPHPKQPRKPPQPPGPGFNFCLASPEVEKHLVVNIGTH CYLALAKGGLSDHVLILDIGHYQSVVELSABVVEEVEKYKATL RRFFKSRGKWCVVPERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAGSQIELLEIPBHSDIKQIAQPGAAYFYVELDTGEKLHFR IKKNPPLOFGRBULASSAILNVPDKSDWRQCQLSKEDEFTLARR FRKDPEPYDFTLDD 6905 1 226 VSKTGEABTITSHYLFPALGVYRTLYLFNWIWNYHFEGFFDLTAI VAGLVQTVLVCDFFYLYITVKLKKSKLSLPA 6906 3 611 SYDDHNGHIDPITAASNLARKMYSIEPADRFKTRIAGKIIPAT ATTTATVSGLVALEMIKVTGGYPFBAYKMFHLALAIPIVVPTET TEVRKTKIRNGISFTIMDEMTVHGKEDFTLLDFINAVEKYGIE PTWVQGVKMLYVPVMPGHAKRLKLMTMIKLVKPTTEKKYVDLTV SFAPDIDGGBDLCAPPYTYYFFBUT TEVRKTKIRNGISFTIMDEMTVHGKEDFTLLDFINAVEKYGIG PTWVQGVKMLYVPVMPGHAKRLKLMTMIKLVKPTTEKKYVDLTV SFAPDIDGGBDLCAPPPPTYYFFBUT GGSSSNASGSGSTLFKOSPLETLKRKSSMKKLSPAPQLGPSS SARLSAVVSAGSLIMWVATS PGRLFRLLYWNAGTTWYRLTTAA SLLDVYVTRFESSLKTEIMFPFRSSLESHHDANMGGDLVFRRRGT GGSSSRASGLVGRKATEDFLGSSGYSSEDDVVGVSDDQQSS SSRLRSAVSRAGSLLMWVATS PGRLFRLLYWNAGTTWYRLTTAA SLLDVYVTRFESSLKTEIMFPFRSSLETHLJWRAGTTWYRLTTAA SLLDVYVTRFESSLKTEIMFLERGAPAGCRGGGLGHED TLALLEGLVSRRAALKEDFRFETAARIQEELSALRAEHQQDSE DLFKKIVRAGSSEARIQQLKEMGRONDESDFFRSCGGLGHED TLALLEGLVSRRAALKEDFRFFTAARIQEELSALRAEHQQDSE DLFKKIVRAGSSEARIQQLKEMGGNVGSSPGSSVKELRRLE DQLAAGLQGELAAALLAGSSAREVGLLPQQQTQAVPDDVSGPFA	6900	3	457	
MEGFIVSOLTRTHOULKKARTNLEVRKLLHQSEAPSLSPTHHHP LADLVGDSNPALRPOEK 6901 1 201 DDNNVQRLETDFKMTLQQGSTLEQWAAWLDNVMMQALKPYEGRP SFPKAARQFLLKWSTYRYHLGFS 6902 2 267 GAPPPPPSOPPROPROPSHIPSIDLTFNPSSALEGQAGAQGA SDMPEPSLOLLPELTMPDELLSYLDPPLPSNSNDDLLSLFKNN, 6903 1 149 RINQVYRQGPTGHILVIDQWVQNFQDESFLFSTVKARSSDGI HILK 6904 464 2092 MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGMPFGSTQDABWEPKYGIKARAIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLMEPVPGYSF SPKDVSSLRMMLCTTSQFKGVDILLTSPWFKCVGNFGNSSGFVD TKKOSSALVSSLATGLRFNYRHAERTYYEELPYSNHTILGEN AGHATEFIALANVGMPEKKYLYAFSIVPMKLMDAABLVKQPPD VTENPYRKSGQEASIGKQILAPVESACQFFFDLNEKQGKKRSS TGRDSKSSPHFKQPKKPPQPPGPCWPCLASPEVEKHLUVNIGTH CYLALAKGGLSDDHVLLIPIGHYGSVVELASPEVEKHLUVNIGTH CYLALAKGGLSDDHVLLIPIGHYGSVVELASEVEEVEKYKATL RRFFKSRGKWCVYFRNYKSHHLOLQVIPVPIGSTTDDIKDAF ITQAGEQGIELLETPEHSDIKQIAQPAAFTYVELDTGEKLPHR IKKNFPLQFGREVLASEAILNVPDKSDWRCQGISKEDETLARR RFKSRGKWCVYFRNYKSHHLOLQVIPVPIGSTTDDIKDAF ITQAGEQGIELLETPEHSDIKQIAQPAAFTYVELDTGEKLPHR IKKNFPLQFGREVLASEAILNVPDKSDWRCQCISKEDETLARR RFKKDEPPYDFTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLUVTLYLCFFYLYTKVKLKKKLSLPA ATTTATVSGLVALEMIKVTGYPFEAYKMFLNLAIPILVVFTET TEVRKTKIRNIGISTI IDMRTWINKEKNFTLALETINAVEKKYGIE PTWVQGVMLVVPVMPGHARRLKLIMHKLVKFTTEKKYVDLTV SFAPDIGGDELLDEPPWRYYFSHMKLLNAMGTURTVRUTTAA ATTTATVSGLVALEPPPRAYSTENKHLEPAPOLGPSS SSGGSSVASGSTLFKOSPLRTLKRKSSNMRLEPAPOLGPSS SSRGGSSVASGSTLFKOSPLRTLKRKSSNMRLEPAPOLGPSS SSRLRSAVSRAGSLLMWATS PGRLFRLLYMAGTITWILTIAA SLLDVYLTRFFSSLKTFLMFLIPLLLICLTYGAWYFYPYGLQ TFHPALVSWAAKDSRRADEGWEARDSSPHGAEGRUSHFNHIL ERLELALABFSSLKWFTMFLIPLLLLICLTYGAWYFYPYGLQ TFHPALVSWAAKDSRRADEGWEARDSSPHFQAEGRUSHENDE TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASGESEARIQUKKSWGSMCJESFQESGGGGGGLHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASGESEARIQUKKSWGSMCJESFGESFSFFSPEN		· .	4-7-I	
LADLVGDSWPALRFQEK 6901 1 201 DDNNVQRLETDFKMTLQQQSTLEQWAAWLDNVMQALKPYEGRP SFPKAARQFLLKWSFYRYHLGFS 6902 2 267 GAPPPPSQPPQAPASSHPHSDLTFNPSSALEGQAGQGA SDMPEPSLOLLPELTNPDELLSYLDPPDLSSNSNDDLLSLFKNN. 6903 1 149 RINQVYRQGPTGIHILVIDQWVQNFQDESCFLFSTVKAESSDGI HILLK 6904 464 2092 MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENTTYLGRKGIFTGSSGLQIVYLGGREGNSGSGVD TKKCGSALVSSLATGLRFYNFFAALERTYYERLPYNHHILQEN AQHATFFILANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLMEKQCRKRSS TGRDSKSSPHPKQPRKPPQPPGCWFCLASPEVEEVEKYATL RRFFKSRGKWCVVFERNVKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQIELLEIPEHSDIKQIQVGAAFTVVEDDTGEKLFHR KKNFPLQFGREVLASEALINVPDKSDWRQCQISKEDEETLARR FRKDFPPTPTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAT VGALVQTVLYCDFFYLVITKVLKKKKLSLPA 6906 3 611 SYDDINGHIDFITAASNLRARMYSIEPADFKYKKIAGKITPAI ATTTATYSGLVALEMIKKVTGGYPEAYKNFLIALAFILVPTET TEVRKTKIRNGISFTIWDRWTVHGKDFTLLDFINAVKEKYGIE PTWVQGVMLYVEVMPGHAKRLKLITMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSLEELHGDANWGEDLFVGRRGG GGSESRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQOSS SSRLKSAVSRAGSLTKMMATSPGLFTLLYWAGTTWYRLTTAA SLLDVFVLTRFFSSLKTFLMFLLPLLLLTCLTYGAWYFYPPGLQ THPALVSWWAAKDSRADEGWBARDSSPHQAEGRWASRVHSL ERRLEALABFESSNWQEANKLELELRQGAPGGGGGGLHED TLALLEGLVSRREAALKEDFRRTAARIQEBLSALRAEHQQDSE DLFKKIVRAQGSERARICQLKSEWGSWTGSFGESFSHER		;		
6901 1 201 DDNNVQRLETDFKMTLQQQSTLEQWAAWLDNVMMQALKPYEGRP 6902 2 267 GAPPPPSQPRQAPSHPHSDLTFNPSSALEGQAGAGA SDMPEPSLDLLPELTNPDELLSYLDPPDLPSNSNDDLLSLFKNN, 6903 1 149 RINQVXGQPTG1HILVJDGWCQNFQDESCFLFSTVKAESSDGI HILL 6904 464 2092 MEASLPVSLSCVLACGDVEGKFDLLFNRVQAIQKKSGNPDLLLC VGNFFGSTQDAEWEEYKTGI KKAPIQTYVLGANNGSTVKYPQDA DGCELAENITYJGRKGIFTGSSGLQIVYLSGTESIMEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWFKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AGHATRFIALANVGNPEKKKLVAFSIVPMKLMDAAELVKQPPD VTENPYRKSGGSASIGKQILAPVESSACOFFPDLNSKQGRKES TGRDSKSSPHKPQPRKPPQPPPGCMFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKMCVVFERNYKSHHLQLQVIPPISCSTTDDIKDAF ITQAQEQQIELLEIP EPHSDIKQIAQPGAAFFYVELDTGEKLPHR IKKNPPLQPGRBVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDPEPYDPTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA ATTTATVSGLVALEMIKVTGGYPFEAYKWFLNLAIPIVVFTET TEVRKTKIRNGISFTIMDRWTVHGKEDFTLLDFINAVEKKYOLE PTMVVGVKMLVYPVMPGHAKRLKLVFTTEKKYVDLTV SFAPDIDGDEDLPGPPWRYYFSHDTD 6907 2 2228 LRGVPVWAGAFRFSGEESTSHLIMSRRSQRLTRYSQGDDGS SSGSGSVAGSGSTJAFKDSPLRTLKKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANMGEDLRVRRRGT GGSESSRASGLVGRKATEDPLGSSSGYSSEDDYVGYSDVDQQSS SGSLASGSSTAFKOSPLRTLYWRSSEDDYVGYSDVDQQSS SGSLASGSSTAFKOSPLRTLYMSRSTWTWRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRAADEGWEARDSSPHYGAEGRVMSRVHSL ERRLEZALABFESSMOKEAWRLERLELGQGAPGCGGGGLHED TLALLEGLUSRREAALEDGTRSTAARIOESLGRAFABHQDDSE DLFKKVVRASQESEARLDGUKSEWSMTGSFGESTSWERRHE				
SPRAARQFLLKWSFYRYHLGFS 6902 2 267 GAPPPPPSQPRQPPQAAPSSHHSDLTFNPSSALEGQAGQAG SDMPBPSQLDLPELTMPDELLSYLDPPDLPSNSNDDLLSLFRMN. 6903 1 149 RINQVYRQFTGIHILVIDQMVQNFQDESCFLFSTVKAESSDGI HILLK 6904 464 2092 MEASLPVSLSCVLACGDVEGKFDLLFNRVQATQKKSGNFDLLLC VGMPFGSTQDAEWEEVKTGIKAPJQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLINEPVPGYSF SPKUVSSLRMMLCTTSQPKGVDILLTSPWPKCVGMFGMSSGEVD TKKCGSALVSSLATGIKFRYHFAALEKTYYERLPYRNHILQEN AOHATFFIALANVGMPEKKKYJAFSIVPWKLMDAAELVKQPPD VTENPYRKSQBASIGKQILAPVEESACQFFFDLMEKGGRKRSS TGRDSKSSHPKQPRKPPQPPGPCMFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLLIPGHYQSVVELSABVUEEVEKYKKTL RRFFKSRGWCVVFERNYKSHLLQLQVIPVPLSCSTTDDIKDAF IKKNFPLQFGREVLASEAILNYPDKSDWRQCQISKEDEETLARR FRKDFPPDFTLDD 6905 1 226 VSKTGBAFTITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAT VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDMMGHDFITAASNLRAKMYSIEPADRFKTKRIAGKITPAI ATTTATVSGLVALEMIKVTGGYFFEAYKNWFLIKABFILVVPTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVMLVYDVMPGHAKKLKLIMLAIPIVVPTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVMMLYVPVMPGHAKKLKLIMLKLKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYSHDTD 6907 2 2228 LKGVPVWAAGAPEFSSGESTSHLIMSRRSQRLTRYSQGDDGS SSSGSSVAGSQSTLFKDSPLRTLKKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDAWWGEDLRVRRROT GGSESSRAGLUGRKATEDFIGGSSGYSSEDDYVGYSDVDQOSS SSRLRSAVSRAGSLLWMWATSPGRIFFRLLYWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLLTTTAWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLLTTTAWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTELWFLLERQGAPGGGGGGLSHED TLALLEGLVSWREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASGESERARIQLKSEUGESFGSSKVELRREE ERRLEEALAAEFSSNWQKERMRLEELELRQGAPGGGGGGISHED TLALLEGLVSWREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASGESERARIQLKSEUGLEPQQQGGGGGGSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE	6901	1	201	
6902 2 267 GAPPPPSQFPRQPPQAPSSHPHSDLTFNPSSALEGGAGQGA 6903 1 149 RINGVYRQGFTGHILVIDQMVQNFQDESCFLFSTVKAESDGI HILLK 6904 464 2092 MERSLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGMFFGSTQDAEWEEVKTGILKRAPIQTYVLGANNQETWKYFQDA DGCELAENTTYLGRKGIFTGSSGLQIVYLSGTESINEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFPALEKTYYERLPYRNHILGEN AOHATEFIALANVGNPEKKKYLYAPSIVPMKLMAABLUKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSHPHQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGISDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSGRGWCVFERNYKSHLQIQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQFGAAYFVVELDTGEKLFHR IKKNFFLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFPYPFTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAT VAGLUQTVLYCDFFFLLYTTKVLKGKKLSLPA 40504QTVLYCDFFFLYTTKVLKGKKLSLPA 6906 3 611 SYDDENGHIDFTAASNLRAHVSLEPADFFKTKRIAGKITPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTYHGKEDDFTLLDFINAVKEKYGIE PTWVVQGVKMLVYPWPGHAKALKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVEVWAAGAFRFSSGEESTSHLIMSRSGQLTRYSGGDDDGS SSGGSSVAGSGSSTJKNDSPLRTLKRKSSNMKRLSPAPDLGPSS DAHTSYYSESLVHESWFPPRSSLESLHGDANWGEDLRVRRRGT GGSESSRASGLWGSTLFKDSPLRTLKRKSSNMKRLSPAPDLGPSS SSGLSSSGSVAGSSTJKNDSPLRTLKRKSSNMKRLSPAPDLGPSS SSGLSSRASGLLWMATSF GFRLFFILLYWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLITCLTYGAWYFYPGLQ TFHPALVSWWAAKDSRRADEGWEARDSSHPQARGGGGGGGSHED TLALLEGLUSRREAALKEDFRRETTARJGELSALRAEHQODSE DLFKKIVANAGESFSNWYKERMRLERLEIRGGAPGGGGGGSHED TLALLEGLUSRREAALKEDFRRETTARJGELSALRAEHQODSE DLFKKIVANAGESEARLOQLKSEWGSMTQESSSVKELRRLE DOLAGLQVELAALALKGSSVAREVYGLPGQTQAVRDDVESGFFA		_	201	
SDMPBPSLDLIPELTMPDBLLSYLDPPPDLPSNSNDDLLSLFERNN. 6903 1 149 RINQVYRQGFTGIHILVIDQMVQNFQDESCFLFSTVKAESSDGI HILK 6904 464 2092 MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKGGNFDLLLC VGMFFGSTQDAEMEEVKTGIKKAPIQTYVLGANNOBTVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKNVSSLRMLCTTSQPKGVDILLTSPWFKCVGMFGNSSGEVD TKKCGSALVSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAPSIVPMKLMDAAELVKQPPD VTENPYRKSGGBASIGKQILAPVEESACQFFFDLMEKGGRKRSS TGRDSKSSPHPKQPRKPPOPPGFCWFCLASPSWEHHLVVNIGTH CYLALAKGGISDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRPFKSRGKWCVFERNYKSHHLQLQVIPVFISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNPPLQFGRBVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDPEPYDPTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKKLSLPA ATTTATVSGLVALEHIKVTGGYPFEAYKNWFLNLAIPIVVPTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVMLVVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSSGEESTHLIMSRRSQRLTRYSQGDDGS SSSGGSSVAGSGSTLFKDSPLRTLKRKSSMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPRSSLEBLHGDAWWGBDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMAATSPGRLFRLLYWMAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFILDFLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRADESVELRDLSSPHFQLAEQRVMSRVHSL ERRLEALABEFSSNWQKEAMRLERLELRQGAPGQGGGGSLSHED TLALLEGLVSRREAALKEDFRRETAARIGEELSALRAEHQODSE DLFKKIVRASQESEARIQUKSEWQSMTQESSPKVELRRLE DQLAGLQQELAALALKGSSVAEGVGLTPQGTQAVRDDVESGFFA	6902	2	267	
6903 1 149 RINGVYRQGPTGIHILVIDQMVQNFQDESCFLFSTVKAESSDGT HILLK 6904 464 2092 MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLILC VGMFGSTQDAEMEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLJTYLGSTESLNEFVPGYSF SPRDVSSLRMMLCTTSGFKGVDILLTSFWPKCVGNFGNSSGFVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAELVKQPPD VTENPYRKSGQEASIGKQTLIAPVESACQFFFDLNEKGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCMFCLASPEVEKHLVUNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKKCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAGEQQIELLEIPEHSDIKQIAQPAAPFYVELDTGEKLFHR IKKNFPLPGFBEVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFPYPDFTLDD 6905 1 226 VSKTGEAETITSHYLPALGVYRTLYLFNWIWRYHFEGFFDLTAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA ATTTATVSGLVALEMIKVTGYPFEAYKNWFLNLAIPIVVPTET TEVKKTKIRNGISFIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVWPGHAKRLKLTMHKLVKFTTEKKYVDLTV SFAPDIDGDEDLFGPPVTYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSFLRTKKRSSMKKLISPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGGDLRVRRRGGT GGSESSRASGLVGKKATEDFLGSSSGYSSEDDYVGSDVDQQSS SSRLSAVSRAGSLIMWAATSPGRLFFILLWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLIPLLLILTCLTGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPQQGGGGGISHBD TLALLEGLVSRREAALKEDFRRSTARIQBELSALRAEHQQDGE DLFKKIVRASQESEARIQQLKSEWGSVTGESFQESSVKELRRE DQLAGLQCELAALALKQSSVAEEVGLLPQQIQAVRDVDSSGFPA			. 207	
HILLK 6904 464 2092 MEASLPYSLSCVLACGDVEGKFDILFNRVQAIQKKSGNPDLLLC VGNFFGSTQDAEWEEYKRIKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESINEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDTLLITSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHILQEN AQHATAFIALANVGNPEKKKYLYAFSIVPMKLWADABELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKGGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEBEETLARR FRKDFEPYPFTLDD 4 226 VSKTGEAETITSHYLFALGVYRTLYLFNWWRYHFEGFFDLIAT VAGLVQTVLYCOFFYLITKVLKGKKLSLPA VAGLVQTVLYCOFFYLYITKVLKGKKLSLPA ATTTATVSGLVALEMIKVTGGYFFEAYKNWFLNLAIPIVVFTET TEVRKYKKRGISFTUMGRTVHGKEDFTLLDFINAVEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDT 6907 2 2228 LRGUPVWAAGAPAFFSSGEESTSHLIMSRSGRUTRYSQGDDDGS SSSGGSSVAGSQSTLFKOSPLRTLKKKSSMKRLISPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEEHHGDANWGBLRVRRRGT GGSESSRAGGLVGKAATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLSAVSRAGSLWMVATSPGREFTLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLITCLTTGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPQQGGGGGISHED TLALLEGLVSRREAALKEDFRRETAARIGBELSALRAEHQQDSE DLFKKLVRASQESEARIQQLKSEWGXNTQESFQESSVKELRRE DQLAGLQCLAALALKQSSVAEEVGLLPQQIQAVRDVDSSGFPA	6903	1	149	
6904 464 2092 MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDABWEEYKTGIKKARPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKUVSSLRMMLCTTSQPKGVDILLTSPWFKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFBALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAELUKQPPD VTENPYKKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGDCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLLLPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKMCVVFERNKSHHLQLQVIPPYISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGRBVLASEAILNVPDKSDWRQCQISKBDEETLARR FRKDFEPYDFTLDD 4 6905 1 226 VSKTGBAETTTSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLXCDFFYLVITKVLKGKKLSLPA ATTTATVSGLVALEMIKVTGGYPFEAYKWFLNLAIPIVVPTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVGVKNLYVPVMPGHARKLKITMHKLVKPTTEKKYVDLTV SFAPDLDGBDLPGPPVHYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSTLEKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSTLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDPJLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATS PGRLFRLLYWWAGTTWRLTTAA SLLDVFVLTRRFSSLKTFLWFLLLLLTCLTYGAWYFYPYGLQ TFHPALVSWMAADDSRRADEGWEARDSSPHFOAGQRGGGGGLSHED TLALLEGLVSRRBAALKEDFREFTAARTQEELSALFAEHQODSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFPCSSVKELRRLE DQLAGLQCSLAALAALGSSVAEEVGLIFQQTQACROPDVESQFFA		-		
VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYPQDA DGCELAENITYLGRKGIFTGSSGLQIVYLGGTESLINEPVPGYSF SPKDVSSLRMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKGGSALVSSLATGLKRYTHFAALEKTYYERLPYRNHIILQEN AOHATRFIALANVGNPEKKYLYAPSIVPMKLMDAABLVKQPPD VTENPYRKSGGEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPQPPPOPCHFCLASPEVEKHLUVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RFFKSRGKWCVVFERNYKSHHLQIQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHBDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFBPYDFTLDD 4 SYNTGREFTISHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRARWYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTINDRWTVHGKEDFTLLDFINAVKEKYGIE PTWVVGGVKNLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVPWAAGAFFRSGGESTSHLIMSRRSQRLTRYSQGDDGS SSSGGSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEZHHDDANMGEDLRVRRRRGT GGSSSRASGLVGRKATEDFLGSSSGYSEDDYVGSDVDQQS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWMAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLLLLTCLTYGAWYFYPSTGL TFPHALVSWAAADSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAWRLERLELRQGAPGQGGGGLISHBD TLALLEGLVSRRRAALKEDFRRETAARIQEELSALRAEHQDDEE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQCLAALAALGSSVAEEVGLIFQQIQAGROFSSKELRLE				1 H 1 1 1 1 X
DGCBLAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQFKGVDILLTSFWPKCVGNTGNSSGEVD TKKCGSALVSSLATGLKPRYHFABLEKTYYREHLQFNNHILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGGBASIGKQILAPVESACGFFFDLNEKGGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILDIGHYQSVVELSAEVVEEVEKKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQFGAAYFYVEDDTGEKLFHR IKKNFPLOFGRBVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 4 226 VSKTGEAETTTSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYTIKVLKGKKLSLPA 6906 3 611 SYDDHRGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAT ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVKKTKIRNGISFTIWDRWTHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGBEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSGEESTSHLIMSRRSQRLTRYSQGDDGS SSSGGSSVAGSQSTLFKOSPLETLKKRSSMWKRLSPAPQLGPSS DAHTSYYSESLVHLESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGKKATEDFLGSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFFLLTWWAGTTWYRLTTAA SLLDVFVLTRFFSSLKTFLWFLLFLLLTCLTYGAWYFYPYGLQ TTHPALVSWWAAKDSRRADEGMEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPQGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQDDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVELRRLE DQLAGLQQELAALALKQSSVAREVGLLPQQIQAVRDDVESGFFA	6904	464	2092	<u> </u>
SPKDVSSLRMMLCTTSQFKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGPPEKKKYLYAFSIVPMKLMAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLMEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCMFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGRBVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 4 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKFTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSVAGSQSTLFKDSPLRTLKKKSSMMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLITTAA SLLDVFVLTRRFFSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPQGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKLVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPQQIQAVRDDVESQFPA	6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC
TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKXLYARFSI VPMKLMDAAELUKQPPPD VTENPYRKSGGBASIGKQILAPVEESACQFFFDLMEKQGKKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVUNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDDF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFSPYDFTLDD 4 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAT VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVYDWPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVPWAAGAFRFSSGEESTSHLTMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPQQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRREHQQDSE DLFKKLVRASQESEAR IQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPQQIQAVRDDVESQFPA	6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFODA
AQHATRFIALANVGNPEKKKYLYAPSIVPMKLMDAAELVKQPPD VTENPYRKSGQBASIGKQILAPVEESACGFFFDLNEKQGRKRSS TGRDSKSSPPHQPRKPPQPPGPWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGRBVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 5905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAT VAGLVQTVLYCDFFYLVITKVLKGKKLSLPA ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTINDRWTYHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRAGSLVGRKATEDFLGSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWMAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWPLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAREVGLLPQQIQAVRDDVESGPFA	6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF
VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQDPBPCVFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFENYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGRBVLASEAILNVPDKSDWRQCQISKBDEETLARR FRKDFEPYDFTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKITPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLFGPPVRYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGSSVAGSQSTLFKDSPLRTLKRKSSMMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRLE DQLAGGLQQELAALALKGSSVABEVGLLPQQIQAVRDDVESGFPA	6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD
TGRDSKSSPHPKQPPKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSABVVEEVEKYKATI RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGRBVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVWPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSGYSSEDDYVCYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPQGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQDDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALIALKQSSVABEVGLLPQQIQAVRDDVESGFFA	6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQFKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN
CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWWRYHFEGFFDLTAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADFKTKRIAGKITPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKUTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSGYSSEDDYVGYSDVDQQSS SSRLSAVSRAGSLLWWVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEANRLERLELRQGAPGQGGGGTSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQODSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAREVGLLPQQIQAVRDDVESQFPA	6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQFKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD
RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGRBVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLIAIPIVVFTET TEVRKTKIRNGISFTIWDRWTYHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVABEVGLLPQQIQAVRDDVESQFPA	6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS
ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGRBVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 2 2228 LRGVPVWAAGAFFFSGEETSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRAGGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAREVGLLPQQIQAVRDDVESQFPA	6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH
IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAT VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRTAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD SFAPDIDGDEDLPGPPVRYYFSHDTD AHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRFFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRADEGWEARDSSPHFQAEQKMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPQQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVABEVGLLPQQIQAVRDDVESQFPA	6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL
FRKDFEPYDFTLDD 6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRFFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVABEVGLLPQQIQAVRDDVESQFPA	6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR
VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVABEVGLLPQQIQAVRDDVESQFPA	6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR
6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 2 2228 LRGVPVWAAGAFRFSSGESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVABEVGLLPQQIQAVRDDVESQFPA				MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR
ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD SSAGGSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVABEVGLLPQQIQAVRDDVESQFPA				MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD
TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 1 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVABEVGLLPQQIQAVRDDVESQFPA	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGRBVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA
TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 1 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVABEVGLLPQQIQAVRDDVESQFPA	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGRBVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI
SFAPDIDGDEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVABEVGLLPQQIQAVRDDVESQFPA	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET
LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVABEVGLLPQQIQAVRDDVESQFPA	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE
SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVABEVGLLPQQIQAVRDDVESQFPA	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE
DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAREVGLLPQQIQAVRDDVESQFPA	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV
GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATS PGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAAR IQEELSALRAEHQQDSE DLFKKIVRASQESEAR IQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVABEVGLLPQQIQAVRDDVESQFPA	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV
SSRLRSAVSRAGSLLWMVATS PGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAAR I QEELSALRAEHQQDSE DLFKKIVRASQESEAR I QQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAREVGLLPQQIQAVRDDVESQFPA	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS
SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAREVGLLPQQIQAVRDDVESQFPA	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS
TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAREVGLLPQQIQAVRDDVESQFPA	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTTVIGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT
ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAREVGLLPQQIQAVRDDVESQFPA	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGRBVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPCHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA
TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAREVGLLPQQIQAVRDDVESQFPA	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLVAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ
DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAREVGLLPQQIQAVRDDVESQFPA	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLVAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL
DQLAGLQQELAALALKQSSVAREVGLLPQQIQAVRDDVESQFPA	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGRBVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKITMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKKRKSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLITCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED
	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGRBVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKKRKSSNMKLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE
WISOFLARGGGGRVGLLOREEMOAOLRELESKILTHVAEMOGKS	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGRBVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE
T	6905	1	226	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPQQIQAVRDDVESQFPA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	-	
ł	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	1	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
,	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
ļ			AREAAASLSLTLQKEGVIGVTEEQVHHIVKQALQRYSEDRIGLA
		1	DYALESGGASVISTRCSETYETKTALLSLFGIPLWYHSQSPRVI
			LQPDVHPGNCWAFQGPQGFAVVRLSARIRPTAVTLEHVPKALSP
		{	NSTISSAPKDFAIFGFDEDLQQEGTLLGKFTYDQDGEPIQTFHF
•			QAPTMATYQVVELRILTNWGHPEYTCIYRFRVHGEPAH
6908	3	780	QVPSAAWLMAVCGLGSRLGLGSRLGLQGCFGAARLLYPRFQSRG
1	J	/00	
			PQGVEDGDRPQPSSKTPRIPKIYTKTGDKGFSSTFTGERRPKDD
1			QVFEAVGTTDELSSAIGFALELVTEKGHTFAEELQKIQCTLQDV
			GSALATPCSSAREAHLKYTTFKAGPILELEQWIDKYTSQLPPLT
			AFILPSGGKISSALHFCRAVCRRAERRVVPLVQMGETDANVAKF
			LNRLSDYLFTLARYAAMKEGNQEKIYKKNDPSAESEGL
6909	3	409	GRLLAVGTDLYGQRSSAPEQELLVQDATPVSNSLLPEKAFSDIP
		4.0	SPYLRGTIKMMQAVRQAFQDQDDRRTWDGRPLTMAATFDDCLYA
			LCVVDTIKRSSQTGEWQNIAIMTEEPELSPAYLISEAMRRSRMS
			LYC
6910	1	1068	LVPVVVIDSYYYGKLVIAPLNIVLYNIFTPHGPDLYGTEPWYFY
	•	1	LINGFLNFNVAFALALLVLPLTSLMEYLLQRFHVONLGHPYWLT
1 .	•	*	LAPMYIWFIIFFIQPHKEERFLFPVYPLICLCGAVALSALQHSF
] :			LYFQKCYHFVFQRYRLEHYTVTSNWLALGTVFLFGLLSFSRSVA
		}	LFRGYHGPLDLYPEFYRIATDPTIHTVPEGRPVNVCVGKEWYRF
			PSSFLLPDNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDQ
			NLEEPSRYIDISKCHYLVDLDTMRETPREPKYSSNKEEWISLAY
1 1			RPFLDASRSSKLLRAFYVPFLSDQYTVYVNYTILKPRKAKQIRK
			KSGG
6911	1184	966	GEDAEEMETGNVANLISIFGSSFSGLLRKSPGGGREEEEGEESG
L		:	PEAAEPGQICCDKPVLRDMNPWSTAIVAF
6912	1	844	AMKPVETHSFQMLFTILSTGSALKAQSYEDAYRCIKSSILLGSI
1	•	<u>;</u>	SGGTDIISCFMGHNFSLPVYKGEIQARNLGMAVEAWNEEGKAVW
1 /			GESGELVCTKPIPCQPTHFWNDENGNKYRKAYFSKFPGIWAHGD
		,,,,,,,	YCRINPKTGGIVMLGRSDGTLNPNGVRFGSSEIYNIVESFEEVE
1 1	*		DSLCVPQYNKYREERVILFLKMASGHAFQPDLVKRIRDAIRMGL
1			SARHVPSLILETKGIPYTLNGKKVEVAVKQIIAGKAVEQGGAFS
			NPETLDLYRDIPELOGF
6913	1643	. 1558	KKSHEESHKEELSYGAQASLPLPCSDFR
6914	1251		
0914	7221	615	ELAAECKSAGYPGTLIPYRCDLSNEEDILSMFSAIRSQHSGVDI
			CINNAGLARPDTLLSGSTSGWKDMFNVNVLALSICTREAYQSMK
	•		ERNVDDGHIININSMSGHRVLPLSVTHFYSATKYAVTALTEGLR
	;		QELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMK
	<u>, , , , , , , , , , , , , , , , , , , </u>		CLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT
6915	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6916	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
1			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
1			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6917	254	652	L
","	434	932	GRSLSFKTFLIWVLTSIYQGGTLMYGALVLFESEFVHVVAISFT
			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6918	28	921	PEAGTRSWREPDPEDLRRFLLSAACRSFPQWLPGGGGGQVSSCS
	ĺ		DTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGSP
			VGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAW
1			LGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGE
]			VFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPW
1			LLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRT
1	ļ		ADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC

Degianing No:	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Noticetide Cortisponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence Servine, T-Threonine, V-Valine, S-Serine, T-Threonine, V-Valine, W-Tytophan, Y-Tytop	1 ~		B .	
Cocation Corresponding Cofirst amino acid Aresidue of Cofirst amino acid Aresidue of Committee	1	nucleotide	l '	
Leleucine, M-Methionine, N-Asparagine, to first smino acid residue of amino acid residue of amino acid sequence sequen				
to first amino acid residue of amino acid aresidue of Sestine, T-Mireonine, V-Valine, W-Trytophan, Y-Tytopine, X-Unknown, *-Stop conditions of Sestine, T-Mireonine, V-Valine, W-Trytophan, Y-Tytopine, X-Unknown, *-Stop code, with the sequence of the seque	1			
amino acid residue of anino acid sequence anino acid sequence (http://pophan.y-myprophan.y				
### residue of amino acid sequence m-Tryptophan, Y-Tyroosine, X-Unknown, *-stop code, /-possible nucleotide deletion, coden, /-possible nucleotide deletion, coden, /-possible nucleotide deletion, coden, /-possible nucleotide deletion, coden, /-possible nucleotide insertion coden, coden, /-possible nucleotide insertion coden,	:	1	1	
amino actd sequence Codon, /-possible nucleotide insertion				
Sequence	1		1	Codon (-nossible nucleotide deletion
6919 650 41 GGRREISGSVECEPTOGLEPERMITLSENTHENVSCOOLOGIOUS RELEKTHENVERANISERVALINGERIMED PYPOLIS SYG ASIDLOKYSHDYADRITANYPWIRESERWINARPPTULE PHYPOLIS ON ASIDLOKYSHDYADRITANYPWIRESERWINARPPTULE PHYPOLIS ON ROAFFEDGGGOVUOLDGRUNGDITUGHEP SVERHTGGANSAR RDPAYFFILES PTHGGLQYDDETEVSLOKETPTUNKESIQTTHE QNDPRAPPKYKIQILSNMGHERTTCLYRVAHGVRTSEGARGS AQGER 6920 1416 591 RAGGERVHITLKKKK 6921 2 1711 MARTSERGPFVINNIARGTIRKMENYLKEKQLCDVLLIAGHLRI PAHRLVLSAVSDYPAAMFTINDVLEAKQERVEMGGVDENLAINGLY OYAYTOVLQUKERTISELLARACLQLIATQVIDOVSHILKQHIP SNCLGIRSFGDAGGCTELLNVAHRYTMEHFIEVIRNGEFILMLS VIRLELSPOLLADLETSSNFTGDLSCOKLIMBANKTHLIBFINSH HIGHMIGERLQFGVAVIDNALVYGGRODLIKTLINVECHNEVOR WILFLEPPOLLADLETSSNFTGDLSCOKLIMBANKTHLIBFINSH HIGHMIGERLQFGVAVIDNALVYGGRODLIKTLINVECHNEVOR BERGNINTVASMSTFRSTVGUVAINNIAVALGERDGSSCLKSNEV FDEPHTINKSLCAPBRIKERGGVAVTINGFLVYGGRODSSCLKSNEV FDEPHTINKSLCAPBRIKERGGVAVTINGFLVVGGROSSCLKSNEV FDEPHTINKSLCAPBRIKERGGVAVTINGFLVVGGROSSCLKSNEV FDEPHTINKSLCAPBRIKERGVAVTINGFLVVGGROSSCLKSNEV FDEPHTINKSLCAPBRIKERGVAVTINGFLVVGGROSSCLKSNEV FDEPHTINKSLCAPBRIKERGSVAVTINGFLVVGGROSSTINDVLAV VARABASTRAVERSTRAVERSKREGGVAVTINGFLVVGGROSSTINDVLAV VARABASTRAVERSTRAVERSKREGGVAVTINGFLVVGGROSSTINDVLAV VARABASTRAVERSTRAVERSKREGGVAVTINGFLVVGGROSSTINDVLAV VARABASTRAVERSTRAVERSKREGGVAVTINGFLVVGGROSSTINDVLAV VARABASTRAVERSTRAVERSKREGGROSSTINDVLAV VARABASTRAVERSTRAVERSKREGGVAVTINGFLVVGGROSSTINDVLAV VARABASTRAVERSTRAVERSTRAVERSKREGGROSSTINDVLAV VARABASTRAVERSTRAVERSTRAVERSKREGGROSSTINDVLAV VARABASTRAVERST		1 .	bequence	
ELEKLIKEVSTVERAMISEVALUTQRILLEPTVERDYDLÄSSY ASIDLOKTSHUTARUTARUTARUTARUTARUTARUTARUTARUTARUTAR	6919		41	
ASIDLOKYSHDYADRYTAYBWRESFWAYADPTVILEPRUPG MCMAPEGDOGGOVUOLORPOKOLSTULAGHPEDVEKSELGTPHL (NDEPARPKYKIQILSINGHTAGHPEDVEKSELGTPHL (NDEPARPKYKIQILSINGHPETVILYRVRAHGVRTSEGAEGS AQGPH 6920 1418 591 EAGGPEKVHLTIKKKK 6921 2 1711 MARTREEGFFVINRAEGTLRKMENYLKEKQLCDVLLIAGHLRI PARHLVLSAVSDYPAAMPTINDVLERKQEBVEMEGVDENALNSIK (YAYATVLVQLKEDTITESILARACLGLOTVQIVDCOSH)LIKQHEN SINCLGIRSFGDAQGCTELLNVAHRYTMEHPIEVIKNQEFLUHLS VIRLPLIPPOLLADLETSSMPTGDLECKLLMARAKYHLHEPIEVIKNQEFLUHLS VIRLPLIPPOLLADLETSSMPTGDLECKLLMBANKYHLHEPISSH HIGTMAGGRIQFGVAVIDNKLYVVGGRODLKTLMTVEKRHDY ERGRUNYVASMSTPRSTVGVALNANGHAWKYHLHEPISSH HIGTMAGGRIQFGVAVIDNKLYVVGGRODLKTLMTVEKRHDY BGRQNNYVASMSTPRSTVGVALNANGHAVATOGELGGALKSMEY FDPHTKMSLCABPAKKRGGVAVATORHAVOGGLGAMLS SRLSDCVSRTDPRGDSNSTVAPLSVPROAVAVCPLGDKLYVVGG DHYLLNTVESTAVDAVANGHAMAYAVGHAPASHHC SRLSDCVSRTDPRGDSNSTVAPLSVPROAVAVCPLGDKLYVVGG VDGHTLATVESTAVANGHAMAYAVGHAPASHHC SRLSDCVSRTDPRGDSNSTVAPLSVPROAVAVCPLGDKLYVVGG VDGHTLATVESTAVANGHAMAYAVGHAPASHHC SRLSDCVSRTDPRGDSNSTVAPLSVPROAVAVCPLGGKLYVVGG VDGHTLATVESTAVANGHAMAYAVGHAPASHHC SRLSDCVSRTDPRGDSNSTVAPLSVPROAVAVCPLGGKLYVVGG VDGHTLATVESTAVANGHAMAYAVGHAPASHHC SRLSDCVSRTDPRGSSSREREREREFEFFPDSTGSSLKGNHTST GLPPAAGSHMKALAPBOTTLGRIKTVTSGAKINGGSTINDVLA- VNTPKDAAQODAKAPEMKKEPLCORQUKULDKKKPEDWB KGAQELFTVULGAHPATGATARTAVAVCPLGGKGTINDVLA- VNTPKDAAQODAKAPEMKKEPLCORQUKULDKKKREBEN KGAQELFTVULGAHPATGATARTAVAVCPLGGAGTINDVLA- VNTPKDAAQODAKAPEMKEPLCORQUKULDKKKREBEN KGAQELFTVULGAHPATGATARTAVAVCPLGGAGTINDVLA- VNTPKDAAQODAKAPEMKEPLCORQUKULDKKREBEN KGAQELFTVULGAHPATGATARTAVAVCPLGGAGTINGTSTAVA VNDFHFVANRENSINGVAGASILSTPHMTISERAGGAGSGILIDSBENG KGAGCANANGSUGGAGTARTAVAMFREPISILENGVANAQUSHIPP ISCTCEGEKALCVNTHWYKSKFRGMSVOSMIGGGVILKTHANG ENVOLDTHILBVYRKISILVGRANGANGGVILKHULH HTKPFYGGKVHRVTARVKHINPNTIVCKARGEMNATGETYLTIGND DATTGYKCEGEKKLCVNTHWYKSKFRGMSVOSMIGGGVILKTHANG HTKPFYGGKVHRVTARVKHINPNTIVCKARGEMNATGETYLTIGND ETVOLOTHILBVYRKISILVGRANGANGANULGGVILTAKTHANGANGHLER GGGAAGAAMAPDSVTENKTIELMCSVPERSMAGCANLVERSMAN BEGGLADAANGDSFVY BEGGLADATARTICSHILDRAGGAGAGALVAGGSGIDLIKKUL BEGGLADATARTICSHILDRAGHARA	0,1,	030	4.1	
MCMAFEGOGGVVIOLPGRVOLBOTTLOHPPSSVEHTGGANSAP RDPAVPFILSFFTHQGQVVPDETWSLAKEFYDESSTQTPHIL ONDPAAPFKVKIQILSNNGHPRFTCLYRVRAHGVRTSEGAEGS AQGPH	1			
6920 1418 591 ERGOFSKVHITIKKKK 6921 2 1711 MNATRSEEQFHVINHAEQITIKMENYLKEKQLCDVLLIAGHLRI 6921 2 1711 MNATRSEEQFHVINHAEQITIKMENYLKEKQLCDVLLIAGHLRI 6921 2 1711 MNATRSEEQFHVINHAEQITIKMENYLKEKQLCDVLLIAGHLRI PARHLUISAVSDVFAAMFINDVLEAKQEBVRNEGVDPHALSILVQ QYAYTUVLQLKEUTIESLLAAALLQLITQVIDVCSNPLLKQLHP SNCLGIRSFGDAQGCTELLAVVARKYTMEHFIEVIKNOGELLLIPA NEISKLLCSDIDINVDESTIFHALMQWGHDVONGQGELGMLLS VILLPLLPPQLLADLETSSMFTDLECQKLLMEANKYHLLPERR SMMGSFRTKRFKSTVGALVARGHDAMMGTTIEKYDLETNSWL HIGMMGGRLQFGVAVIDNKLYVVGGRDGLKTLATVVECRPVGK IMTVMPPMSTRRIGLAVATLEGPMYAVGGHDAMSTITTEKYDLETNSWL HIGMMGGRLQFGVAVIDNKLYVVGGRDGLKTLATVVECRPVGK IMTVMPPMSTRRIGLAVATLEGPMYAVGGHDADASSHC GRONNYVASMSTERSTVGVVALNNKLYALGGROGSSCLKSMEY FDPHTAKKSLCAPMSKRRGGVQVATYNGFLYVVGGHDAPASHC SRLSDCVERYDPKGBSMSTVAPLSVPRAVAVCPLGDKLYVVGG YDGHTLANTVESYDAQRMEMKESFPVAJIGRAGACVVVVKF FDPHTAKKSLCAPMSKRRGGVGVATYNGFLYVVGGHDAPASHC SRLSDCVERYDPKGBSMSTVAPLSVPRAVAVCPLGDKLYVVGG YDGHTLANTVESYDAQRMEMKESFPVAJIGRAGACVVVVKF FDPHTAKKSLCAPMSKRRGGRGVGVATYNGFLYVVGGHDAPASHC SRLSDCVERYDPKGBSMSTVAPLSVPRAVAVCPLGDKLYVVGG VDGHTANTVARKSVPRREEEREKERFEKFFDESTSEELKQNIHSTT- GLPPANGKWYMKGLAPERKTEREKERFEKFFDESTSELKQNIHST- FDPAGTHERVFRORGEREEREKERFEKFFDESTSELKQNIHST- FDPAGTHERVFRORGEREEREKERFEKFFDESTSELKQNIHST- FDPAGTHERVFRORGEREEREKERFEKFFDESTSELKQNIHST- FDPAGTHERVFRORGEREEREKERFEKFFDESTSELKQNIHST- FDPAGTHERVFRORGEREEREKERFEKFFDESTSELKQNIHST- FDPAGTHERVFRORGEREEREKERFEKFFFDESTSELKQNIHST- FDPAGTHERVFRORGEREEREKERFEKFFFDESTSELKQNIHST- FDPAGTHERVFRORGEREEREKERFEKFFFDESTSKENGT- FDPAGTHERVFRORGEREEREKERFEKFFFTDESSELKQNIHST- FDPAGTHERVFRORGEREEREKERFEKFFFTTDESSELKQNIHST- FDPAGTHERVFRORGEREEREKERFEKFFTTT- FDPAGTHERVFRORGEREEREKERFEKFFTT- FDPAGTHERVFRORGEREEREKERFEKFFTT- FDPAGTHERVFRORGERETTENT- FDPAGTHERVFRORGERETTENT- FDPAGTHERVFRORGERETTENT- FDPAGTHERVFRORGERETTENT- FDPAGTHERVFRORGERETTENT- FDPAGTHERVFRORGERETTENT- FDPAGTHERVFRORGERETTENT- FDPAGTHERVFRORGERETTENT- FDPAGTHERVFRORGERETTENT- FDPAGTHERVFRORGERETTENT- FDPAGTHERVFRORGERETTENT- FDPAGTHERVFRORGERETTENT- FDPAGTHERVFRORGERETTAL FDPAGTHERT- FDPAGTHERVFRORGERT- FD	İ	1		
ONDPPAAPFKYKIQLISMMCHPRFTCLYRVRAHGVRTSEGAEGS AQGPH				DDENIERI I GERMIOGI OUNDORNIGI GURRONINIA
6920 1418 591 RAGGPBKVHLTLKKKK 6921 2 1711 MNATSSERGFRVINTHARGTICKMENYIKEKOLODVILIAGHLRT PAHRLVILSAVSDYPAMMETNULEKOLODVILIAGHLRT PAHRLVILSAVSDYPAMMETNULEKOLODVILIAGHLRT PAHRLVILSAVSDYPAMMETNULEKOLODVILIAGHLRT SINCLGIRSFGDAGGCTELLAVARKYTMEHFIEVIKNOEFILLKOLHB SINCLGIRSFGDAGGCTELLAVARKYTMEHFIEVIKNOEFILLKOLHB SINCLGIRSFGDAGGCTELLAVARKYTMEHFIEVIKNOEFILLKOLHB SINCLGIRSFGDAGGCTELLAVARKYTMEHFIEVIKNOEFILLKOLHB SINCLGIRSFGDAGGCTELLAVARKYTMEHFIEVIKNOEFILLKOLHB SINCLGIRSFGDAGGCTELLAVARKYTMEHFIEVIKNOEFILLKOLHB SINCLGIRSFGDAGGCTELLAVARKYTMEHFIEVIKNOEFILLKOLHB SINCLGIRSFGDAGGCTELLAVARKYTMEHFIEVIKNOEFILLKOLHB SINCLGIRSFGDAGGCTELLAVARKYTMEHFIEVIKNOEFILLKOLHB SINCLGIRSFGDAGGCTELLAVARKYTMEHFIELDIKNOEMISTLAVITORGOLOMSYLINTVERKOH BEGROMMYVASMSTPRSTUGVVALINKKLYALGGROGSSCILKMEY PDPHTTKINGLCAPMEKREEFIERERKFFLESTGSELKOMIHSTT. GLEPANGKWMYKGLAPEDKTLERIKVYSGGKLMGGGSTINDVLA- VINTYRDAAQODAKAENIKKEEPICRGOKHRKLYAVYON KAJQERLETVVLSGWYINKSGGKVRLTFFLEQDQUMIGTKEETEK LPMGSIKMVVGBEIGHEDYMMARGIGDTESGELKOMIHSTT. GLEPANGKWMYKGLAPEDKTLERIKVYSGGKLMGGGSTINDVLA- VINTYRDAAQODAKAENIKKEEPICRGOKHRKLYWYWWYDTOY VDAIKDTVLGKWOYF UDAIKDTVLGKWOYF UDAIKDTVLGKWOYF UDAIKDTVLGKWOYF UNDELFTUNKERPSEFICHGROHRKUNGVERDUMIGTEETTEK COMPONIKCHVOHRAPROGLIPTSGELKOMIHSTENGKY SGTSDRIRFTVNRRISIVGFGLYSSINGFTUNGVISHEPI SCHOOLOMARGENGUARENTYFFFSSENORNGTSIBDGUT LEIFTY 6924 2210 1235 PEERVICTVEYYYLTAFHEGRKGALAKKPYNPT IGETFHCSWEVF KDRYRKKRTASRSPASCHEHMADDFSKSYKLRFVAGOVSHHPP ISCYCCEKERKUNTHAVIKSFROMMSVGSWGIGGGVLELLE HGEEVYFTLPSAVARSILTIPWELGGKVSINCAKTUSYSATVIF HTKPFYGGKWRTVASKHMPHTNIT VCKALGEWGCILEFTYNNG ETKYLDTYTLDVYPKKIRPLEKGEMSRILKREVTRYLRIGDI DAATEQKRHLEKOQUSERKRICHTETHNING ETKYLDTYTLDVYPKKIR PLEKGGMSSRIKKRYEKOLICHTVTALD ETKYLDTYTLDVYPKKIR PLEKGGMSSRIKKRYCKOLCKULCH SCHOMARGAMBEPDSVIEDRTTEIMCSVPRSIMIKGCALLOKSOMLICHETTNOM ETKYLDTYTLDVYPKIR PLEKGGMSSRIKHRONGCRILLEFTYNNG ETKYLDTYTLDVYPKKIR PLEKGGMSSRIKHRONGCRILLEFTYNNG ETKYLDTYTLDVYDKIR PLEKGGMSSRIKHRONGCRILLEGHANGT ETKYLTDTYLLAVARGABRUTCHTORDSILLEGHANGT LODIETESSWARGGRHILKER JOGGSSBNITIKHNISC LODIETESSWARGGRHILKE JOGGSSBNITIKHNISC UDAAT		1		
6920 1418 591 RAGOPSKVEILTILKKK 6921 2 1711 MINATRSEQFHVINHABOTTRKMENYLKEKQLCDVILLIAGHLRI PARRLUSAVSDYPAMPTNOVLEAKQEVKMEGVDYNLIAGHLRI PARRLUSAVSDYPAMPTNOVLEAKQEVKMEGVDYNLISLIK QYAYTGVIQLKENTISLLAARCILGUTQVIDVCSNFLKQLHP NEISKILCSDDINVPDEETIFHALMOWVCHDVONRGGELGHLLEA NEISKILCSDDINVPDEETIFHALMOWVCHDVONRGGELGHLLEA YIRIPLIPPOLIADLETISSMFTGBLEGGVILLAMEMKYHLLEBER YIRIPLIPPOLIADLETISSMFTGBLEGGVILLAMEMKYHLLEBER SMMOSPRTKPRKSTVGALXAVOGGMAMKGTTTIEKYDLERTNSWL HIGTMMGRELQFGVAVIVAKLYVVGGREDGHSYLINTVERRDP EGROWNYVASMSTPRSTVGALVANJOGHDOMSYLINTVERRDP EGROWNYVASMSTPRSTVGALVANJOGHDOMSYLINTVERRDP EGROWNYVASMSTPRSTVGALVANJOGHDOMSYLINTVERRDP EGROWNYVASMSTPRSTVGALVANJOGHDOMSYLINTVERRDP EGROWNYVASMSTPRSTVGALVANJOGHDOMSYLINTVERRDP EGROWNYVASMSTPRSTVGALVANJOGHDOMSYLINTVERRDP EGROWNYVASMSTPRSTVGALVANJOGHDOMSYLINTVERRDP EGROWNYVASMSTPRSTVGALVANJOGHDOMSYLINTVERRDP EGROWNYVASMSTPRSTVGALVANJOGHDOMSYLINTVERRDP EGROWNYVASMSTPRSTVGALVANJOGHDOMSYLINTVERRDP EGROWNYVASMSTPRSTVGALVANJOGHDOMSYLINTVERRDP EGROWNYVASMSTPSTVGALVANJOGHDOMSYLINTVERRDP EGROWNYCHALDROPHAMAPOLITICATION TO THE THE THE TOP TO THE THE TO THE THE TOP TO THE THE TO THE THE TO THE THE TO THE TO THE THE TO THE THE TO THE THE TO THE THE TO THE TO THE THE TO THE THE TO THE THE TO TH				
6921 2 1711 MNATRSEEGFHUINHAEGTLRKMENYLKEKQLCDVLLTAGHLRI PARHLVISAVSDYPAMPTINDVLEAKQEBVRMEGUPDALISIUV QYAYTOVLOKEDTIESILÄAACLQUTQUTOVCSNFLIKQLHP SINCLGURSACLGUTQUTQUVCSNFLIKQLHP SINCLGURSGTGDAQCCTELLINVAHKYYMEHFIEVIKNGEFLLLPA NEISKLLGSDINVPDEETFHAIMMOWLONGFLGELGHLA YIRLPILIPPOLLADLETSSMFTGDLSCOKLIMMEAMYHLLDERR SINMGSBETREPKRESTVGALVAVORDHAMKUPTURKOPFLLLPA HIGTMINGRELQFGVAVIDNKLYVVGGRDGGKTLNTVEKVDE BEGRNNYVASHSTRESTVAVVALNINKLYAHGERDGSSCLKSMEY FDPHTMKMSLCAPMSKRRGGVGVAVTINGFLVAVGGBASHTINTVEKVDE BEGRNNYVASHSTRESTVAVVALNINKLYAHGERDGSSCLKSMEY FDPHTMKMSLCAPMSKRRGGVGVAVTNGFLVAVGGBLAPASHNE SRLSDCVBRYPPKGDMSSTVAPLSVPROKYLGEDKLYVVGG YDGHTVLNTVSSYDAQRNSKKERGVGVAVTNGFLVAVGGBLAPASHNE SRLSDCVBRYPPKGDMSSTVAPLSVPROKYLGEDKLYVVGG YDGHTVLNTVSSYDAQRNSKKERGVAVATNGFLVAVGGBTINDVLAV VNTPKDAQQDAKABERKKEPLCRQKGHRKVLDKKGFGDLWFSV KGAGRELPTVPLSGMNINKSGERGEREKEKPFGBEVEKPFFDEDWFSV KGAGRELPTVPLSGMNINKSGERGEREKEKPFGDEVFDSV KGAGRELPTVPLSGMNINKSGERGEREKEKPFGDVFSV KGAGRELPTVPLSGMNINKSGCVRVLFFKLEGDQLWIGTRGETER LPMSSTKNVSEPIEGHEDYHMMAPGLGFTBASYMVWAVPTDY VNTPKDAQQDAKABENKKEPLCRQKGHRKVLDKKGFBDWFSV KGAGRELBTVPLSGMNINKSGCVRVLFFKLEGDQLWIGTRGETER LPMSSTKNVSEPIEGHEDYHMMAPGLGFTBASYMVWAVPTDY VNDFKLHFTVNFKRVSKVLAFRAGAKTRVDLKYMPTDY VNTPKDAQQDAKABENKKEPLCRQKOHRKVLAKAGAGALKYMPTDY VNTPKDAQQDAKABENKKEPGCVRCO VNDFLHFTVNFKRVSKVLAFRAGALKKFVNDAGAGSTINDVLAV VNTPKDAQAGAGAGAASATSTVRFWREDFTSILENVCYTACATLKKG DISHYTYNFKRYSKYLAFVVAGAGAGAGAAGAAGAGAAGAAGAAGAAGAAGAAGAAGA	6920	1418	591	
PAHRLVLSAVSDYPAAMFINDVLEAKQEEVRMEGVDPNALNSIJV QYAYTEVLQLKEDTIESLLAARCLIGITQVIDVCSNPLIKQLHP SNCLGIRSFGDAQCCTELLAVAKLYTMEHPIEVIKNGEFLLEPA NEISKLLCSDDINVPDEETIFHALMOWVCHDVONRGGELGHLLS YIRLPLLPPOLLADLETSSMPTGBLEGGVLLAPMEMKYHLLEPER SMMSSFRTTPRKSTVGALVAVGGNDANKGTTTIEKVDLETNSWL HIGMMGRERLOFGVAVIUNKLYVVGGRDEROSSCIKSMEY FDPHTNKWSLCAPMSKRRGGVGVATINGFLYVVGGRDASASHC INTVMPPMSTURHGLGVATLGCPMYAVGGHDGMSYLINTERNDP BGRONNYVASMSTPRSTVOVALINNKLYLINTEVCDPVGK IWTVMPPMSTURHGLGVATLGCPMYAVGGHDGMSYLINTERNDP BGRONNYVASMSTPRSTVOVALINNKLYLINTEVCDPVGK IWTVMPPMSTURHGLGVATLAGCPMYAVGGHDGMSYLINTERNOVA SRLSDCVBRYDPKOBWSTVAPLSVPRDAVAVCHLGKLYVVGG LOFGHTLANTVSSYDAQRMSKERPVAVGGROSSCIKSMEY FDPHTNKWSLCAPMSKRRGGVGVATINGFLYVVGGDAPASHC SRLSDCVBRYDPKOBWSTVAPLSVPRDAVAVCHLGBLKYVGG GLPPANGKWMYKGLAPDENKEEPUPDSTGSELKONIHSTIT. GFPANGKWMYKGLAPDENKEEPUPDSTGSELKONIHSTIT. VINTENDAQQDAKABENKKEPLCROKCHKVLDKKBGGSTINDVLAV VINTENDAQQDAKABENKKEPLCROKCHKVLDKBGGSTINDVLAV VINTENDAQQDAKABENKKEPLCROKCHKVLDKBGGSTINDVLAV VINTENDAQQDAKABENKKEPLCROKCHKVLDKBGGSTINDVLAV VINTENDAQADAKABENKKEPLCROKCHKVLDKBGGSTINDVLAV VINTENDAQADAKABENKKEPLCROKCHKVLDKBGGSTILSDREV VINTENDAYANGSGVRUTPRVAKEPLSTURGGSTILSDREV VIDAKDTVLGROYP VIDAKDTVLGGVYSTRAMSPOLGENTARTEVGAPASSAGV UNFFLHFTVINRFRISIVGFGLVGSTHGFQVBSSMGV SGTSDRIFFTVINRFRISIVGFGLVGSTHGFQVBSSMGV SGTSDRIFFTVINRFRISIVGFGLVGSTHGFQVBSSMGV SGTSDRIFFTVINRFRISIVGFGLVGSTHGFTHVAVTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSGNINNGTSIBDGQIP ELIFYT ELIFYT G924 2210 1235 PEERVICFVBYYLTAPHEGRKGALAKKPYNFIIGETFHCSWEVP KDRVRFRKTASRSPASCHEHMAADDPSKSYKLLEVVARGVSHIPP ISCFYCEGERERLCVNTHVMKSKFMGMSVCVSMIGEGVILKLE HGBEYYFTLDSAYARSILTIEWSELGKVSINCAKTGVSATVIF HTKPFFGGKKRTVANTWMKSKFMGSVCVSMIGEGVILKLE HGBEYYFTLDSAYARSILTIEWSELGKVSINCAKTGVSATVIF HTKPFFGGKKRTVANTWMKSKFMGNUTSVISGGMIKKLI ERMVRTDFLWGLISGRFGWDGYLFKRRPTDGPDNSFYSLLYPKL JOHNESSDQVEFVEHLISRNCHYGHGGHINSVLKMLGNDGPFTIALP EQGLDHIAEM LISHLANGLARGACABLUCKGWISGGGILG SPLESTLMGLEVGSFRGWGGYLGYRRETHOPEPNSFYSLYPKL JOHNESSDQVEFVEHLISRNCHYGHGGHINSVLKMLGHTISMDIS LERNSTTDERVANTOSLOS TVEWNOVTIGERUALDTARGALHTURGALHTURGSUCCHYTOSSOS T				1
OYATTGULGLEGOTIESULANARCHIQUIDUCSNFLIKQLHD SNCIGIES FODAGGCTELLAVARCHITMEN IEVIKNGEFLLPA NEISKLCSDDINVPDETIFHALMQWGGHVUNROGELGHLLS YIRLPILIPPQLLADLETSSMFTGDLECQKLLMEAMKYHLLEERR SMMGSFTKPRSTYGGLAVAUGMDAMKYHLLEERR SMMGSFTKPRSTYGGLAVAUGMDAMKYHLLEERR HIGTMMGRRLQFGVAVIDNKLYVVGGRGGLKTLMTVECFDPVGK IMTVMPPMSTHRHGLGVANTLGGPMYAUGHGSVLIKTMYTGERDD EGROMYVASMSTPRSTYGVVALNIKKLATGGGGSCLKSMEY FDPHTMKMSLCAPMSKRRGGVGVATYNGFLYVVGGHDAPASNHC SRLSDCVERYDPRGDSNSTVAPLSVPRDAVAVCPLDDLLYVUGG YDGHTYLNTVESYDAQRNEMKERVFVNIGRAGACVVVVKLP LTPPAGTRIEVVDRERERERERERFKFFLSTGSELKONTISTT. GLPPAMQKVMYKGLAPEDKTLRFIKVTSGAKINGGSTINDVLAV VNTPKDAAQDAKAEBREERERFKFFLDSTGSELKONTISTT. GLPPAMQKVMYKGLAPEDKTLRFIKVTDGRAKVLDKKREPDVPFGV KGAQERLPTVPLSGMYMKSGGKVRLTPFKLBODQLHTGYKEETER LPMGSIKNVVSEPIEGHEDYHMMAPQLGPTEASYYWVWAVPTQY VDAIKDTVIGKNQVIG FORDATARSYNVANDAGGSTINDVLAV VNIPLHFTVNFKRVLIGKALSLIKFPIMTI EFFAAGPAGSGILSDREV VNIPLHFTVNFKRKVLGKALSLIKFPIMTI EFFAAGPAGSGILSDREV VNIPLHFTVNFKRVLIGKALSLIKFPIMTI EFFAAGPAGSGILSDREV VNIPLHFTVNFKRVLIGKALSLIKFPIMTI EFFAAGPAGSGILSDREV VNIPLHFTVNFKVLYGKALSLIKFPIMTI EFFAAGPAGSGILSDREV VNIPLHFTVNFKVLYFTAFHEGKGALAKKFYNFT IGETHCSWEVF KORVFKKTAGRSPASCHERPMADDPSKSYKLKFVAEQVSHHPP ISGYCECEBKRLCVNTHWHTKSKFMGMSUGVSMIGEGVURLLE HGREYVFTLPSAYABILIT PROWEDSKSYKLKFVAEQVSHHPP ISGYCECEBKRLCVNTHWHTKSKFMGMSUGVSMIGEGVURLLE HGREYVFTLPSAYABILIT PROWEDSKSYKLKFVAEQVSHHPP ISGYCECEBKRLCVNTHWHTKSKFMGMSUSVSMIGEGVURLLE HGREYVFTLPSAYABILIT PROWEDSKSINCATGYSATAVF HTXPFYGGKVHRVTABVKHNPTNTIVCKAHGEMNGTLEFTYNNG ETKVIDTTILLEVIPKKIR PLEENGGFMSRRILMERTTRILKGID DAATEGKRHLEEKGRVBERKRENLETHRKKKFI GEGGGSGILG SPLESTLMSLEVGSFFV DQMSSBOUGVEFVELLISTENGCYPTSLMLGCANLVESMCAL SCLQSMPSVRCLGISNGTSSVIVSKKRPSEGNYQKEKOLCIKYF DQMSSBOUGVEFVELLISTENGCYPTSLMKRKFILDERNIKKKLI ERRWRTDELMKGLSERRGHDQVLKKNRPTOFPHNFKSLYPKI IQDIETIESMMCGERNICRG TERCHVYCHGHINSVLKMLDGDFTIALP EQGLDHIAEN ILSYLDARSLCAABLVCKEMQEVISEGEMLMKKLI ERRWRTDELMKGLIKGIAGCLQYRDFIVVSGSDDNTIRLMDIEC GACLEVLISCHBELVRCTRPDNRTVSGAYDGKIKWDLQAALDP RAPASTLCLRTLVBHGGNFTSPSGTYTTISS	0,721	4	1/11	
SNCIGIRS FIGDAGGTELLAWARKTMERHIE LYNGGEFLLLPA NEISKLLGSDINVPDEBTIFHALMGWYGHDVONROGGLGMLLS YIRLFILPPQLLADLETSSMFTGDLECQKLLMEAMKYHLIPERR SMMGSPRTKPRKSTVGALYAVGGMDAMKGTTTIEKYDLRTNSWL HIGTMAGRILGEGWAY LDNKLYVVGGRDGMKYTLTVERWDP EGRQNNYVASMSTPRSTVGVALINKLAGGDGSSCLKSMBY FDPHTMKMSLCAPMSKRGGVGVATYNOFILYVVGGHDAPASNHC SRLSDCVERYDPRGDSMSTVAPLSVPROAVCPLGDKLYVVGG YDGHTVLNTVESYDAQRNEWKERPVDNIGRAGACVVVVKLP FDPHTMKMSLCAPMSKRRGGVGVATYNOFILYVVGGHDAPASNHC SRLSDCVERYDPRGDSMSTVAPLSVPROAVCPLGDKLYVVGG YDGHTVLNTVESYDAQRNEWKERPVDNIGRAGACVVVVKLP 6922 1075 369 LTPPAGITHEVKDRERERERERERREKFPLDSTGSLKONTISTIT. GLPPAMGKWMYKGLAPEDKTLREIKVTGGAKINGGGSTINDVLAV VNTPKDAAQQDAKABEMKKEPLCGKQGHRKVLDKKRPBDVMPSV KGAQERLPTVPLSGMYMKKGGKVRLTPKLEQQLWIGTKERTEK LPMGSIKNVVSEPIEGHEDYHMMAPGLGPTEASYYWWYPTGY VDAIKDTVLJGKNQYF 6923 2469 1660 LGLFCILPJOTCAVLERDTLSIRESRLFGAVVRWAEAECGRQQ LPVTFGNKGKVLGKALSLIREPJMTIEFFAAGPAGSGILSDREV VNIPLHFTVMFKPREVI IDEPRCCIRECCINEPQUSERWGY SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIQIIEFEKK QTIGGNDTGFSCDGTAMTFRVMFKEPIELLENVCYTACATLKGP DSHYGTKGKLKVVUETPAASKTVFFFSENNINTSISTEDQQIP EIIFYT 6924 2210 1235 PERRVICFVBYYLTAPHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQUSHHPP ISCFYCECEBERLCVNTHWMTKSKPMMMSUGWSMIGGGVLRLLE HGEEVYFTLBSAYARSILTIPWVLEGKVSINCATGYSATVIF HTKPFYGGKVIRVYTABVKINPTNTIVCKAGGEWINGTLEFTINNG ETKVIDTTILDVYPKK IRPLERCGGRWINKERINFETTRYLKIGDI DAATECKRILEBKGRVBERKRENLRTPWKKPYFIQEGDGSGILQ SPLESTLMGLEVQSFPV BGGAGAAAMEPDSVIEDKTIELMCSVPRSIMLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVGRKRPSEGSVQKEKLCIKKF LGOMETILSVLAGRENGDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESSMRGGRINLCRIGGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVGRKRPSEGSVYCKERCLIKKFL IGNIETIESSMRGGGRINLCRICTGTDNRTVSGADPPNSFYRSLYPKI IQDIETIESSMRGGGRINLCRICTGTDNRTVSGADPPNSFYRSLYPKI IQDIETIESSMRGGRINLCRICTGTDNRTVSGADPNSFYRSLYPKI IQDIETIESSMRGGRINLCRICTGTDNRTVSGADPNSFYRSLYPKI IQDIETIESSMRGGRINLCRICTGTDNRTVSGADPNSFYRSLYPKI IQDIETIESSMRGGRINLCRICTGCDRTDNRTVSGADPNTIRLMDIEC GACLRVLEGHBELVRCIRFDNRTVYSGADPGRIKWMDLQAALDP NVPPSAQMGTTSPSRTYTYTISR		+		
NEISKLLCSDDINVPDEETIFHALMQWVGHDVQNRQGELGHLLE YIRLPLPPQLLADLETSSMFTGDLECQKLMEAMKYHLLPERR SMMQSPRTKPRSTVGALYAVGGMDAMKGTTTIEKYDLGTNSWL HIGTMNGRRLQEGVAVIDNELYVVGGRDGLKTLINTVECFDPVGK IWTVMPPBMTHRHGLGVAVIDNELYVVGGRDGLKTLINTVECFDPVGK FROMPMTHRHGLGVANTLGGMTAVGGRDGSSCLKSMEY FDPHTNKWSLCAPMSKRRGGVGVATYNGFLYVVGGHDAPASNHC SRLSDCVBRYDPKGDSWSTVAPLSVPRDAVAVCPLGDKLYVVGG YDGHTVLNTVESYDAQRNEWKERVPVNIGRAGACVVVVKLP LTPPAGITRIEVVDRERBERERBERFEKPFLDSTGSELKGNINSTT GLPPAMQKWMYKGLAPEDKTLRRIKVTGGAKINGGGSTINDVLA- VNTPKDAAQQDAKABENKKEPLCRQKQHKVLDKGKPEDVMPSV KGAQERLPTVPLSGMTMKSGGKVLTFKLEDDGLWIGTKERTEK LPMSIKNVVSEPIEGEDYHMMAPQLGPTEASYYWVXWVPTQY VDAIKDTVLGKNQVY VDAIKDTVLGKNQVY VNFLHFTVNFKPKVSTIDERCCLRGKECCINRPQQVSSMEV SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDGVVUNGLEFERE 6923 2469 1660 LGUFCILFIDTUCAVLERDTLSIRESRLFGAVVRWAEAECQRQ LPVTFGNKQKVLGKALSLIRFPLMTIEEFAAGPAQSGILSDRV- VNNFLHFTVNFKPRVEVIDERCCLRGKECCINRPQQVSSMEVY SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDGVVIQLITEVEKK QTLGNDTOFSCOCTANTFVWFKEVFIELDPNCTTACATLKGP DSHYGTKGLKKVVHETPAASKTVPFFFSSPGNNNGTSIEDGQIP EIIPYT 6924 2210 1235 PERVICTVBYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRWCKRTAGRSPASCHEHPMADPSKSYKLFYAEQUSHIPP SGCYCEGEKRLCUNTWWTKSKFMGWNGVSMTGGEGVLRLLE HGBEYVFTLPSAYARSILTIPWBLGGKVSINCAXTGYSATVF HTKPFYGGKVHRVTAEVKHNPTNTIVCKHAGEWNGTLEFTYNNG ETKVIDTTTLEVYFKKIRPLEKQGMSSINLARETTRLRIGDI DAATEQKRHLEEKQRVEERRRENETPWRKYFIQEGDGSGILQ SPLESTLMLSEVGSFVY DQMSESDQVEFVEHLISRNCHGMGHINSILKPMQRFTTALP EQGLDHIABNILSVLDAFDLIKSKCHGPHNSILKPMQRFTTALP EQGLDHIABNILSVLDARSLCCAPEDPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRNNSTKUMDKTSLECLKVLTGHRGSVULCLQYDGENIVFX IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRNNSTKUMDKTSLECLKVLTGHRGSVULCLQYDGSDATTLKUDIEC GACLRVLEGHEBLVRCIRPDNRRIVSGSDATTLKUDIEC GACLRVLEGHEBLVRCIRPDNRRIVSGSDATTLKUDIEC GACLRVLEGHEBLVRCIRPDNRRIVSGSDATTLKUDIEC GACLRVLEGHEBLVRCIRPDNRRIVSGSDATTLKUDIEC NVPPSAQMETTSPSRTYTYTISR	1	j		
YIRLPILIPPOLLADLETSSMTGGLECOKILMEANKYHILPERR SMMSPRTKPRKSTVADALYAUGMAKGTTTIEKYULRTNSMI, HIGTMNGRRLQFGVAVIDNKLYVVGGRDGLKTLNTVECFNPVGK IWTVMPPMSTHRHGLGVATLEGPMYAVGGHDGWSYLNTVERMPP BGRQMWYVASMSTPRSTVGVVALNNKLYAIGGRDGSSCLKSMEY FDPHTNKWSLCAPMSKRRGGVAVTVNGFLYVVGGHDAPASNHC SRLSDCVERYDPRGDSWSTVAPLSVPRDAVAVCPLGDKLYVVGG YDGHTYLNTVESYDAQRNEWKEVPVNIGRAGACVVVVKLP 6922 1075 369 LITPPATIENTVENDERSKREKFREKFPLDSTGSELKONTHSIT. GLPPAMQKWMYKGLAPEEKTREKFKPLDSTGSELKONTHSIT. VNTTKDAAQQDAKABENKKELCRQKQHRKVLDKKKPEDVWPSV KGADERLPTVPLSGMYNKSGGKVSTKLEKOPQLWIGTKERTEK LPMGSIKNTVSBPIBGHEDYHMMAFQLGPTBASYYWVYWVPTQY VNJEHHTVNPKSPMYNKSGGKVSTKEKCOLNRFQOQUSSWGY SGTSDRIFFTVNRRISIVGFGLVGSLHGFDDYQWIQTIEYBKK QTLGQNDTGFSCDGTANTFRVMPKEPIELIPNVCYTACATLKGP DSHYGTKGLKKVVHETPAABKTVPFFFSSFGNNNGTGIBDQQIP EIIFYT 6924 2210 1235 PEREVICFVBYSLTAFHEGRKGALAKKPYNPTIGETFHCSWEVP KDRVKKRTASRSPASCHEHMADDPSKSYKLRFVARQUSSHHPP ISCFYCECEKKLCVNTHVWTKSKFMGMSVGVSMIGEGVIRLLE HGBEYVFTLPSAYARSILTIFWWELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHRPTNTIVCKAHGEWRNTLEFTYNNG ETKVIDTTILPVYPKKIRPLEKGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHRPTNTIVCKAHGEWRNTLEFTYNNG ETKVIDTTILPVYPKKIRPLEKGGRVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHRPTNTIVCKAHGEWRNTLEFTYNNG ETKVIDTTILPVYPKKIRPLEKGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHRPTNTIVCKAHGEWRNTLEFTYNNG ETKVIDTTLLPVYPKKIRPLEKGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHRPTNTIVCKAHGEWRNTLEFTYNNG ETKVIDTTLLPVYPKKIRPLEKGGRVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHRPTNTIVCKAHGEWNTLEFTYNNG ETKVIDTDLWKGLISERCCRERKERLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVGSPPV 6925 2 1653 RGGAAGAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVGRRRPSGENNKGVCLQYDDEKITSG LRNNS.KIHDKSLLSRCCKCULTGHTGSVLCLQYDDERVITCSSDS TVENDVDNTGSVLNTLIHHBEALHINSYLKPHLQFDFTALP EQGLDHIABNILSYLDARSLCABELVCKSBORVITCW UNDASATDITLRRVLVGHRAAVNVUPFDDKYTVSASGGNTIKW STSTCEFVVTLIMGKRGIALCLAVERGSDSTILVW STSTCEFVVTLIMGKRGIALCLAVERGSGSDTILKW STSTCEFVVTLIMGKRGIALCAGELVCKSGRGNTLRWDICGGRACHVUPGAALDP RAPASTICLRTLVEHSGRVFRLOFDSFYLSSSHDDTILIWDFL NVPPSAGANETSSPSTRTYTISS	1			
SMMGSPRTKPRKSTVGALYAVGGNDANKGTTTIEKYDLRTNSWL HIGTMRGRRLGFGVAVIDNKLYVVGGGDLKTLNTVECFNPVGK INTVMPPMSTHRHGLGVAVIDNKLYVVGGDCLKTLNTVECFNPVGK FDPHTMKUSLCAPMSKRRGGGVAVTNGFLYVVGGHDAPASNHC SRLSDCVERYDPRGDSWSTVAPLSVPRDAVAVCPLGDKLYVVGG YDGHTYLNTVESYDAQRNEWKEVPVNIGRGAGCVVVVKLP 1075 369 LTPPAGTRHEVRDRRERERERERKEREKPDLDSTGSELKGNTHSIT. GLPPAMGKWMYKGLAPEDKTLREIKVTSGAKIMGGGSTINDVLA- VNTPKNDAQQDAKAERENKKELVGHRVLDKKKEDGVPTVLA- VNTPKNDAQQDAKAERENKKELVGHRVLDKKKEDGVPSTVLA- VNTPKNDAQQDAKAERENKKELVGHRVLDKKKEDGVPSTVLA- VNTPKNDAQQDAKAERENKKELVGHRVLDKKKEDGVPSTVLA- VNTPKNDAQQDAKAERENKKELVGHRVLDKKKEDGVPSTVLA- VNTPKNDAQQDAKAERENKKELVGHRVLDKKKEDGVPSTVLA- VNTPKNDAQQDAKAERENKKELVGHRVLDKKKEDGVPSTVLA- VNTPKNDAQQDAKAERENKKELVGHRVLDKKKEDGVPSTVLA- VNLFLHFTVNGKVLIGKAELSIRPFLMT IEEFAGPAGAGILSDRFW VNLFLHFTVNPRRISIUGFGLVSHTGHTVAGNIGLISPBKK QTLGQNDTOFSCOETANTFRWNREPIELLPNVCTTACATLKGP DSHYGTKGLKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKKRTASRSPASCHEHMADDPSKSYKLRFVARQUSHHPP ISCFYCECEKRELCUNTHWTKSKMOSVGVSMIGSVURLLE HGESYVFTLPSAYARSILTIEWVELGGKVSINCAKTGYSATVIP HTXPFYGGKHRVTARVKHNDTSITUCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKGGPMESRNLWREVTFYLRLGDI DAATEQKRHLERKQRVERKRENLRTPWKPKYFIQEGGGGILQ SPLESTLMGLEVGSFPV 6925 2 1653 RGGAGGAAMEDDSVIEDKTIELMGSVPRSLMLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKPDGGPNSFTSLIPKI IQDIETIESNMCGRHNLGRIQCRILVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKPDGPNSFTSRIPFII IQDIETIESNMCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKINDENTSLEERKGNDQVIJKRDTDGPNSFTSLIPKI IQDIETIESNMCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKINDENTSLECKVULTGHTGSVLCLUYDDERVIVTGSSDS TVKVMDVNGSVLNILHHERANGHVTQSSDNTTLRMDISC GACLRVLEGHBELVRCIRFDNKRIVSGSSDOTILKW STSTCEFVVTLINGKRGTALCLYNGERVLVSGSSDOTILKW STSTCEFVVTLINGKRGTALCLYNGERVLVSGSSDOTILKW STSTCEFVVTLINGKRGTALCLYNGERVLVSGSSDOTILKW STSTCEFVVTLINGKRGTALCLYNGERVLYSGSSDOTILKW STSTCEFVVTLINGKRGTALCLYNGERVLYSGSSDOTILKW STSTCEFVVTLINGKRGTALCLYNGERVLYSGSSDOTILKW STSTCEFVVTLINGKRGTALCLYNGERDELVVSGSSDOTILKW STSTCEFVVTLINGKRGTALCLYNGERDELVVSGSSDOTILKW STSTCEFVVTLINGKRGTALCHAURPTUSS		:		
HIGTMMCRELQGCVAVIDNKLYVVGGRDGLKTLNTVECKNDVG INTVMPPMSTHRHGLGVATLEGPMYAVGGHDGWSYLNTVERMDP BGRQMNYVASMSTPRSTVGVVALNNKLYAIGGRDGSSCLKSMEY FDPHTNKWSLCAPMSKRRGGVATTNGFLYVVGGHDAPASNHC SRLSDCVERYDPRGDSWSTVAPLSVPRDAVAVCPLGDKLYVVGG YDGHTYLNTVESYDAQRNEWKEEVPVNIGRAGACVVVVKLP 6922 1075 369 LTPPAGITHEVRDRERERERERKEKFFLDSTGSELKQNTHSIT. GLPPAMQKVMYKGLAPBENKTREIK KVTSGAKTMGGSTINDVLA, VNTPKDAAQQDAKABENKKEPLCRQKQHRKVLDKGKPEDVMPSV KGAQERLPTVPLSGMYNKSGGKVRLTFKLEQDQLMIGTKERTEK LPMSSIKNVVSBPIBGHBDYHMAPPGLGFTERSYYWVYWPTCY VDAIKDTVLGKMQYF 6923 2469 1660 LGLPCILPIDTLCAVLERDTLSIRESRLFGAVVRNAREAECQRQQ LPVTFGNKQKVLGKALSLIRFPLMTIEEFAAGPAQSGILSDREV VNLFLHFTVNPKPRVEYIDRPRCCLGKSKCCINRFQQVESRWGY SGTSDRIFFTVMRRISI VIGFGLGSCHSCTUNRFQQVESRWGY SGTSDRIFFTVMRRISI VIGFGLGSCHSCTUNRFQQVESRWGY SGTSDRIFFTVMRRISI VIGFGLGSCHSCTUNRFQQVESRWGY SGTSDRIFFTVMRRISI VIGFGLGSCHSCTUNRFQQVESRWGY SGTSDRIFFTVMRRISI VIGFGLGSCHSCTUNRFQQVESRWGY SGTSDRIFFTVMRRISI VIGFGLGSCHSCTUNRFQQVESRWGY SGTSDRIFFTVMRRISI VIGFGLGSCHSCTUNRFQQVESRWGY SGTSDRIFFTVMRRISI VIGFGLGSCHSCTUNRFQQVESRWGY BLIFTT 6924 2210 1235 PERRYLCFVBYLITAFHEGRKGALAKKPYNPI IGETFFCSWEVP KDRVKVRRTASRSPASCHEHMADDPSKSYKLRFVARQUSHHPP ISCFYCECEBKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGBEYYFTLPSAYARSILTIFWWLLGGKVSINCAKTGYSATVUF HTXPFYGGKVHRVTARVKHPMTIV VCKAHGEWNSTLEFTYNNG ETKVIDTTILPVYPKKIRPLEKGGPMESRILMERVTRYLRLGDI DAATEGKRHLERKQRVBERKRERNLRTPMKFKYF IQEGDSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKT IELMCSVPRSLWLGCANLVESMCAL SCLGSMPSVRCLQI SIGRTSSVIVSRRPSBECMYQKEKOLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAEN ILSYLDARSLCAAELVCKSWGRVISEGMLKKLI ERMVRTDPLWKGLGBRRGWDQYLFKRRPDGPPNS FYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKII IGG LRDNSIKINDKTSLECLKVLTGHTGSVLCLQYDDEKII IGG LRDNSIKINDKTSLECLKVLTGHTGSVLCLQYDDEKII IGG LRDNSIKINDKTSLECLKVLTGHTGSVLCLQYDDEKVISGDS TVRVMDVNTGBVLANTLHHHEAALHLRFSNGLMVTCSKDRS IAV WDMASATDITLRRVLVGHRAAVMVUDFDDKVIVSASSDNTIKW STSTCEFVVTLINGHKGRIAGLALQVRDRLVVSSSSDNTIKWM STSTCEFVVTLINGHKGRIAGLALQVRDRLVVSSSSDNTIKWM STSTCEFVVTLINGHKGRIAGLALQVRDRLVVSSSSDNTIKWM STSTCEFVVTLINGHKG	1			
INTYMPPMSTHRIGLGVATLEGPMYAVGGHGMSYLMYVERWID BGROMYVASMSTPRSTVGVVALINKLYAIGGRDGSCLKSMEY FDPHTNKWSLCAPMSKRRGGVGVATYNGFLVVVGGHAPASNIC SRLSDCVERYDPKGDSWSTVAPLSVPRDAVQCLGKLKYVGG- YDGHTVLINTVESVDAQRNSWKERSPVNIGRAGACVVVVKLD 6922 1075 369 LTPPAGTRHBVRDREREREREREFPLDSTGSELKQNIHSTT- GLPPAMQKVMYKGLAPEDKTLREIKVTSGAKIMGGSTIMDVLA- VNTPKDAAQQDAKAEENKKEPLCRÇKQHRKVLDKGKEPDVMFSV KGAQERLPTVPLSGMYNKSGGKVRLTFKLEQDQLWIGTKERTEK LPMSS IRNVVSEPLEGHEDYHMAFQLGPTEASYYWVYWVPTQY VDAIKDTVLGKWQYF 6923 2469 1660 LGIFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGNKOKVLGKALSLIRPIMTIEEFAAGPAQSGILSDREV VNLFLHFTVMPKPRVBYIDRPRCCLRGKECCINRFQQVBSRWGY SGTSDRIRPTVNRSISIVGFGLYGSILGFDTVQVNIQIIEYBKK QTLGQNDTGFSCDGTANTFRWFKEPIBIHDVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSFONNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVBYYLTAPHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKRKTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHIPP ISCFYCECEBKRLCVWTHWTASKKMGMSVGVSNIGGBVLRLLE HGESYVFTLPSAYARSILTIPWVBLGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTASVKHNDTIVCKAHGEWBGTLEFTYNNG ETKUIDTTLPVYPKXIRPLEKCQPMESRNLWREVTRYLRLGDI DAATEGKRHLEEKQRVBERKRENLRTEWKRYTFIGEGOGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAMBPDSVIEDKTIELMCSVPRSLMLGCANLUVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVBHLISRMCHYQHGHINSYLKPMLCRDFITALP EQGLDHIABNILSYLDARSLCABELVCREPGRYVSSGMWKKLI ERWYRTDPLWKGISERRGMDGVIKRPTTORPFYFSLYPKI IQDIETIESNWRCGRHILQRIQCRSENSKGYVCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLUQYDERVIVSGSDDTIKUM UMMASATDTILRRVLUGHBAANVAVDFDDKYIVSASGDDTIKWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVMDLQAALDP RAPASTLCLCRTLVEHSGRVFRLQFDEFQIISSSHDDTILIMDFL NVPPSAQNDSTRSPSRTYTYISS	1	,		
### ### ##############################	1	,		
FDPHTNKMSLCAPMSKRRGGVGVATYNGFLYVVGGHDAPASNHC SRLSDCVBRYDPKIDSBWTVAPLSVPAVAVCYLGKDKLYVGG YDGHTYLNTVESYDAQRNBWKEEVPVNIGRAGACVVVVKLP 6922 1075 369 LTPPAGIRHBVRDREEREREREREREFEPDSTGSELKQNIHSIT. GLPPAMQKVMYKGLAPEDKTLREIKVTSGAKIMGGSTINDVLA- VNTPKDAAQQDAKAEENKKEPLCRQKQHRKVLDRGKPEDVMPSV KGAQERLPTVPLSGMYNKSGGKVRLTFKLEQDQLMIGTKERTEK LPMGSIKNVVSBEPIEGHEDYHMAPQLGPTEASYYWVYAWPTQY VDAIKDTVLGKMQYF 6923 2469 1660 LGLFCILPIDTLCAVLERTLSIRESRLFGAVVRWAEAECQRCQ LPVTFGMKORVLGKALSLIRFPLMTIEEFAAGPAQSGILSDREV VNLFLHFTVNPKPRVEYIDRPRCCLRGKCCINRFQQVESRWGY SGTSDRIRFTVNRRISIVOFGLYGSIHOPDTYQVNIQIIEYBKK QTLGQNDTGFSCOGTANTFRVMFKEPISILEDVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVLCFVBYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPWADDPSKSYKLRFVARQUSHHPP ISCFYCECEBKRLCVNTHVWTKSKPMMSVUSMIGEGVLRLE HGBEYYFTLPSAYARSILTIPWLGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTASVKHNPTNTIVCKAHGEMWGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQPMESRNLMREVYTRYLRLGDI DAATECKRHLEEKQRVBERKRENLRTPMKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFFV 6925 2 1653 RGGAAGAMEPDSVIEDKTIELMCSVPRSLMLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKPSERNYCKEKDLCIKYF DQWSESDQVEFVEHLISRNCHYQHGHINSYLKPMLQRDFITALP EQGLIGHAENILSYLDARSLCABLVCKEMGRYUSGMMKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDERVITSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRS IAV WDMASATDITLRRVLVGHRAAVNVVDFDDYXIVASGGDBTIKWD STSTCEFFVETLMGHKRGIACLGYPRDLYVSGSSDNTIRLMDIEC GACLRVLEGHBELVRCIRPDWXRTVSGAYDGKIKVNDLQAALDP RAPASTLCLRTLVEIGGRVFRLUGSSSNDTTILMDIEC GACLRVLEGHBELVRCIRPDWXRTVSGAYDGKIKVNDLQAALDP RAPASTLCLRTLVEIGGRVFRLUGSSSNDDTILIMDFL NVPPSAQNSTRSPSRTYTYISS	1	ŀ		
SRLSDCVERYDPKGDSWSTVAPLSVPRDAVAVCPLGDKLYVVGG- YDGHTYLNTVESYDAQRNEWKEEVPVNIGRAGACVVVVLLP 1075 369 LTPPAGTRHEVRDRERERERERERERERERERERERERERERERERERE	1			
6922 1075 369 LTPPAGIRHEVRDREREREREREKFPLDSTGSELKQNIHSIT. GLPAMQKVMYKGLAPEDKYTLREIKVTSGAKINGGSTINDVLA' VNTPKDAAQQDAKABENKKEPLCRQKQHRKVLDKGKPEDVMPSV KGAQERLPTVPLSGMYNKSGGKVRLTFKLEQDQLWIGTKERTEK LPMGSIKNVVSEPIEGEEDYHMMAFQLGPTEASYYMVYMVPTQY VDAAKDTVLGKWQYF 6923 2469 1660 LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGMKQKVLGKALSLIRPPLMTISEFAAGPAQSGILSDREV VNLFLHFTVMPKPRVEVIDRPRCCLRGKECCINFQQVBSRWGY SGTSDRIRFTVNRRISIVGHSGSIHGPTDYQVNIQIIEYBKK QTLGQNDTGFSCDGTANTFRUMKEEPIELLPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKPYNPTIGETFHCSWEVP KDRVKKRRTASRSPASCHEHPMADDESKSYKLRFVAEQVSHHPP ISCFYCECEBKRLCVNTHVWTKSKFMGMSVGSWSMIGEGYLRILE HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKHRVTABVKHMPTNTIVCKAHGEMNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKGCPMESNILMEEVTRYLKGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFFV 6925 2 1653 RGGAGAAMBPDSVTEDKTIELMCSVPRSLMLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLAELVCKSMGVISEGMWKKLI ERMYRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRGGRINLQRIQCRSENSKGVVCLQYDEKVITSG LRNNSIKIMDKTSLECLKVITGGSVLCLQYDERVIVTGSSDS TVEWWDDNTGEVLNTLIHHRAVLHLRFSNGLMVTCSKORSIAV WDMASATDLTRRVLVGHRAANVEVDFDKYTVASSGDRTIKWW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSDDTITKWM WDMASATDLTRRVLVGHRAANVEVDFDKYTVSSASGDRTIKWM STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDDTITKWM STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDDTITLWMDIEC GACLRVLEGHEBLVRCTRFDNKRIVSGAYDGKIKVMDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILLWDILL NVPPSAQNETRSPSRTYTVISR				
6922 1075 369 LTPPAGIRHEVRORERERERERERERERERERERERERERERERERER FLOORINGSTENDULA WITH KOAAQQDAKABENKKEPLCRQKQHRKUDKGKPEDVMPSV KGAQERLPTVPLSGMYMKSGGKVRLTFKLEQDQLWIGTKERTEK LPMGSIKNVVSEPIEGHEDYHMAFQLGPTEASYYWYWVPTQY VDAIKDTVLGKWQYF 6923 2469 1660 LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGKKQKVLGKABLIRFPLMTI BEFAAGPAQSGILSDREV VNLFLHFTVWPKPVEVEVI IDPCCLIRKFQQVBSRWGY SGTSDRIFFTVNRRISIVGFGLYGS IHGPTDYQVNIQIIEYEKK QTLGQNDTGFSCDGTANTFRWMKEPIELLPNVCYTACATLKGP DSHYGTKGLKKVVLETPAASKTVFFFFSSPGNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKPYNPTIGETFHCSWEVP KDRWCPKTLSFKER SPASCHEHPMADDPSKSYKLRPVAEQVSHHPP ISCFYCECEEKRLCVNTHVWTKSKFMGMSVGVSMIGEGVIRLLE HGEEYYFTLPSAVARSILTIPWVLGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTVABVKHNFTIVCKAHGEMGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEERQRVBERRRERIRTTWKPKYFIQEGDGSGILQ SPLESTIMGLEVQSFFV 6925 2 1653 RGGAAGAMEPDSVIEDKTIELMCSVPRSLMIGCANLVESMCAL SCLQSMPSVRCLQISINSTSSVIVSRKRPSEGNYQKKKLLI ERWYRTDPLWKGLSERRGWDVLFKNRLI IQDIETIESNWRCSHCHUCHYF GGGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMWKKLLI ERWYRTDPLWKGLSERGWWCLQYDDEKIISG LRRNSIKIMDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRWNDYNTGEVLNTLIHNNEAULHRFSNGLWYTCSKORS IAV WDMASATDITLRRVLVGHRAAVNVDFDDKYIVSASGDRTIKWW STSTCEFVRTLNGHKRGIACLQYRDRLVVSASGDRTIKWW STSTCEFVRTLNGHKRGIACLQYRDRLVVSASGDRTIKWW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDLEC GACLRVLEGHBELVRCTRFDNKRIVSGAYDGKIKWDLQAALDP RAPASTLCLRTLVEHSGRVFRLOFBFGIISSSHDDTILIWDLEC GACLRVLEGHBELVRCTRFDNKRIVSGAYDGKIKWDLQAALDP RAPASTLCLRTLVEHSGRVFRLOFBFGIISSSHDDTILIWDLEC GACLRVLEGHBELVRCTRFDNKRIVSGAYDGKIKWDLQAALDP RAPASTLCLRTLVEHSGRVFRLOFBFGIISSSHDDTILIWDLEC GACLRVLEGHBELVRCTRFDNKRIVSGAYDGKIKWDLQAALDP RAPASTLCLRTLVEHSGRVFRLOFBFGIISSSHDDTILIWDLEC GACLRVLEGHBELVRCTRFDNKRIVSGAYDGKIKWDLQAALDP RAPASTLCLRTLVEHSGRVFRLOFBFGIISSSHDDTILIWDLEC GACLRVLEGHBELVRCTRFDNKRIVSGAYDGKIKWDLQAALDP RAPASTLCLRTLVEHSGRVFRLOFBFGIISSSHDDTILIWDLEC GACLRVLEGHBELVRCTRFDNKRIVSGAYDGKIKWDLQAALDP RAPASTLCLRTLVEHSGRVFRLOFBFGIISSSHDDTILIWDLEC GACLRVLEGHBELVRCTRFDNKRIVSGAYDGKIKWDLQAALDP RAPASTLCLRTLVEHSGRVFRLOFB	· ·			
GLPPAMOKVMYKGLAPEDKTIREIKVTSGAKIMGGGSTINDULA- VNTPKDAAQQDAKABENKKEPLCROKQHRKVLDKKYEBUVMPSV KGAQERLPTVPLSGMYNKSGGKVRITFKLEQDQLWIGTKERTEK LPMGSIKNVVSEPIEGHEDYHMMAFQLGPTEASYYWVYWVPTQY VDAIKDTVLGKWQYF 6923 2469 1660 LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECORQQ LPVTFGRKQKVLGKALSLIRFPLMTIEEFAAGPAQSGILSDREV VNLFLHPTVNPKPRVEYIDRPRCCLRGKECCINRFQQVBSRWGY SGTSDRIRFTVNRISIUGFGLYGSIHGFTDYQVNIQIIEYBKK QTLGONDTGFSCDGTANTFRVWFKEPIELLPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVBYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKFKTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISCFYCECEBKRLCVNTHVWTKSKFMGMSVGVSMIGEGVIRLLE HGESYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEGKKSILAKKPYNPIQEGDGSGILQ SPLESTLMGLEVQSFFV 6925 2 1653 RGGAAGAMEPDSVIEDKTIELMCSVPRSLWIGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSECNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQQLDHIAENILSYLDARSLCAAELVCKEWGRVISEGMLWKKLI ERWYRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRNNSIKIMDKTSLECLKVITGHTGSVLCLQYDDEKIISG LRNNSIKIMDKTSLECLKVITGHTGSVLCLQYDDEKIINGSSDS TVRWDVNTGFVLNTLIHHNEAVLHLRFSNGLMVTCSKORSIAV WDMASATDITLRRVLVGHRAAVNVUDFDDKYIVSASSDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGSYDKIKWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILLWDFL NVPPSAQNETRSPSRTTYTISR	6922	1075	369	
VNTPKDAAQQDAKAEENKKEPLCRQKQHRKVLDKGKPEDVMPSV KGAQERLPTVPLSGMYNKSGGKVRLTFKLEQDQLWIGTKERTEK LPMGSIKNVVSEPIEGHEDYHMMAFQLGPTERASYYWVYWPYTQY VDAIKDTVLGKWQYF 6923 2469 1660 LGIFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECORQQ LPVTFGMKQKVLIGKALSLIRFPLMTIEEFAAGPAQSGILSDREV VNLFLHPTVNPKPRVEYIDRPRCCLRGKECCINRFQQVESRWGY SGTSDRIRFTVNRRISIVGFGLYGSIHGFTDYQVMIQIIEYBKK QTLGQNDTGFSCDGTANTFRWMFKEPIEILPNVCYTACATLKGP DSHYGTKGLKKVVLETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISGCFYCECEBKRLCVNTHVWTKSKPMGMSVGVSMIGEGULRLLE HGBEYVFTLPSAYARSILTIPWELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKUIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWIGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKPSEGNYQKEKDLCIKYF DOWSESDQUEFVEHLISHMCHYOHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKRRPTDGPPNSFYRSLYPKI IQDIETIESSWRCGRHULQTICRSENSKGYVCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDEKIITGSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVUDFDDKYIVGSSDSTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDDKRTVSGSYDGKKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL	1			l ·
KGAQERLPTVPLSGMYNKSGGKVRLTFKLEQDQLWIGTKERTEK LPMSSIKNVVSEPIEGHEDYHMMAFQLGPTEASYYWVYWYPTQY VDATKDTVLGKWQYF 6923 2469 1660 LGLFCILFIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGNKQKVLGKALSLIRFPLMTIEFFAAGPAQSGILSDREV VNLFLHFTVNPKPRVEYIDRPRCCLRGKECCINRFQQVESRWGY SGTSDRIRFTVNRRISIVGFGLYGS IHGPTDYQVNIQIIEYBKK QTLGQNDTGFSCDGTANTFRVMFKEPIEILPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDFSKSYKLRFVAEQUSHHPP ISCFYCECEBKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGBEYVTTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVIRVTABVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPJEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVGRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHTAENILSYLDARSLCAAELVCKEMGRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVHLURFSNGLMVTCSKDRS IAV WDMASATDITLRRVLUGHBELVRCIRFDURFVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDRRIVSGAYPGKIKVWDLQAALDP RAPASTLCLRTLVEHSBRCYFRLQFBEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	İ	· ·		T'
LPMGSIKNVUSEPIEGHEDYHMMAFQLGPTEASYYWVYWVPTQY VDAIKDTVLGKWQYF 6923 2469 1660 LGFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGNKQKVLGKALSLIRFPLMTIEEFAAGPAQGGILSDREV. VNLFLHFTVNPKPRVEYINPRCCLRGKECCINRFQQVESRWGY SGTDRIRFTVUNRFISIVGFGLYGSILGPTDYQWIQIIEYEKK QTLGQNDTGFSCDGTANTFRVMFKEPIEILFNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDFSKSYLLRFVAEQUSHHPP ISCFYCECEBKRLCUNTHWWTKSKFMGMSUGVSMIGEGURLLE HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKGPMESRALWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRNCHYQHGHINSYLKDHLQRDFITTALP EQGLDHTAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKLSERRGWDQYLFKNRFTDEPNSFKSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVHLURFSNGLMVTCSKORSIAV WDMASATDITLRRVLUGHBELVRCIRFDDKRIVSGSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDNKRVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSRCVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR			,	
VDAIKDTVLGKWQYF 6923 2469 1660 LGJFCILFIDTLCAVLERDTLSIRESRLFGAVVRWAEAECORQQ LPVTFGNKQKVLGKALSLIRFPLMTIBEFAAGPAQSGILSDREV. VNLFLHFTVNPKPRVEYIDRERCCLRGKECCINRFQQVESRWGY SGT5DRIRFTVNRRISIVGFGLYGSIHGPTDYQWNIQIIEYEKK QTLGQNDTGFSCDGTANTFRVMFKEPIEILPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSFGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PERVICFVBYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISCFYCECEBKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGBEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEMNGTLEFTTNNG ETKVIDTTTLPVVPKKIRPLEKQGPMESNNLWREVTRYLRGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPYFYLGGDI SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCABELVCKEWQRVISEGMLWKKLI ERMYRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRINLQRIQCRSENSKGVVCLQYDDEKIISG LRNDSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGBVLNTLIHHNEAVHLLFSNGLMVTCSKDRSIAV WDMASATDITLRRVLYGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRYFLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	1			
LPYTFGNKQKVLGKALSLIRFPLMTIBEFAAGPAQSGILSDREV VNLFLHFTVNPKPRVBYIDRPRCCLRGKECCINRFQQVBSRWGY SGTSDRIRFTVNRKISIVGFGLYGSIHGPTDYQVNIQIIEYBKK QTLGQNDTGFSCDTANTFRVMRKPIBEILPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEBRVICFVBYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISCFYCECEBKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGBEYVFTLPSAVARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKGGPMESRNLWREVTRYLRIGDI DAATEQKRHLEEKQRVBERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGBVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKXIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDNRRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTTTYISR				
LPVTFGNKQKVLGKALSLIRFPLMTIBEFAAGPAQSGILSDREV VNLFLHFTVNPKPRVBY IDRPRCCLRGKECCTNRFQQVBSRWGY SGTSDRIPFTVNRRISIVGFGLYGSIHGPTDYQVNIQIIEYBKK QTLGQNDTGFSCDGTANTFRVMFKEPIBLLENVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIBDGQIP EIIFYT 6924 2210 1235 PEBRVICFVBYYLTAFHEGRKGALAKKPYNPTIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVABQVSHHPP ISCFYCECBKRLCVNTHVWTKSKFMGMSVGVSMIGGGVLRLLE HGEEYVFTLPSAYARSILTIPWVBLGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHNPTMTIVCKAHGBWNGTLEFTTNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVBERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAMBEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAABLVCKEWQRVISEGMLWKKLI ERNVTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGBVLNTLIHNHEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVCHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCLRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	6923	2469	1660	LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECOROO
SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIQIIEYEKK QTLGQNDTGFSCDGTANTFRWFKEPIEILDNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVBYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISCFYCECEBKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGEEYVFTLPSAYARSILTIPWVBLGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVBERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSKKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFTTALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERNVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGGVLNTLIHHNEAVLHLRFSNGLMVTCSKORSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	1			· · · · · · · · · · · · · · · · · · ·
QTLGQNDTGFSCDGTANTFRVMFKEPIEILPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEBRVICFVBYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRPVAEQUSHHPP ISCFYCECEBKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGEEYVFTLPSAYARSILTIPWVBLGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFFV SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMYRTDFLWKGLSERRGWDQVLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIGCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	1			VNLFLHFTVNPKPRVEYIDRPRCCLRGKECCINRFQQVESRWGY
DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVBYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQUSHHPP ISCFYCECEBERLCUNTHWWTKSKFMGMSVGVSMIGEGVLRLLE HGEEYVFTLPSAYARSILTIPWVBLGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVBERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMBPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LKRNSIKIWDKTSLECLKVLTGHTGSVLCLQYDDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIQIIEYEKK
6924 2210 1235 PERRVICFVRYYLTAFHEGRKGALAKKPYNPI IGETFHCSWEVP KDRVKPKTASRSPASCHEHPMADDPSKSYKLFVAEQUSHHPP ISCFYCECEBKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGESYVFTLPSAYARS ILTIDWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTI VCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVVPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDDEKIISGSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTTISR	•	,	*	
PERVICFVBYYLTAFHEGRKGALAKKPYNPI IGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISCTYCECEBKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGESYVFTLPSSAVARS ILTI DWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTI VCKAHGEWNGTLEFTYNNG ETKVIDTTLPVVPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVBERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR		·		DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP
KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQUSHHPP ISCFYCECEBKRLCUNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGEEYVFTLPSAYARSILTIPWVBLGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVBERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPNLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTIGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVUDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	· .		<u> </u>	
ISCFYCECEBKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGBEYVFTLPSAYARSILTIPWVBLGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVBERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	6924	2210	1235	PEERVICFVBYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP
HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGBVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTTRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR		· .	1	KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP
HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGYYCLQYDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGBVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	1		•	ISCFYCECEEKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE
ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRIGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGBVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				
DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDDEKIIVGSSDS TVRVWDVNTGBVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				
SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDDEKVIVGSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				· · · · · · · · · · · · · · · · · · ·
RGGAAGAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				
SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGBVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR		· · · · · · · · · · · · · · · · · · ·		
DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	6925	2	1653	
EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				
ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR		·		
IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				
LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGBVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				
TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	1			
WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				
STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				
GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR]			
RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	1 1			
NVPPSAQNETRSPSRTYTYISR	1			
		ļ		
SGRVAMDGLGLQFPEQGFPAGPPLLPPHMGGHYRDCQSLGAPPL				
	6926	1	733	SGRVAMDGLGLQFPEQGFPAGPPLLPPHMGGHYRDCQSLGAPPL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Doquemoc	\=possible nucleotide insertion)
			DGYPLPTPDTSPLDGVDPDPAFFAAPMPGDCPAAGTYSYAQVSD
			VAGDDEDDAGDMUDDI CDEDAGDG I DOGLI ADDGALUURUGANG
			YAGPPEPPAGPMHPRLGPEPAGPSIPGLLAPPSALHVYYGAMGS
			PGAGGGRGFQMQPQHQHQHQHQHPPGPGQPTPPPEALPCRDGT
.		1	DPSQPAELLGEVDRTEFEQYLHFVCKPEMGLPYQGHDSGVNLPD
6927	2		SHGAISSVVSDASSAVYYCNYPDV
0327	2	1484	LTLCGDIQLMLAQNANNRAAHLEEFHYQTKEDQEILHSLHRESS
ı		1	CQGFAWATDLSTDLESQLSVSCKCYEAANBILQFRDLKSQNPEH
			YVQVLKRMGNIRNEIGVFYMNQAAALQSERLVSKSVSAAEQQLW
1			KKSFSCFEKGIHNFESIEDATNAALLLCNTGRLMRICAQAHCGA
			GDELKREFSPEEGLYYNKAIDYYLKALRSLGTRDIHPAVWDSVN
Į		1	WELSTTYFTMATLQQDYAPLSRKAQEQIEKEVSEAMMKSLKYCD
ļ			VDSVSARQPLCQYRAATIHHRLASMYHSCLRNQVGDEHLRKQHR
,	•		VLADLHYSKAAKLFQLLKDAPCELLRVQLERVAFAEFOMTSONS
ı	,		NVGKLKTLSGALDIMVRTEHAFQLIQKELIEEFGQPKSGDAAAA
l			ADASPSLNREEVMKLLSIFESRLSFLLLQSIKLLSSTKKKTSNN
			IEDDTILKTNKHIYSQLLRATANKTATLLERINVIVHLLGQLAA
			GSAASSNAVQ
6928	1086	777	EAIDLINNLLQVKMRKRYSVDKTLSHPWLQDYQTWLDLRELECK
l			IGERYITHESDDLRWEKYAGEQGLQYPTHLINPSASHSDTPETE
			ETEMKALGERVSIL
.6929	1749	607	RDQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG
ļ			NLHQHDPQDLRHNGNVVVAGRPSCSRGPRRAIQKPQPAGGRRSG
		,	RGPAAGGLCLQPPDGGTCVPEEPPVPPMDWEALEKHLAGLQFRE
.		*	QEVRNQGQARTNSTSAQKNERESIRQKLALGSFFDDGPGIYTSC
1			SKSGKPSLSSRLQSGMNLQICFVNDSGSDKDSDADDSKTETSLD
.		, ·	TPLSPMSKQSSYSDRDTTEEESESLDDMDFLTRQKKLQAEAKM
-			ALAMAKPMAKMQVEVEKQNRKKSPVADLLPHMPHISECLMKRSL
			KPTDLRDMTIGQLQVIVNDLHSQIESLNEELVQLLLIRDELHTE
. }			QDAMLVDIEDLTRHAESQQKHMAEKMPAK
6930	131	545	FKDTANVFVSLFQMRNNFRHYFIEPSQLKLFYDVITWIVTQVAI
:	-=', '''		SYTVVPFVLLSIKPSLTFYSSWYYCLHILGILVLLLLPVKKTOR
- 1	**		RKNTHENIQLSQSKKFDEGENSLGQNSFSTTNNVCNQNQEIASR
	•	,	HSSLKO
6931	2	659	FVERLPNRPACLLVASGAAEGVSAQSFLHCFTMASTAFNLQVAT
		. 039	PCGVAMETIDUEDONA DESCAPEDA WAY TO THE TOTAL OF THE POPULATION OF T
. 1			PGGKAMEFVDVTESNARWVQDFRLKAYASPAKLESIDGARYHAL
1			LIPSCPGALTDLASSGSLARILOHFHSESKPICAVGHGVAALCC
:	•		ATNEDRSWVFDSYSLTGPSVCELVRAPGFARLPLVVEDFVKDSG
6932		7.7.	ACFSASEPDAVHVVLDRHLVTGQNASSTVPAVQNLLFLCGSRK
3334	2	1131	FVDSPGQGEQAEEEEGGIQMNSRMRAHSPAEGASVESSSPGPKK
- 1			SDMCEGCRSLAAGHPGYISHDKETSIKYVSHQHPSHPQLFSIVR
- 1			QACVRSLSCEVCPGREGPIFFGDEQHGFVFSHTFFIKDSLARGF
1			QRWYSIITIMMDRIYLINSWPFLLGKVRGIIDELQGKALKVFEA
			EQFGCPQRAQRMNTAFTPFLHQRNGNAARSLTSLTSDDNLWACL
			HTSFAWLLKACGSRLTEKLLEGAPTEDTLVQMEKLADLEEESES
	1		WDNSEAEEEEKAPVLPESTEGRELTQGPAESSSLSGCGSWQPRK
		•	LPVFKSLRHMRQVGGRGTAHHELRRRANHGLCLPTRLASGPSTL
			KTLQEVTDSLLGGWLMAQGVGGII
6933	1431	890	SLNLHCTLPPPPHQYPAGYPSDKEGKKPKGQSKKQPSGTTKRPI
1		i	SDDDCPSASKVYKASDSAEAIEAFQLTPQQQHLIREDCQNQKLW
į.	İ		DEVLSHLVEGPNFLKKLEQSFMCVCCQELVYQPVTTECFHNVCK
j			DCLQRSFKAQVFSCPACRHDLGQNYIMIPNEILQTLLDLFFPGY
1			SKGR
6934	3030	2588	
	2030	4900	DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTFIIVLAFIV
-		l	CWTPFFFVQMWSVWDANAPKBASAFIIVMLLASLNSCCNPWIYM
1		ļ	LFTGHLFHELVQRFLCCSASYLKGRRLGETSASKKSNSSSFVLS
- 1			HRSSSORSCSQPSTA
		·	

CEO	Dwodie	Decidence and	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
6935	886	543	NSALYVAGGNDGTSCLNSVERYSPKAGAWESVAPMNIRRSTHDL
0,555		3.3	VAMDGWLYAVGGNDGSSSLNSIEKYNPRTNKWVAASCMFTRRSS
			VGVAVLELLNFPPPSSPTLSVSSTSL
6936	1347	567	RSHRROFLSRALLEFFGKSHPPPHRLFRKSLNVGLHYSHIPFLT
6936	134/	26/	
	ļ		TCLHFLRKRLQKGEVGLSVETSKPQVPVGGLSRKKVPQEPWATV
			MEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRALLQLRGLDPS
			LPSPLPNLGPQGPALTPEQENILHTTQTDCYNNLAACLLQMBPV
1			NYERVREYSQKVLERQPDNAKALYRAGVAFFHLQDYDQARHYLL
			AAVNRQPKDANVRRYLQLTQSELSSYHRKEKQLYLGMFG
6937	1	727	AVEFRCCPGRDPACFARGWRLDRVYGTCFCDQACRFTGDCCFDY
			DRACPARPCFVGEWSPWSGCADQCKPTTRVRRRSVQQEPQNGGA
			PCPPLEERAGCLEYSTPQGQDCGHTYVPAFITTSAFNKERTRQA
1			TSPHWSTHTEDAGYCMEFKTESLTPHCALENRPLTRWMOYLREG
1	· ·	· ·	YTVCVDCQPPAMNSVSLRCSGDGLDSDGNQTLHWQAIGNPRCQG
1.			TWKKVRRVDQCSCPAVHSFIFI
6938	3	719	NSRKLELAERVDTDFMOLKKRROSSEKENDSGTLDTVGAVVVDH
0,530	3	713	I
1			EGNVAAAVSSGGLALKHPGRVGQAALYGCGCWAENTGAHNPYST
1		•	AVSTSGCGEHLVRTILARECSHALQAEDAHQALLETMQNKFISS
1	i	•	PFLASEDGVLGGVIVLRSCRCSAEPDSSQNKQTLLVEFLWSHTT
Ì		,	ESMCVGYMSAQDGKAKTHISRLPPGAVAGQSVAIEGGVCRLGEP.
			SELTLQAECEASQRHFRT
6939	3	810	KVTAPRRPQRYSSGHGSDNSSVLSGELPPAMGRTALFHHSGGSS
			GYESLRRDSEATGSASSAPDSMSESGAASPGARTRSLKSPKKRA
	[·		TGLQRRRLIPAPLPDTTALGRKPSLPGQWVDLPPPLAGSLKEPF
1			EIKVYEIDDVERLORPRPTPREAPTOGLACVSTRLRLAERROOR
		· •	LREVQAKHKHLCEELAETQGRLMLEPGRWLEQFEVDPELEPESA
1		-	EYLAALERATAALEQCVNLCKAHVMMVTCFDISVAASAAIPGPQ
1 .			BADA
6940	1188	496	GKMAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQ
1 05±0	2200	450	VVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAV
		•	,
			LADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGS
			TYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLL
		i .	KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILS
	<u> </u>	<u></u>	EVTPDQSKPEN
6941	1	713	SLSRADSDPHGPHTCGHVLNVIIGSNVLALAEAQRQAEALGYQA
[VVLSAAMQGDVKSMAQFYGLLAHVARTRLTPSMAGASVEEDAQL
1			HELAAELQIPDLQLEEALETMAWGRGPVCLLAGGEPTVQLQGSG
1	;		RGGRNQELALRVGAELRRWPLGPIDVLFLSGGTDGQDGPTEAAG
1		,	AWVTPELASQAAAEGLDIATFLAHNDSHTFFCCLQGGAHLLHTG
			MTGTNVMDTHLLFLRPR
6942	1	246	GDYVERYDPKTDTWTMGAPLSMPTNAVGGCLLGDRLYADGGYDG
			QTYLNTMESYDPOTNEWTQMASLNIGRAGACVVVIKQP
6943	. 1	739	PMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLG
0,43	• •	737	
			HSPAGGSITETLVQGDKTEYLLTALEPKPTYIICMVTMETTNAY
			VADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAGIIGGA
			VALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDYMESG
	,		TKKDNSILEIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLCK
L			ATHTIGYGTTRGYRDGGIPDIDYSYT
6944	960 '	156	VANILLNGVKYESELTGSSERAEQPLSVGRLCSTICNMPKALRT
]			LCVNHFLGWLSFEGMLLFYTDFMGEVVFQGDPKAPHTSEAYQKY
1 1			NSGVTMGCWGMCIYAFSAAFYSAILEKLEEFLSVRTLYFIAYLA
[FGLGTGLATLSRNLYVVLSLCITYGILFSTLCTLPYSLLCDYYQ
1	· '		SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVLGPLTSA
			VGSANGVMYFSSLVSFLGCLYSSLFVIYEIPPSDAADEBHRPLL
l i	'		
			LNV

WO 01/53312

Г	SEQ	Predicted	Predicted end	
	ID	beginning		Amino acid segment containing signal peptide
			nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
-	i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
-	i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	i	amino acid	sequence	Codon, /=possible nucleotide deletion,
- [-		sequence		
F	6945	2067		\=possible nucleotide insertion)
1	0342 1	2067	179	EGEDRGLPRTMGAALGTGTRLAPWPGRACGALPRWTPTAPAQGC
	ì			HSKPGPARPVPLKKRGYDVTRNPHLNKGMAFTLEERLQLGIHGL
	ì	!	ļ ,	IPPCFLSQDVQLLRIMRYYERQQSDLDKYIILMTLQDRNEKLFY
	l l			RVLTSDVEKFMPIVYTPTVGLACQHYGLTFRRPRGLFITIHDKG
	ì	·		HLATMLNSWPEDNIKAVVVTDGERILGLGDLGCYGMGIPVGKLA
	l			LYTACGGVNPQQCLPVLLDVGTNNEELLRDPLYIGLKHQRVHGK
-	ı			AYDDLLDEFMQAVTDKFGINCLIQFEDFANANAFRLLNKYRNKY
	į.			CMFNDDIQGTASVAVAGILAALRITKNKLSNHVFGFQGAGEAAM
1	i			G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLIVQGRDH
1	ì			LNHEKEMFAQD\HPEVNSLEEVVRLVKPTAIIGVAAIAEA\FTE
1	l			QILRDMASFHERP\IIFALSNPTSKAECTA\EKCYRVTEGPRGF
-	i			FAS\GSPF*GVLIWEMGKTFIPGGRGNNA*RVPRGWQLGVHSPG
	l	Ì		GDPGHIP\DEIFLPDSRAKLPQEVSEQHLSQGRLYP\PLST\IR
1				NVFLRIAIKVFD*GYKHNLV\SYYPEPKD\KEAFCKIPGSYTPD
	Ì			YDSFYT/VDSYIWAOGKAMNVOTV
+	6946	133	2551	SCEYSGITVAPGDPCPGVAHLLAPSMASDTPESLMALCTDFCLR
1			1667	
	Ì			NLDGTLGYLLDKETLRLHPDIFLPSEI\CDRLVNEYVELVNAAC
				NF\EPHE\SFFNPLFRDPRKQPASRRIHL\RED\LVQD\QD\LE
	١		1	AIRKQDL\VEL\YLTN\CEKLSAKSLQTLRSFSHTLGVP*AFFG
-	j			C\TNILLLRKENPGGL/CEDEYLFNPTCQVLVKDFTFEGFSRLR
	Ì			F\LKLGRMIDWVPVES\LLRPLNSLAALDLSGIQTSDAA\FLTQ
	1			WKDSL\VSLVL\YNMDLSDDHIR\VIVQLHKLRHLDISRDRLSS
	1	l		YYKFKLTREVLSLFVQKLGNLMSLDISG\HMILENCSISKIGKR
	İ	ŀ	i i	EAGQTSI\EPSK\SSIIPFRGFEGGPLQF\LGVF*GIFCGRLTH
	ļ			IPAYKVSGDKNEEQVLNAIEAYTEHRPEITSRAINLLFDIARIE
-	.	'	•	RCNQLLRALKLVITALKCHKYDRNIQVTGSAALFYLTNSEYRSE
1	}	ļ		QSVKLRRQVIQVVLNGMESYQEVTVQRNCCLTLCNFSIPEELEF
	İ			QYRRVNELLLSILNPTRQDESIQRIAVHLCNALVCQVDNDHKEA
	ļ		i	VGKMGFVVTMLKLTQKKLLDKTCDQVMEFSW\SALWNITDETPD
		٠.		NCEMFLNFNGMKLFLDCLNEFPEKQELHRNMLGLLGNVAEVKEL
	1		İ	RPQLMTSQFISVFSNLLESKADGIEVSYNACGVLSHIMFDGPEA
1	1		İ	WGVCEPQREEVEERMWAAIQSWDINSRRNINYRSFEPILRLLPQ
1		†	İ	GISPVSQHWATWALYNLVSVYPDKYCPLLIKEGGMPLLRDIIKM
	. J			ATARQETKEMARKVIEHCSNFKEENMDTSR
-	6947		1682	
	/		1007	TSVSTIPRGLASARPOSRSWRCCPVWRRSPGRARGRGLKMLNVP
		}		SQSFPAPRSQQRVASGGRSKVPLKQGRSLMDWIRLTKSGKDLTG
	,]	, ,		LKGRLIEVTERELKKHNKKDDCWICIRGFVYNVSPYMEYHPGGE
				DELMRAAGSDGTELFDQVHRWVNYESMLKECLVGRMAIKPAVLK
	ļ			DYREEEKKVLNGMLPKSQVTDTLAKEGPSYPSYDWFQTDSLVTI
1		}		/EHIY*TEGYQFRLNNS*SSE*FLYSRNNY*GLLISYTYW/R*A
	1	}		MRFRKIFLCGL/CESVGKIEIVLQKKENTSWDFLGHPLKNHNSL
1	1	ł		IPRKDTGLYYRKCQLISKEDVTHDTRLFCLMLPPSTHLQVPIGQ
1		ļ		HVYLKLPITGTEIVKPYTPVSGSLLSEFKEPVLPNNKYIYFLIK
		1		IYPTGLFTPELDRLQIGDFVSVSSPEGNFKISKFQELEDLFLLA
		1		AGTGFTPMVKILNYALTDIPSLRKVKLMFFNKTEDDIIWRSQLE
	1	. 1	ļ	KLAFKDKRLDVEFVLSAPISEWNGKQGHISPALLSEFLKRNLDK
İ		i		SKVLVCICGPVPFTEQGVRLLHDLNFSKNEIHSFTA
\vdash	6948	104	58	PDGAHSFFPDEYFTCSSLCLSCGVGCKKSMNHGKEGVPHEAKSR
	-			CRYSHQYDNRVYTCKACYERGEEVSVVPKTSASTDSPWMGLAKY
	- 1	1		
	1			AWSGYVIECPNCGVVYRSRQYWFGNQDPVDTVVRTEIVHVWPGT
1	- 1	!		DGFLKDNNNAAQRLLDGMNFMAQSVSELSLGPTKAVTSWLTDQI
1	ļ	ļ	ļ	APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGEGFCDSCSSK
	ł	j		TRPVPERGWGPAPVRVCDNCYEAR/TRPVSCYRGTSGR*RRRRT
\vdash				QETVB
	6949	152	4656	GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGGGGGKIRTRRCH
L				QGPIKPYQQGRQQHQGILSRVTESVKNIVPGWLQRYFNKNEDVC

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
"""	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i 'l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
:	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Podrettos	\-possible nucleotide insertion)
		· · 	SCSTDTSEVPRWPENKEDHLVYADEESSNITDGRITPEPAVSNT
1 1			PERCETTOTA CT/ VEDUC TRUCK MOUNT AND A SOCIETY CONTROL OF THE CT/ VEDUC TRUCK AND A SOCIETY CONTROL OF THE CT/
1			BEPSTTSTAST\YPDVLTRVSLYRSHLNFSMLESPALHCQPSTS SAFPIGSSGFSLVKEIKDSTSOHDDDNISTTSGFSSRASDKDIT
1 1			
1			VSKNTSLPPLWSPEAERSHSLSQHTATSSKKPAFNLSAFGTLSP
1			SLGNSSILKTSQLGDSPFYPGKTTYGGAAAAVRQSKLRNTPYQA
1 1			PVRRQMKAKQLSAQSYGVTSSTARRILQSLEKMSSPLADAKRIP
1			SIVSSPLNSPLDRSGIDITDFQAKREKVDSQYPPVQRLMTPKPV
1 [SIATNRSVYFKPSLTPSGEFRKTNQRIDKKCSTGYEKNMTPGQN
]			REQRESGFSYPNFSLPAANGLSSGVGGGGGKMRRERHAFVASKP
j		•	LEEEEMEGPVLPKISLPITSSSLPTFNFSSPEITTSSPSPINSS
1			QALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF SVPVAKTABLSGSSSTLEPIISSSAHHVTTVNSTNCKKTPPEDC
1			
]			EGPFRPAEILKEGSVLDILKSPGFASPKIDSVAAQPTATSPVVY TRPAISSFSSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC
[ļ		ON A MET COMPANY CONTRACTOR OF COMPANY CONTR
	j		QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET
1 1			MTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC
1			VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC
]			ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS
1 1	: 1		SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP
			MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL
j			SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR
			VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA
1 1			TKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGEG
[]			KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE
			SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS
1 1		,	AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST
			SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG
	. '		ATTTSSSAGSSFVFGTGPSAPSASPAFGANQTPTFGQSQGASQP
1			NPPGFGSISSSTALFPTGSQPAPPTFGTVSSSSQPPVFGQQPSQ
ļ [SAFGSGTTPNSSSAFQFGSSTTNFNFTNNSPSGVFTFGANSSTP
1			AASAQPSGSGGPPFNQSPAAFTVGSNGKNVFSSSGTSFSGRKIK
į į	1		TAVRRRK
6950	2585	411	PRPGSRSGLCRRAGERGAVRAGGLSRRTRAE*IMDELHYODTDS
	-555	744	DVPEQRDSKCKVKWTHEEDEQLRALVRQFGQQDWKFLASHPPNR
[TDQQCQYRWLRVLNPDLVKGPWTKEEDQKVIELVKKYGTKOWTL
i E	ł	ſ	IAKHLKGRLGKQCRERWHNHLNPEVKKSCWTEEEDRIICEAHKV
l Í	•		LGNRWAEIAKMLPGRTDNAVKNHWNSTIKRKVDTGGFLSESKDC
į į	I		KPPVYLLLELEDKDGLQSAQPTEGQGSLLTNWPSVPPTIKEEEN
1	. !		SEEELAAATTSKEQEPIGTDLDAVRTPEPLEEFPKREDQEGSPP
į l			ETSLPYKWVVEAANLLIPAVGSSLSEALDLIESDPDAWCDLSKF
ı l			DLPEEPSAEDSINNSLVQLQASHQQQVLPPRQPSA\LVPSVTEY
ı İ			RLDGHTISDLSRSSRGELIPISPSTEVGGSGIGTPPSVLKRQRK
, 1		j	RRVALSPVTENSTSLSFLDSCNSLTPKSTPVKTLPFSPSQFLNF
[[1	WNKQDTLELESPSLTSTPVCSQKVVVTTPLHRDKTPLHQKHAAF
. 1	1		VTPDQKYSMDNTPHTPTPFKNALEKYGPLKPLPQTPHLEEDLKE
			VLRSEAGIELIIEDDIRPEKQKRKPGLRRSPIKKVRKSLALDIV
			DEDMKLMMSTLPKSLSLPTTAPSNSSSLTLSGIKEDNSLLNQGF
ļ			LQAKPEKAAVAQKPRSHFTTPAPMSSAWKTVACGGTRDQLFMQE
į.		ĺ	LQAKPEKAAVAQKPRSHFTTPAPMSSAWKTVACGGTRDQLFMQE KARQLLGRLKPSHTSRTLILS
6951	1940	239	
	1740	433	AGPDDTMKRSLQALYCQLLSFLLTLALTEALAFATQEPSPRESL
1			QVLPSGTPPGTMVTAPHSSTRHTSVVMLTPNPDGPPSQAAAPMA TPTPRAEGHPPT\TPSPPSLRQ*PPPILKAP/SSTGPAPAAMAT
1		1	
		ı	
		ľ	TSSKPEGRPRGQAAPTILLTKPPGATSRPTTAPPRTTTRRPPRP

	T =		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TVPSNTSWAPTTTSLGPAKDKPGLRRAAQGGGSTFTSQGGTPDA
		ľ	TAASGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCYP\CT
	}		SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTTPQAP
ļ			THPSRVSESTISGAKEETVA\PSP*PTGCPVLSPQWYPQPQAIS
			STAWSPPGPGSLGQQGTSPMWPRGTNRSTEPPSA*ARWISPG*S
1			WPSACPSPP\LCPADGVLHEEEEEDRQPGEQPEAYGNNTHHPGT
1			TFQQAC\RGAAPGEIPVPLKPLRTQLSEPRSPANGDYRDTGMVP
			С
6952	658	304	PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE
			PTPRLVLLLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT
6953	15.5		ASRQARGELRLCLTTAVRGTSPSVSPVCQSS
0953	1512	349	NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES
1 .			FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
			PLLELCQCPLCQLDCGSREQLIAHVYQHTAAVVSAKSYM\CPVC
			GRALSSPGSLGRHLLIHSEDQRSNCAVCGARFTSHATFNSEKLP
		,	EVLNMESLPTVHNEGPSSAEGKDIAFSPPVYPAGILLVCNNCAA
1			YRKLLEAQTPSVRKWALRRQNEPLEVRLQRLERERTAKKSRRDN
ł ,			ETPEEREVRRMRDREAKRLQRMQETDEQRARRLQRDREAMRLKR
			AIETPEKRQARLIREREAKRLKRRLEKMDMMLRAQFGQDPSAMA
6954	010		ALAAEMNFFQLPVSGVELDSQLLGKMAFEEQNSSSLH
0954	819	1	PPPPFIIPSHPREAGT*AG*KRSGDSECSPPVEQ*A*TRAAAQN
			*PQR*RWTEGNSPQASAVATPGQGASPAAPRCTP*PSRRHRRLP
İ			PGARPPAG*AAPAPTKPWLAGPASAPQPGAAPLSPPAPPLIRTR
			*CAGAAARGRPRRDRSPRPRTPGGCSWSEPRTPPAVSASAQTPS
	,		DAG*AGGR*GQRQRPSTGR*PPGVGGAGRSHRREGTIPGNPHPR
			AS*RAGWQR*PGP/REWGL*EPQGEEMSGPGGPGGAPPNQVGSS
6955	1968	782	VMQAMSTGI
0000	1300	782	PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRRARRTMPFLGQD
1'			WRSPGWSWIKTEDGWKRCESCSQKLERENNHCNISHSIILNSED
1 . [GEIFNNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKESTK
	· 🔅		ERHGYCTLGEAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLTS
1 1			LSGVAQKNYFNILDKIVQKVLDDHHNPRLIKDLLQDLSSTLCIL
]			/N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\NG
1			LTLSDLPLHMLNNILYRFSDGWDIITLGQVTPTLYMLSEDRQLW
	,		KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAKEQY GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLFK
			GDILMFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLFK
6956	8605	3839	QTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQSS
1			DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAAS
1 1			PEISPEVCPAASTVVSPAVFSVVSPASSAVLPAVSLEVPLTASV
			TSPKASPVTSPAAAFPTASPANKDVSSFLETTADVEEITGEGLT
			ASGSGDVMRRRIATPEEVRLPLQHGWRREVRIKKGSHRWQGETW
	ļ		YYGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMPVGDFF
1			EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKEV
1 1	•		PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAKI
[]	1		AKSKKKMRQKVQRGECQTTIQGQARNKRKQETKSLKQKEAKKKS
1	1		KAEKEKGKTKQEKLKEKVKREKKEKVKMKEKEEVTKAKPACKAD
1 1	1		KTLATQRRLEERQRQQMILEEMKKPTEDMCLTDHQPLPDFSRVP
; l			GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLQEGL
			LCQGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSEI
1	ŀ		PLTRDNVSEILRCFLMAYGVEPALCDRLRTQPFQAQPPQQKAAV
, !			LAFLVHELNGSTLIINEIDKTLESMSSYRKNKWIVEGRLRRLKT
;		İ	VLAKRIGRSEVEMEGPEECLGRRRSSRIMEVISGMEEEEEEESI
j			AAVPGRRGRRDGEVDATASSIPELERQIEKLSKRQLFFRKKLLH
]]	ļ		SSQMLRAVSLGQDRYRRRYWVLPYLAGIFVEGTEGNLVPEEVIK
	J		KETDSLKVAAHASLNPALFSMKMELAGSNTTASSPARARGRPRK
└── <u></u>	L	[

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence		\=possible nucleotide insertion)
			TKPGSMQPRHLKSPVRGQDSEQPQAQLQPEAQLHAPAQPQPQLQ
			LQLQSHKGFLEQEGSPLSLGQSQHDLSQSAFLSWLSQTQSHSSL
ŀ			LSSSVLTPDSSPGKLDPAPSQPPEEPEPDEAESSPDPQALWFNI
	:		SAQMPCNAAPTPPPAVSEDQPTPSPQQLASSKPMNRPSAANPCS
			PVQFSSTPLAGLAPKRRAGDPGEMPQSPTGLGQPKRRGRPPSKF
	1		FKQMEQRYLTQLTAQPVPPEMCSGWWWIRDPEMLDAMLKALHPR
1			GIREKALHKHLNKHRDFLQEVCLRPSADPIFEPRQLPAFQEGIM
			SWSPKEKTYETDLAVLQWVEELEQRVIMSDLQIRGWTCPSPDST
1			REDLAYCEHLSDSQEDITWRGRGREGLAPQRKTTNPLDLAVMRL
			AALEQNVERRYLREPLWPTHEVVLEKALLSTPNGAPEGTTTEIS
			YEITPRIRVWRQTLERCRSAAQVCLCLGQLERSIAWEKSVNKVT
1			CLVCRKGDNDEFLLLCDGCDRGCHIYCHRPKMEAVPEGDWFCTV
1			CLAQQVEGEFTQKPGFPKRGQKRKSGYSLNFSEGDGRRRRVLLR
1	[· · · · · · · · · · · · · · · · · · ·		GRESPAAGPRYSEEGLSPSKRRRLSMRNHHSDLTFCEIILMEME
1	·		SHDAAWPFLEPVNPRLVSGYRRIIKNPMDFSTMRERLLRGGYTS
	١.	•	SEEFAADALLVFDNCQTFNEDDSEVGKAGHIMRRFFE\SRWEEF
1	1		YQGKQGQSVRQGRWGVTLWHLPPTFQTKTCHFHLLMLPWVQTQV
L			RYNPDF
6957	82	3514	HLIVAMPEPTKKEENEVPAPAPPPEEPSKEKEAGTTPAKDWTLV
1			ETPPGEEQAKQNANSQLSILFIEKPQGGTVKVGEDITFIAKVKA
l			EDLSEKPTINGSRKWMDLASKAGKHLQLKETFERHSRVYTFEMQ
		•	IIKAKDNFAGNYRCEVTYKDKFDSCSFDLEVHESTGTTPNIDIR
}]		SAFKRSGEGQEDAGELDFSGLLKRREVKQQEEEPQVDVWELLKN*
			TKPSEYEKIAFQYESPTCSGMLKRLKRSIREEKKSAAFAKILDP
			VYQVDKGGRVRFVVELADPKLEVKWNKNGQELRPSTKYIFEDTR
		•	CQSILNIDNCQMTDDSEYYVTAGDEKCSTELLVREPPIMVTKQL
	·		EDTTDYCGERVELECEVSEDDAQVKWFKNGEEIILVQTRYRIRV
			EGKKHILIIEGATKADAADYSVMTTGGQSSAKLSVDLKPLKILT
1		:	PLTDQTVNLGKEICLKCEISENIPGKWTKNGLPVQESDRLKVVH
1			KGRIHKLVIDHALTEDEGDYVFAPDAYNVTLPAKVHVIDPPKII
ļ	• •		LDGLDADNTVTVIAGNKLRLEIPISGEPPPKAMWSRGDKAIMEG
i .	:		SGRIRTESYPDSSTLVIDIAERDDSGVYHINLKNEAGRAHASIK
			VKVVDFPDPPVAPTVTEVGDDWCIMNWEPPAYDGGSPILGYFIE
			RKKKQSSRWMRLNFDLCKETTFEPKKMIEGVAYEVRIPAVNA\I
1 1	:		GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI
.	:.		GAAGLDGYVLEYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKD
			LIDKTKFTITGLPTDAKIFVRVKAVNAAGASEPKYYSQPILVKE
1 1			IIEPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPELTWKKD
; I			GAEIDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVE
) I			TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT
; !		,	GYTIQKADKKSMEWLRVIEHIIEPVPHTELVIGNEYYFRVFSEN MCGLSFDATMTVFSAULABDCVIVVNDUVEDBDESEADMETODI
1	1		MCGLSEDATMTKESAVIARDGKIYKNPVYEDFDFSEAPMFTQPL VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMFS
			NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ
6958	274	1663	PRTSRVKTEGSOGSSAMDFSVKVDIEKEVTCPICLELLTBPLSL
""	.	T002	DCGHSFCQACITAKIKESVIISRGESSCPVCQTRFQPGNLRPNR
[HLANIVERVKEVKMSPQEGQKRDVCEHHGKKLQIFCKEDGKVIC
1	l	İ	WVCELSQEHQGHQTFRINEVVKECQEKLQVALQRLIKENQEAEK
]		ļ	
]	!		LEDDIRQERTAWKNYIQIBRQKILKGFNEMRVILDNEEQRBLQK
1 1	1	ł	LEEGEVNVLDNLAAATDQLVQQRQDASTLISDLQRRLRGSSVEM
	Í		LQDVIDVMKRSESWTLKKPKSVSKKLKSVFRVPDLSGMLQVLKE
]		1	LTDVQYYWVDVMLNPGSATSNVAISVDQRQVKTVRTCTFKNSNP
1 1	ł		CDFSAFGVFGCQYFSSGKYYWEVDVSGKIAWILGVHSKISSLNK RKSSGFAFDPSVNYSKVYSRYRPQYGYWVIGLQNTCEYNAFEDS
			SSSDPKVLTLFMAV\LPVVLGFS
		1	COODE VALUE LIVA /DEA ADOLO
6959	1	1469	SLVHVVEFGRGIEDFPYLFFQLTHCQQRICSVTQAGVQWCDHSS

Second Predicted Predicted Predicted Predicted Predicted Predicted Prediction Despiration Academy partic Acid, Be Contrasponding Corresponding Cofficial Company Corresponding Cofficial Company	SEQ	Predicted		
Docation Corresponding			Predicted end	Amino acid segment containing signal peptide
Cortasponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence PPPClime, O=Glutamine, R=Arginine, PPPClime, O=Glutamine, R=Arginine, PPPClime, V=V=V=V=V=V=V=V=V=V=V=V=V=V=V=V=V=V=V=				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
to first amino acid residue of amino acid residue of amino acid sequence Perfoline, Q-Goltumaine, R-Arginine, S-Serine, T-Threonine, V-Valine, S-Serine, T-Threonine, V-Valine, S-Serine, T-Threonine, V-Valine, W-TryPtophan, Y-Tyrosine, Y-Wolknown, *-Stop Codon, /-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide for the transport of the transport of the transport of the transport of the transport of the transport of the transport of the transport of the transport of the transport of the transport of the transport of the transport of the transport of transport of the transport of transport of the transport of tr	l NO:			Grucamic Acid, r=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid amino acid sequence #Tryptophan, Y=Tyxosine, X=Unknown, *=stop coden, /=possible nucleotide deletion, \possible nucleotide insertion) Loportgonosynthylantizethylanderpy				n=nistidine, l=isoleucine, K=Lysine,
### amino acid residue of amino acid sequence ###				Debuggine, Memethionine, Neasparagine,
mino acid sequence W-Tryptopham, Y-Trytocine, X-Unknown, *-stop Coden, /-possible nucleotide deletion, Coden, /-possible nucleotide deletion, Coden, /-possible nucleotide deletion, Coden, /-possible nucleotide insertion) IOPOTEMINSSHIELLISSEDYMENGETERIPEDEVE WTELEDROGRYTPHPODLLAALFILLIVALIAMRLAFERFIGLPLS RNIGVEDOTRROVENDATION ROUTE ROUTE THOUTON ROUTE ROUTE ROUTE THOUTON ROUTE ROUTE ROUTE THOUTON ROUTE ROUTE ROUTE HPVAVILMITES VSANILLE (SENVILLED SENVILLE COMMING YOU COLAF LIFSEY PITRIVILET FOIL INTITYSES ISSEME HPVAVILMITES VSANILLE (SENVILLED SENVILLE COMMING YOU COLAF LIFSEY PITRIVILET FOIL INTITYSES ISSEME HITTAT AKKARKEMOEP TRSF RGEPDLSTLTHS IVERRYLABGES HILPERKOALKRUVEES ROUTE KEENPRA SKANESS SERSE (SEGNIL PAGGES SEREEKE YERGK KEENPRA SKANESS SERSE (SEGNIL PAGGES SEREEKE YERGK KEENPRA SKANESS SERSE (SEGNIL PAGGES SEREEKE YERGK KORKMALIST SEEDS LEREWED SERSE ALE PURT PARK YENDER KEENPRA SKANESS SERSE SEREE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SKANESS SERSE SERSE PURT REVENDER KEENPRA SERSE SERSE SERSE PURT REVENDER KEENPRA SERSE SERSE SERSE PURT REVENDER KEENPRA SERSE SERSE SERSE PURT REVENDER KEENPRA SERSE SERSE SERSE PURT REVENDER KEENPRA SERSE SERSE SERSE PURT REVENDER KEENPRA SERSE SERSE SERSE PURT REVENDER KEENPRA SERSE SE				
### sequence Codon, /-possible nucleotide deletion,		I	1	
Appossible nucleotide insertion		1	1	w=Tryptopnan, Y=Tyrosine, X=Unknown, *=Stop
### ILDERORGEVIPHODILAALPLATVILAMINISTREPTICIPLE ### WITHERDRORGEVIPHODILAALPLATVILAMINISTREPTICIPLE ### ### ### ### ### ### ### ### ### ##			sequence	codon, /=possible nucleotide deletion,
### WISLEDRIGKYPHFOOLLALALPLALVILLAMEAPERFIGLES RHIGHVENDTRICKYRNATIKEHFITGERPRERGISLADAQCOL TILOQTORM PERRENGDERQLITKECCRASMERLEYIS.SETYCGISL LYHESSULAPWORD YROCTILECARDSERA LYHWYLLEUS LYHESSULAPWORD YROCTILECARDSERA LYHWYLLEUS LYHESSULAPWORD YROCTILECARDSERA LYHWYLLEUS PYLSLLI ELPPOVERKOGGS SI KEPPHYDPPETA \ \text{PYKSQVIH} HFVAVILMTPSYSARLLRIGSLVLLHDSSDYLLEACKWYRWIGH YQUCCALFILESSYPTTRIVEFTOLLTITYTESISREGFF GYYFFRGLIALLQLIAUFFSYSARTUFFTOLLTITYTESISREGFF GYYFFRGLIALLQLIAUFFSYSARTUFFTOLLTITYTESISREGFF GYYFFRGLIALLQLIAUFFSYSARTUFFTOLLTITYTESISREGFF GYYFFRGLIALLQLIAUFFSYSARTUFFTOLLTITYTESISREGFF GYYFFRGLIALLQLIAUFFSYSARTUFFTOLLTITYTESISREGFF GYYFFRGLIALLQLIAUFFSYSARTUFFTOLLTITYTSYRKGQMSKOITSKORTH RHTTAT RHTTAT ### CARRY CONTROL OF THE PROPERTY OF THE PROPE		sequence	<u> </u>	
RNIGVREDUTRGVRPNATILEKHFLTGGREPKEPGISLLANGGE TIQQTGREPKRENGDERGASWEPKETSSFVGGLSV LYHESNLANDVMCDREYBOLTLSCRANGERGES LYWWTLLIS EYLSLLILELPEVENKGOGPS LYKPWTLLIS FYLSLLILELPEVENKGOGPS LYKPWTLLIS FYLSLLILELPEVENKGOGPS LYKPWTLLIS HPVAVILHTESYSANLLRIGSLVALLHDSSDYLLEACKWYNYM VQCVCALFLIESPYPYTRILLPPOLITYTTYSKREGPF GYYFRIGLIMLLQLIHTYRSCLILRAILSYPKKGQMKKDIESDY LESDSSERARAGEPLQLKNGTAGGPPRAPTDGPRERVAGRITN RHTTNT 6960 387 2068 AKRARERMGEP\TRSPF\KGRPDLSTLTHSIVRRYLAHSGRS HLEPERGALKALVEREPLKWQVDRAASREBKLDITKKKREPF PCSDEFRREFRENSESSESSERSSFDYFGFPAKNOVASKSHTHEN KENPERA\SKAVESSBEEKGVARESBEEKGVKKK TRKEVVKKOAGKASVSKKGARESBESSERSDPVGFPAKNOVASKSHTHEN KENPERA\SKAVESSBEEKGVARESBESSERGENGVKKKK TRKEVVKKOAGKASVSKKGARESBESSERGENGVKKKK KGTKSLKSSSGSSERSELLAQKKGCARESBESSERGENGVKKK KGTKSLKSSGSSESSESSELSLAQKKGCARESBESSERGENGVKKK FRESSMASSIGSSBEDLEGENGENEWEERERSENGDK PRTESNIGBRESAREERSCKGAKGAKELGSSEDEBGKGBFSTA KGSRKMAALGSTGGESDLEREVSDERAGGPGGERKINESKENG SRKMAALGSTGGESDLEREVSDERAGGPRGGERKINESKENG KGSRKMAALGSTGGESDLEREVSDERAGGPGGGERKINESKENG KGSRKMAALGSTGGESDLEREVSDERAGGPGGGERKINESKENG KGSRKMAALGSTGGESDLEREVSDERAGGPGGGERKINESKENG KGSRKMAALGSTGGESDLEREVSDERAGGPGGGERKINESKENG KGSRKMAALGSTGGESDLEREVSDERAGGPGGGERKINESKENG KGSRKMAALGSTGGESDLEREVSDERAGGPRGGATHRICKSTYL ACQHIENTKILLGSCCHKERLSI LEABLEALGMKGTPSLGCK ALKGGERAAEVAGLOVANI TIGGGSPRRTATAMPHGEAAPPGG LYRRTLDSDERRPRAP POWSHINGI I SSDGESN FORSSPITKANTELLE I STINLICKGI FYLLSEKBAGRMRRIGGFL LYRRTLDSDERRPRAP POWSHINGI I SLOGESN LYRRTLDSDERRPRAP POWSHINGI I SLOGESN LYRRTLDSDERRPRAP POWSHINGI I SLOGESN THE STATEMPH THE ST				
LYHESHUAND/MCDRYPNOLITISCPADABRA/SLYWWILELD LYHESHUAND/MCDRYPNOLITISCPADABRA/SLYWWILELD PYLSILIRLPPDVKRKGGGSSIKPRPHYPPSTANDPKCQUTH HFVAVILMFSYSANLLENSGYLLLUSSGYLLLUSACKYNYMG YQQVCDALFLIPSFVFFYRLVLFPTQILYTTYRSISNRGFF GYYFPROLIMILQLLHYPROCILIAMINSFMKKCGMEKNIRSDY EESDSSERAAAQBELQLIKNGGGFRAPTDGFRSKVAGRINTS GYYEPROLIMILQLLHYPROCILIAMINSFMKKCGMEKNIRSDY EESDSSERAAAQBELQLIKNGGGFRAPTDGFRSKVAGRINTS RHTTAT 6960 387 2068 AKWARKEKMGEPYTRSFF\RGRPDLSTLTHSIVRRFYLAHSGRS HLEPBEKQALKRIVEEEPLKMQVDEAASREDKLDLTKKKKRPPT PCSDSPRKRFFRYNSSESSESSEASSDYTGPGAVAGRSISTHTE KENPRRA\SKAVESSSDERRQNLPAQRGEESSSEBEEKGYKGK KOKSLKESGOSEBELLAQKKEQREBEKSEBEEKGHAK KOTKSLKESGOSEBELLAQKKEQREBEKSEBEEKGHKKK KOTKSLKESGOSEBELLAQKKEQREBEKSEBEEKGHNK PRTRSINGRKSAABEERSGKGAAKRILGBSERNINSSKKS GRKGATRSGSSSDGSPEAKGGKASGGRROEDHPAWRILKRYIR ACGHENYALLGSCCSHKERLSILRABLEALGHKGTPSICKCR ALKEGREBAABVASLDVANI IGGGGRRRATHAWFLIGRAPPGG ALKEGREBAABVASLDVANI IGGGGRRRATHAWFLIGRAPPGG ALKEGREBAABVASLDVANI IGGGGRRRATHAWFLIGRAPPGG ALKEGREBAABVASLDVANI IGGGGRRRATHAWFLIGRAPPGG ALKEGREBAABVASLDVANI IGGGGRRRATHAWFLIGRAPPGG ALKEGREBAABVASLDVANI IGGGGRRATHAWFLIGRAPPGG ALKEGREBAABVASLDVANI IGGGGRRATHAWFLIGRAPPGGF ALKEGREBAABVASLDVANI IGGGGRRATHAWFLIGRAPPGGF ALKEGREBAABVASLDVANI IGGGGRRATHAWFLIGRAPPGGF ALKEGREBAABVASLDVANI IGGGGRRATHAWFLIGRAPPGGF ALKEGREBAABVASLDVANI IGGGGRRATHAWFLIGRAPPGGF ALKEGREBAABVASLDVANI IGGGGRRATHAWFLIGRAPPGGF ALKEGREBAABVASLDVANI IGGGGRRATHAWFLIGRAPPGGF ALKEGREBAABVASLDVANI IGGGGRRATHAWFLIGRAPPGGF ALKEGREBAABVASLDVANI IGGGGRRATHAWFLIGRAPPGF ANDVLLCOLLINMIPEDLICLKENTGLHDAYACAGGFISTSCKSFET TTGPPHRATPISDHEALMATTPYNGGVIYALAVAGGFYISCKSFET TTGPPHRATPISDHEALMATTPYNGGVIYALAVAGGFYISCKSFET TTGFPHRATPISDHEALMATTPYNGGVIYALAVAGGFYISCKSFET TTGFPHRATPISDHEALMATTPYNGHOPPGGKANGGFBCHEN ADVVLLCOLLINMIPEDLIGCCLLKENTGLHDAYACRYDIFHOGENG ADVVLLCOLLINMIPEDLIGCCLLKENTGLHDAYACRYDIFHOGENG ADVVLLCOLLINMIPEDLIGGCCLLKENTGHDAYACRYDIFHOGENG ADVVLLCOLLINMIPEDLIGGCCLLKENTGHDAYACRYDIFHOGENG ADVVLLCOLLINMIPEDLIGGCCLLKENTGHDAYACRYGGGEB ADVVLLCOLLINGRARGADOPEOQUALLYANGAGGFI ADAVCLCAGAGGGRAATLLWTTSVGLOWA				
LYHESHUADPUNCHORDYS IKRPENTPED KATA ÞEKDUTH PYLSLILILIPDVIKRIGGISS IKRPENTPED KATA ÞEKDUTH HFVAVILIMTPSYSANLILIGSLVILLHOSDYILIBACKMINYM YQOVCDALFLITSPYFYTRIVLFTGILTTYYTES SIRREFF GYYFTRGLIMLIGLHVFWSCILIBMINSTRKKGMEKKOIRKNINSDY LESDSSEBRAAAGBELGUKNGTAGGRPAPTTOGRSRVAGKINN HITTAT AKMARKKMÖEP YTRSFF\KGRPBLSTLTHSIVRRYNLAHSGRS HLEPBEKQALKRIVSEBELMKOVDBAASREDALDITKKKKRPPT PCSDPERKIFTRYSBSSIGSEASSPUYGPPAKNGVASKSHTHE KEENPRAJ SKAVAESSDEERGROPLÞAGNGESBEERGKYKKEGN KGTKSLKESSGSEBELLAKKKORDEREVEEBEEKGYKK KGTKSLKESSGSEBELLAKKKORDEREVEEBEEKGYKK KGTKSLKESSGSEBELLAKKKORDEREVEEBEEKGYKK KGTKSLKESSGSEBELLAKKKORDEREVEEBEEKGYKK KGTKSLKESSGSEBELLAKKKORDEREVEEBEEKGYKK KGTKSLKESSGSEBELLAKKORDEREVEEBEEKGYKK KGTKSLKESSGSEBELLAKKORDEREVEEBEEKGYKK KGTKSLKESSGSEBELLAKKORDEREVEEBBEKGORK PRTESNGRRKSADERBSCKKASGKRRGBDHPAWRIKKYIK ACGAHRINKKLIKSCCSKREKESILIABEELAGHKGTFSLKKCH ALKGGRBAAEVASLDVANIISGSGRRRGBDHPAWRIKKYIK ACGAHRINKKLIKSCCSKREKESILIABEELAGHKGTFSLKKCH ALKGGRBAAEVASLDVANIISGSGRRRGBDHPAWRIKKYIK KGSRKABLISSTSGBEBLERSFIRGITSGSGE LYKRTLDSDEERPRAPPONSHIKGIISSEBERGKAGSKRGBDHPAWRIKKYIK ACGAHRINKKLIKSCCSKREKESILIABEELAGHKGTFSLGKKCH ALKGGRBAAEVASLDVANIISGSGRRRGBDHPAWRIKKYIK ALKGGRBAAEVASLDVANIITSGSGRRRGBDHPAWRIKKYIK ALKGGRRAALDVANIITSGSGRRRGBDHPAWRIKKYIK ALKGGRRAALDVANIITSGSGRRRGBDHPAWRIKKYIK ALKGGRRAALDVANIITSGSGRRRGBDHPAWRIKKYIK ALKGGRRAALDVANIITSGSGRRRGBDHPAWRIKKYIK ALKGGRRAALDVANIITSGSGRRRGBDHPAWRIKKYIK ALKGRRAALDSGLGCLLKERTGALHATAANTAATHEOPTSGSBG NTWYKKNCYVSQGLKPPFPFGVRIDTVALHAVAGFYILFHVQEWNG LYPAGABELQIVITLIKARGAGAGAAALLAHL LALLCULAAGGGGBAAILLIMTPSVGLUVAAGAFYLFHVQEWNG LYPAGABELQIVITLIKARGAGAPYLFHVQEWNG MYMPKNCYVSQGELKPPPFGVRIDTVALLVAAVSGFYISCKSPET TTGFDPHRGTPLSDHBALMATLFVRHSPFQONBSGRAGLIVHH. SGWILMAVYHLLHBEVNGOLDTYALRAVAGAFYLFHVQEWNG LYPAGABELQIVITLINGGRRAALDLAFTYNGHTYSKILAAGAG ADVVLLCCGLIMBPFGLLARITFILARDRINGTSCDLICGSSAKGEICHLIN LHIPSNYLETILBGRRINGHFFOUTVERHSPRGSBGGSARGES PFPQBKLLLTYBORGBFCOUTVERHSGRAGGLIVHL LALLCULAAGGGGRBAAILLMTPSVGIVLMAGAFYLFHVQEWNG LYPAGABELQIVITLARRARGADDEPGQLAALLACGMGGGB PFPGDKLLLTYGRRGRGFCOUTVERHSGRSGRAFTENSE TTGFG	1			1
FYLSLLIRLPDVKRKGGGFSSIKPRPHYDPSTAN)DFKEQUTE HPFVAVILHTSYSANILLRIGSKULLLHUSSYLLVLKHOSDKEKKWYNYKG YQQVCDAFFLTSFFYFTRLUFFTOLINTTYYESISNEGPFF GYYFPRGLIMLLQLLHVFNSCLILRMLYSFMKKGCMKKINSDV EESDSSERAAAGBELQLKNGTAGGPRPAFTDGFRSVAGRLITN RHTTAT 6960 387 2068 AKWARRKEMEPYTRSFFYRGRPDLSTLTHSIVRREYLAHSGRS HLEPBEKQALKRIVZBEFLKMQVDEAASREDKLDLTKKGKRPPT PCSDFBRKRFPRSSBSSGSEASSFDVFGPAGNASSKITH KENPFRA SKAVESSDEERGRDLPAGRGESSEREERGYKGK TRKKPUVKLOADCKASVSTRKOARESSBEEREGYKGK KGTKSLKSSBOSEGEBILAQKKSQREBEVEEEKEEDEERGDKK PRTRSNGRRESAREERSCKQKSQAKGLLGDSDSEERGKSAASGG DDSGRREPPYQRKSSENTGLKGGKLSGSSEDEDBOGGGPTAKVEGK KGTKSLKSSBOSEGEBILAQKKSQREBEVEEEKEEDEERGDKK PRTRSNGRRESAREERSCKQKSQAKGLLGDSDSEERGKGRASGG KGSRKNAALGSTSGEEBDLERVSDSEAGGGPQGERKNIKK KGSRKNAALGSTSGEEBDLERVSDSEAGGGPQGERKNIKK RGSRKNAALGSTSGEEBDLERVSDSEAGGGPQGERKNIKK ACGAHRNYKKLIGSCCSHKERLSILRAELAGHKGTPSLGKCK ALKGGRERAAPSSDLOWANI ISGGRPRRTAMPLGEAPPGG LYRRTLDSDEERRPRAP DDMSINNGI ISSGGPRRRTAMPLGAPT ACGAHRNYKKLIGSCCSHKERLSILRAELAGHKGTPSLGKCK ALKGGRERAAPSSDLOWANI ISGGRPRRTAMPLGAPTHEAGA LCVFSKHPIQELTQHITTLINGVETPHIHHDWSGKAVGLIVHL SGMVLANVHLHABYNNGQUITJAHRVAQAMELAGFHHTSK ADVVLLCODLNMIPBDLGCCLLKENTGHADALTSTROFTGSSEG NTWYRNCYUSQCELKP PFFGVILTYLVLKVASGFYISCKSFET TTGFPPHRGTFLSDHEALMATLFVRHSPFQGNPSSTHGP\AGRS PL/MCVLKKABLDGSLGGMA/ARMWAITFAVSGFYISCKSFET TTGFPPHRGTFLSDHEALMATLFVRHSPFQGNPSSTHGP\AGRS PL/MCVLKABLDGSLGGMA/ARMWAITFAVSGRSKAGGRAFALLWTSKAGAPYLEHVDSVMG LYRAQABLGVHLGRRAEADGLGFPBOLYALLVAGAPYLEHVDSVMG LYRAQABLGVHLGRRAEADGLGFBFDLYALLVAGAPYLEHVDSVMG LYRAQABLGVHLGRRAEADGLGFBFDLYALLVAGAPYLEHVDSVMG LYRAQABLGVHLGRRAEADGLGFBPDLYALLVAGAPYLEHVDSVMG LYRAQABLGVHLGRRAEADGLGFBDLYALLVAGAPYLEHVDSVMG LYRAQABLGVHLGRRAEADGLGFBOLYALLVAGAPYLEHVDSVMG LYRAQABLGVHLGRRAEADGLGFBOLYALLVAGAPYLEHVDSVMG LYRAQABLGVHLGRRAEADGLGFBOLYALLVAGAPYLEHVDSVMG LYRAQABLGVHLGRRAEADGLGFBOLYALLVAGAPYLEHVDSVMG LYRAQABLGVHLGRRAEADGLGFBOLYALLVAGAPYLEHVDSVMG LYRAQABLGVHLGRRAEADGLGGGGRAATLLWTSVGNOGGFGCERCTEG TTGFPHRGTTLSDHEALMATLFYNGNDTYNHHGDFGSSCANGCHALAGG PFPGOKLLGSYDS EIDSVCNOGNVFG GLOBGGDFTCG TTGFPHRGTTLSDHEALMATLFYNGNDTYNHHGDFGSGCANGCHAG	1			
HEVAULIMTESYSAMLIAEIGSLVILLIHOSDYLLEACKWYNYMG YQQVCDALFLIEPSPYPYTHLIHOPTOILTYPESISNEGEPE GYYETRIGILMALQILHVFWSCLILEMIJSFMKKGQMEKDIRSDV EESDSSEBAAAQEPLQLKNGTAGGRRPAPTDGYRGRVAGKITN HTTAT 387 2068 AKMARKKMQEPYTRSFFYKGRPDLSTLTHSIVRRRYLAHSGRS HLEPBEKQALKRIVVEEPSLIMQVDEAASREDKLDLTKKKKRYPFT PCSDERRKFFRNSSBESGSEASSDVYGPPAKNGVASRSHTHE KERNPRA\SKAVESSDEERGRODLPAQNGESBEERGKYKKVEGN KOTKSLKESSOSESERILAGKKGREERVEESBEERGYKKVEGN KOTKSLKESSOSESERILAGKKGREERVEESBEERGYKKVEGN KOTKSLKESSOSESERILAGKKGREERVEESBEERGKYKKVEGN KOTKSLKESSOSESERILAGKKGREERVEESBEERGKYKKVEGN KOTKSLKESSOSESERILAGKKGREERVEESBEERGKYKKVEGN KOTKSLKESSOSESERILAGKKGREERVEESBEERGKYKKVEGN KOTKSLKESSOSESERILAGKKGREERVEESBEGKGKRASSG RKGATRGSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRIKKYIK ACGARMYKKLLGSCCSEKERLSITLRAELEAGHKGTFSLGKCK ALKSQRERAABALGSTSGESPLERRYSDSAGGPQGFRKNRSSKKS SRKGATRGSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRIKKYIK ACGARMYKKLLGSCCSEKERLSITLRAELEAGHKGTFSLGKCK ALKSQRERAABVASLDVANIISGSGRFRRSTATAMYBLGEAAPGG LYFRTLBSDEERRPAPPONSHINGIISSGSCBLINGKTFSLGKCK ALKSQRERAABVASLDVANIISGSGRFRSTATAMYBLGEAAPGG LYFRTLBSTFFILERFRAPHNINGKISTLAGKTFSLGKKTSLGKT ALKSQRERAABVASLDVANIISGSGRFRSTTAMYBLGFALV KORSPHALLEEWWSGDPTYLARKLAGKTSTLICHTATURGTIGSC LCVFSKHPIQELTQHITYLINGYPMIHHGDWFSGKAVGLIJV-HL SGWULNAVYTHLHABYNGQUTJAHRVAQAMELAQPIHHTSKK ADVULLCODLMMIPEDLGCCLLKENTGHDAVLSTFICKSFET TTGFDPHRGTPLSDHEALMATLFVVGLUDAVLATSTFIPFGSSEG NTWYRKNCYUSQOEKKPPPGWALDVIJKAXAAGFYLIFHVQEWNG LYRAQABLQHVUGRARRAQDLOFPROHATALTTPPFGSSEG NTWYRKNCYUSQOEKKPPPGWALDVIJKAXAAGFYLIFHVQEWNG LYRAQABLQHVUGRARRAQDLOFPROHATLFTDPFGSEG NTWYRKNCYUSQOEKKPPPGWALDVIJKAXAAGFYLIFHVQEWNG LYRAQABLQHVUGRARRAQDARBAATLTFTDPFGSEG NTWYRKNCYUSQOEKKPPPGWALDVIJKAXAGGFYLISCKSFET TTGFDPHGTPLEDHEALMATLFVHNSCHGLFULLAGGGGGGGRATLLHTTSVGLUWAGAPYLIFHVGEWNG LHRSSDEKCHDINHPEDLOFCLUKRWTGHAPTYLAHTSKK ADVULLCOBLUMHPEDLOFCLUKRWTGHAPTYLAHTSKK ADVULLCOBLUMHPEDLOFCLUKRWTGHAPTYLAHTSKK ADVULLCOBLAMBPEDLOFCLUKRWTGHAPTYLAHTSKK ADVULLCOBLAMBPEDLOFCLUKRWTGHAPTYLAHTSKK ADVULLCOBLAMBPEDLOFCLUKRWTGHAPTYLAHTSKK ADVULLCOBLAMBPEDLOFCLUKRWTGHAPTYLAHTSKK ADVULLCOBLAMBPEDLOFCLUKRWTGHAPT			·	
GYPFMGLMLJQLLVPFWSCLILMLYSTYMSISMRGPF GYYFFMGLMLJQLLVPFWSCLILMLYSTYMKKGQMEKDIRSDV EESDSSEBAAAQEPIQLKNGTAGGPRAPTDGPRSRVAGRLTN RHTTAT 6960 387 2068 AKWARRKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS HLEPBEKQALKRLVBEEPLKMQVDRAASRENKLDLFKKKREPPT PCSDPERKFPFNSESSESSESSASPYDYDARGWASRSHTHE KENNPRA\SKAVESSASPYDYDPAKNGVARSHTHE KENPRA\SKAVESSASPYDYDARGWASRSHTHE KENPRA\SKAVESSASPYDYDARGWASRSHTHE KENPRA\SKAVESSASPYDYDARGWASRSHTHE KENPRA\SKAVESSASPYDYDARGWASRSHTHE KENPRA\SKAVESSASPERGREDLPAGREESSEEREKGYKKK TRKKPVVKAOAPKKASVEKOKASKASELESDVGTTAKVVEON KGTKSLKSSGCSSEBEILAGKEORSEEVEEREKEEDERKODKK PRTESNGGRKGARGSRGKOKGAGKRIGGSSEDEEDSKKGPTA KGSRNARLGSTEGBESDLEREVSDEAGGGPOGEKKADSKS SRKGRTRSSSSSGLOSP BEKKGOKGAGSGRAGDHPAMMIKRYIR ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLCKCK ALKCGEERAAVASLDVANIISGGGPPRANDFIGEAPPGE LYRRTLDSDEERPRAPPDWSHNGIISSDGESN NGSSPDLALLEEWSGOPOYLROKLSPTYPAAHHPRSGIIGSC LCVFSKHPIQEITQHIYTINGYPYMIHHDDWFSGKAVGLLVHL SGWLKAAVYTHLBABYNRQKDITLAHRVAAVABLAGPHHTISK ADVULCODLMMIPEDLGCCLLKEWTGHDAYLETREFKGSESS NTWPPRICTVSQOELEPFFFOVENDIVYLYXAVSGFYISCKSFET TTGFDPHRGTPLSDHBALMATLFVRRSPPQONESTHEP\AERS PL/MCVCLKEALDOSSIGJAMA\QARWA\TFA\SYVIGIGI\LL LALLCULAAGGGAGRAAILLMTPSVGLIVMAGAFYLFHOYENG LCVFSKHPIQEINGHLFRAEKADDLISPEDLAWALL\LQQQEGDRTKSG CLVFSKHPIQEINGHLFRAEKADDLISPEDLAWALL\LQQQEGDRTKSG ADVVLLCGDIMMIPEDLGCCLLKEWTGHDAYLETREDFKGSESS NTWPRICTVSQQELKPFFOVENDIVYLYXAVSGFYISCKSFET TTGFDPHRGTPLSDHBALMATLFVRRSPPQONESTHGP\AERS PL/MCVLKEALDOSSIGJAMA\QARWA\TFA\SYVIGIGI\LL LALLCULAAGGGAGRAAILLMTPSVOLLVHAAVASPIHHTSK ADVVLLCGBLMMIPEDLGCCLLKEWTGHDAYLETREDFKGSESS NTMVPRICTVSQQELKPFPGOVENDYVLYXAVSGFYISCKSFET TTGFDPHRGTTLSDHBALMATLFVRRSPPQONESTHGP\AERS PL/MCVLKEALDOSSIGJAMA\QARWA\TFA\SYVIGIGI\LL LALLCULAAGGGAGRAAILLMTPSVOLLVHAAYSTHGDFKSCKOCLUHH SGMVLMAYYTHLHAEVNRQNDIVALAFVARGAPATLFFROYSCKS PLYMCVLKEALDOSSIGJAMA\QARWA\TFA\SYVIGIGI\LL LALLCULAAGGGAGRAAILLHTPSVOLLVKRASSESTHGPSVARS PLYMCVLKEADLOSSIGJAMA\QARWA\TFA\SYVIGIGI\LL LALLCULAAGGGAGRAAILLHTPSVOLLVKRASSESTHGPSVARS PLYMCVLKSTTLLERPROKGHPCDVTVTRHGSMRRAGCCULAAGS PFFQOKLLIGKTSISTE TTGFTHTTRLERPROKGHPGDSVATI	1			
GYFFRIGLMILGOLLHVFWSCLILRMINS PHYKKGOMEKDIESDY EESDSSERAAAQEPIQLKKNTAGGPRAPTDGPRSPVAGRITM RHTTAT RHTTAT AKMARRKEMQEP\TRESF\RGPPLSTLTHSIVRRYLAHSGRS HLEPEEKQALKRIVEEEPLKMQVDEAASREKHTIP KEENPERA JSKAVESSDEERKGALRESEEBEKGVLLVRKKREPPT PCSDPERKRFFFNSSESGSGSASSPYFOPPARNGVASRSHTHE KEENPERA JSKAVESSDEERKGARESEBEREKGVAFAKVEER RGTYSLKSSEGSEBELLGVAKGARESEBEREKGVAFAKVEER KGTYSLKSSEGSEBELGVAKGARESEBEREKGVAK RGTYSLKSSEGSEBELGGSEBELLGVAKGARESEBEREKGVAK RGTYSLKSSEGSBEELLGAKGKGARESEBERGEVAFAKVEER RGSRKMARLGSTGGEBDLEERVSDESAGGPQGERKNESSKK SRKGRTRSSSSSDSDFPARKGGKARSGSREGDHPAWRIKKTIR ACGAHRIVKHLGSCCSHKERELSILRAELBALGMKGTPSLGKCR ALKEGREBABVASLDVANITISGGEPRRTTAMPLGBRAPPGE LYRRTLISDSDERPPPAPPBOHMBGILSGLALGMKGTPSLGKCR ALKEGREBABVASLDVANITISGGEPRRTTAMPLGBRAPPGE LYRRTLISDSDERPPPAPPBOHMBGILSGLALGMKGTPSLGKCR ALKEGREBABVASLDVANITISGGEPRRTTAMPLGBRAPPGE LYRRTLASDSERPPPAPPBOHMBGILSGLALGMKGTPSLGKCR ALKEGREBABVASLDVANITISGGEPRRTTAMPLGBRAPPGE LYRRTLASDSERPPPAPPBOHMBGILSGLALGMKGTPSLGKCR ALKEGREBABVASLDVANITISGGEPRRTTAMPLGBRAPPGE LYRRTLASDSERPPAPPBOHMBGILSGLALGMKGTPSLGKCR ALKEGREBABVASLDVANITISGGEPRRTTAMPLGGRAPPGE LYRRTLASDSERPPAPPBOHMBGILSGLALGMKGTPSLGKCR ALKEGREBABVASLDVANITISGGEPRRTTAMPLGGRAPPGE LYRRTLASDSERPPAPPBOHMBGILSGESM GSPLALLTUNSYPMHHEDDFSGKAVGLLUHL SGMVLAAVYTHILHESVINGCLILKBWTGLHDAYLETTEDFKGSEBG NTMY FRICTVSQQELKPPFFOVRIDVLYLKAVSGFYISCKSFET TTGGPBHRGTISGNHMIPEDLGCLILKBWTGLHDAYLETTEDFKGSEBG NTMY FRICTVSQQELKPPFFOVRIDVLYLKANGAPTLHHTSKK ADVVLLCGLIMMHPEDLGCCLLKBWTGLHDAYLETTEDFKGSEBG NTWYFRICTVSQQELKPPFFOVRIDVLYLKANGAPTHHTSKK ADVVLLCGLIMMHPEDLGCCLLKBWTGLHDAYLETTEDFKGSEBG NTWYFRICTVSQUEKAPPFFOVRIDVVLYKAVSGFYISCKSFET TTGFPHRGTTLGBHRAMTLVFRHSPOQUNSSERHGP\BERGE LLALLCULAAGGAGGEAAILLMTPSVGLIVKANGAPTHFHTSKK ADVVLLCGLIMMHPEDLGCCLLKBWTGLHDAYLETTEDFKGSEBG NTWYFRICTVSGUEKAPPFFOVRIDVVLYKAVSGSERHGFOLDVL LYRAQAELQHVLGRAREAQDLGPPEPQLVALL\LJCGGGGRTKEG NTWYFRICTVSGUEKAPPFFOVRIDVVLYKAVSGSERHGFOLDVL LYRAQAELGHVLGRAREAQDLGPBPGGSSAPFGGFGLAP PFFONLLLUSKRICHSPENDHMBGPSFTGTHERSGORGFYL LHARSISCHERDFYVDRONGSGERREGGEFTGGGSFTGGGGFTKEG PFFONLLLUKKRYFTAMFGGSFFFGGVSSAP				1
EESDSSERAHAAGEPLQLKNGTAGGGPRAPTDGGPRSRVAGRLITN HITTAT AKMAREKERQEF\TRSFF\KGERPLSTLTHSIVERRYLAHSGRS HLEPBEKQALKRLVEEEPLKWQVDEAAGREDKLDLTKKGKRPFT PCSDFRKRFFFNSSBSSGSSASSPDYFGPPAKNGVAGSRSHTHF KENPPRA\SKAVESSUSERGKDLDAGRGESSSEERKGYKGK TRKKPVVKAQAPCKASVSRKQARESSESBEABVQGTARKVEGN KGTKSLKSSEQSSEERILAGKKGGRAFERSEBERGYKGK KGTKSLKSSEQSSEERILAGKKGGRAFERSEBERGKYKGK PRTRSNGRYRSASEBERSCKGKSQAKELLGBDSBEERGKTKGK KGTKSLKSSSSSEDGSPOLKGGKRLGGSSEDEEDSGGRPTA KGSRKARLUSISTGGESDLEEFEVDEBEAGGOPQCERKNESSKAS DDGGRRBPPVQRKSEDRTQLKGGKRLGGSSEDEEDSGGRPTA KGSRKARLUSISTGGESDLEEFEVDEBEAGOOPQCERKNESSKAS SRKGRTRSSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIR ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTFSLKKCR ALKGREERAAVASLUVANIISGGGRPRAFMPTGGAAPPGG LYRRTLDSDEERRPAPPDMSHNGGISSDGESN NGSFDLALLEEWSROPTQVLRGKLSPTYPAAHRFRSGITGSC LCVFSKHPIGPLTGHTTMOSPTMIHADPFSKAVGLUVHL SGMVLALVYTHLHAEVNRQKDIVLAHRVAQAMELAPTHHTSKX ADVVLLCGDLMHPEDLGCCLLKEWTGHDAYLETRDFKGSEBG NTWPRNCYVSQGELKPFFFGVRIDYVLYKAVSGFFISCKSFET TTGFDEHRGTFLSDHEALMATLFVRRSPPQONPSSTHGP\AERS PL/MCVLKERALDGSLGJAMA\QARWA\TFA\SYVIGLG\LL LALLCVLAAGGGAGRAAILLATPSVGLVUMAGAFYLFHQEVNG LYRAQAELGHVLGRARRAGDLGFPGLVARAVATHELFUNGTHAY LYRAQAELGHVLGRARRAGDLGFPGLVARAVATHELFUNGTHAY SGWVLAAVTHILAEVNRGOPVLRGKLSPTYPAAHRFRSGITGSC LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVHL SGWVLAAVTHILAEVNRGOPVLRGKLSPTYPAAHRFRSGITGSC LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVHL SGWVLAAVTHILAEVNRGOPVLRGKLSPTYPAAHRFRSGITGSC LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVHL SGWVLAAVTHILAEVNRGOPVLRGKLSPTYDARHFRSGITGSC NTWPRNCYVSQGELKPFPFGVRIDYVLYKAVSGFFIHTNSKGSER NTWPRNCYVSQGELKPPFFGVRIDYVLYKAVSGFFIHTNSKGSER NTWPRNCYVSQGELKPPFFGVRIDYVLYKAVSGSFRAPGLFCLNF TTGFDPHRGTTLSDHEALMATATLVRNSPPQONBSSTHGP\BERS PL/MCVCLKEALDGSIGJGMA\QARWA\TFA\SYVIGIGL\LL LALLCLAAGGGAGRAFALLHTPSVGVLVWAGAPYLFHQDSVNG LYRAQAELGHVLGRAREAQDLGPPPQLVALL\LGGGGDGTPRG PPSSSTGGSGSDTGSGTLGSGTGSPGGSCTCSGGGDFTRSG PFFOOKLLIGVSSIETESTGSDTGSGTGSFGGTGNGGGGFTRSD PFFOOKLLIGVSSIETESTGSDTGSGTGSFGGTGNGGGDTPRG TPSSGTGGGSGDTGSGTGSGTGSFGGTGSGTGSGTGGTGSFTGGTGCTGCTGTTASSPF TTTGTTHCRKGSGCTFETDTQARTHTRAGGPGPTNGCTGASSPF RSPGG				
RHTTAT AKWARREKMOEP\TRSFP\KGRPDLSTLTHSIVERRYLAHSGRS HLEPEEKQALKRLVEEEPLKMQVDEAASREDKLDLTKKGKRPPT PCSDPERKRFFFNSSSSGSEASSPYFGPPAKNGVARSSINTHF KEENPRAN, SIKANESSDEEREEKGNLDAGRGEESSEEEREKGYKEK KENPRAN, SIKANESSDEEREEKGNLDAGRGEESSEEEREKGYKEK KGTSKLKSSGOESEELLAGKKKGREEVEEREEEDEKKOMK KGTSKLKSSGOESEELLAGKKKGREEVEEREEEDEKKOMK PRTSSNGRRSARERSCKOKSQAKELLADDSSEEROKAASSG DDSGORDR PVQKRSCRETVOLKAGKELLGSSEEDEENGKGREPTA KGSRKMARLGSTSGEESDLEREVSDEAGGGPQGERKINGSKKS SRKGRTRSSSSSSDSPBAKGGKAGSGRRGBHPAWMIKKYIK ACCHANINYKHLISSCCSHKERLSLIARBLEALGHKGTPSLGKCK ALKEQREEAABVASLDVANIISGGSPRRRTAMPDGBAAPPGE LYRRTLDSDEERRPPAPPDWSHNRGIISLEALGHKGTPSLGKCK ALKEQREEAABVASLDVANIISGGSPRRRTAMPDGBAAPPGE LYRRTLDSDEERRPAPPDWSHNRGIISLEALGHKGTPSLGKCK ALKEQREEAABVASLDVANIISGGSPPRRTAMPDGBAAPPGE LYRRTLDSDEERRPAPPDWSHNRGIISLEALGHKGTPSLGKCK ALKEQREEAABVASLDVANIISGGSPRRRTAMPDGBAAPPGE LYRRTLDSDEERRPAPPDWSHNRGIISLEALGHKGTPSLGKCK ALKEQREEAABVASLDVANIISGGSPPRRTAMPDGBAAPPGE LYRRTLDSDEERRPAPPDWSHNRGIISLEALGHKGTPSLGKCK ALKEQREEAABVASLDVANIISGGSPPRRTAMPDGBAAPPGE LYRRTLDSDEERRPAPPDWSHNRGIISLEALGHKGTPSLGKCK ALKEQREEAABVASLDVANIISGGSPPRRTAMPDGBAAPPGE LYRRTLDSDEERRPAPPDWSHNRGIISLEALGHKGTPSLGKCK ALKEQREEAABVASLDVANIISGGSPPRRTAMPDGBAAPPGG LYRRTLDSDEERRPAPPDGVLRQLSPTYDAHHREGLGKCK ALKEQREEAABVASLDVANIISGGSPPRRTAMPDGGSEBAPPGBLOKK ADVULLCHALEEVMSGDPGVLRQLLSPTYVALKAGSEVLLUHL LALLCULAAGGGGAGAA LLHTPSVGLUHAASTLGFLGFLK SGWLAAVYTHLHAEVNGGGGGAGAA LLHTPSVGLUHAASTLGFLGFLK SGWLAAVYTHLHAEVNGGGAGAAA LLHTPSVGLUHAASTLGFLGFLK SGWLAAVYTHLHAEVNGGGAGAAA LLHTPSVGLUHAAGAPTLAFTSCGC LCVFSKHPIGELTCHTYTLINGYPYNHHHODMFSGKANGLUHHL SGWLAALGEBAABVASCHULCHHL SGWLAAGABCAHULCHAAATLTVRHSPGCHLAWAGAPTLAFTSCGCC LCVFSKHPIGELTCHTYTLHATTSVGLUHAAGAPTLAFTSCGCC LCVFSKHPIGELTCHTYTLHATTSVGLUHAAGAPTLAFTSCGCC LCVFSKHPIGELTCHTYTLHATTSVGLUHAAGAPTLAFTSCGCC LCVFSKHPIGELTCHTYTLHATTSVGLUHAAGAPTLAFTSCGCC NTMYPKNCYVSQOELKPPFFGVRIDYVLYKAVSFYISCKSFET TTGFPPHRGGGGGGAAALLAHTSTSCCCCC NTMYPKNCYVSQOELKPPFFGVRIDYVLYKAVSFYISCKSFET TTGFPTHRGGGGGGAAAALLAHTSVGSSCAAPGGGGGGAAPGGCAAAAAACAGGGGAAAAAAAAAA	1	1		
AKMAREKENGEP \TRESFY\MGREDLSTLTHSIVRRRYLAHSGRS HLEPEEKQALKRLVEEEPKMQVDEAASREVALDTIKKGKRPFT PCSDEBRKFRFNSBSESGSEASSPDYGFPAKNGVARSSHTHP KEENPRRA\SKAVEESSDEERGRDLPAQRGEESSEEBEKGYKGK TRKFVVKKQAPGKASVSRKQAREESSEEBEKGYKGK KGTKSLKESEQSSEEGILAQKKGREEVEEERKEEDEEKGYKGK KGTKSLKESEQSSEEGILAQKKGREEVEEERKEEDEEKGYKGK PRTENGRKSAREERSECKGKGAQARTGBOSBEEBGKEASASG DDSGRDRPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTA KGSRKMARIGSTSGEBEDLERBVSDSEAGGGPGGEKKRSSKKS SRKGRTRSSSSSSGSSEPEAKGGKAGSGEDEDPAWMRLKRYIK ACGAHRNYKKLLGSCCSHKERISILRABLEALGMKGTPSLGKCR ALKEQRERAEVSALDVANIIGSGGREEPDHAWMRLKRYIK ACGAHRNYKKLLGSCCSHKERISILRABLEALGMKGTPSLGKCR ALKEQRERAEVSALDVANIIGSGGREEPHAPAMPLGBAPPGE LYRRTLDSDEERPRAPPDWSHIRGIISSDCESN KORSTBALALEEVWSEQDPQYLRGGLSPTYPAAHHERSGIIGSG LYFSKHPIQELTCHIYTLNGYFYMIHHGDWFSGKAVGLLVLHI SGMVLHAVYTHIHABYMRGKDIYLAHGAMELAGPHHTSKK ADVULLCODLMMHEDDLGCCLLKENTGIHDAYLETTDFKGSEBG NTMYPKNCYVSQQELKPFPFGVRIDYLWAGSFYISCKSFBT TTGFDPHRGTELSDHEALMATLFVHSPFQQMPSSTHGP\AERS PL/MCVCLKEBALDGSLGLGMA\QARWMA\TFA\SYVIGLGI\LL LALLCULAAGGGAGEAALLLWTPSGULWAGAFYLFHVQEVMG LYRAQBELCHVLGRARRAQDLLSPFBQLVALL\LGQGEGDRTKSG OKSPHDLALLEEVWSEQDPQYLRQKLSPTYPAAHHFRGIIGSG SGMVLHAAVYTHLHABYMRQKDIYLAHRAQAMELAGPTHITYSK ADVULCGDLIMHEDDLGCCLLKEWTGIHDAYLETTDFKGSEBG LCVPSKHPIGGLTQHIYTINGYTMIHHGDWFSGKAVGLUVLH SGMVLHAAVYTHLHABYMRQKDIYLAHRAQAMELAGPTHITYSK ADVULCGDLIMHFSTWALTHAGAGAGAAFALLATARVAGAMELAGPTHITYSK ADVULCGDLIMHFSTWALTHAGAGAGAAFALLATARVAGAMELAGPTHITYSK ADVULCGDLIMHFSTWALTHAGAGAAFALLATARVAGAMELAGPTHITYSK ADVULCGDLIMHFEDLGCCLLKEWTGIHDAYLETTDFKGSEBG NTMYPKNCYVSQGELKPFPFGVRIDYLARVAGSFYLSKSFBT TTGGPBHRGTFLSDHRALMATLFVHSPPQDAMSSAHCHPTHITSK ADVULCGBLAMHFEGLGGCLLKEWTGIHDAYLETTDFKGSEBG NTWYPKNCYVSQGELKPFPGWRIDYLAVAGSGRAVGLALLAGE PL/MCVCLKEALDGSLGLGMA\QARWMA\TTA\SYVIGLGL\LL LALLCULAAGGGAGEAAILLWTPSGULWAGAFYLFINQEVAG LYRAQBELQHYLGRARRAQDLOPPEGLYALL\LGQGGGGDGTRKG TTGGPBHRGTPLSDHRALMATLFVHSPCDVAGGGGRACHACHAGA PFPQDKLLLGYSDIETDFXCNGGGFCCONTRIBGN LHRENSULVETINGGNGGHFCCDVYTHGGGGGDATKGC RSFYSGANVSHHETALGJERDHHMEDPSWTTHKRSQOMBCH THENGGGGSSATTSGYGGGSBATTGCOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				
HLEPBEKQALKRIVBEEPLKMQVDEAASREDKLDLTKKGKRPPT PCSDFERKRFFRNSESSEGSEASSBOTGEPDALDAGEESSEEBEKGYKCK KEENPRAR JSKAVEBSSBOERGROLD-PAQRGEESSEEBEKGYKCK TRKKPVVKKQAGKASVSKQARRESSESSEERGYKCK KGTKSLKSESGESSEELLAJKKEGREESSEEBEKGYKCK KGTKSLKSESGESSEELLAJKKEGREESBERGEBKGDKK KGTKSLKSESGESSEELLAJKKEGREESBERGDKK PRTRSNGRRKSAREERSCKQKSQAKRLIGDSDSEEGKEAASG DDSGRDRBPPVQRKSEDRTQLGGGKRLSGSSEDBESGKGEPTA KGSRKWARLGSTSGEEBDLERSVSDSEAGGEPQGERKNRSSKKS SRKGRTKSSSSSSDGSPAKGGKAGSGRGEDHPAWMILKRYTK ACQAHENYKKLIGSCCHKKRISILISELALGMKGTPSLGKCR ALKEQREEAAEVASLDVANIISGSGRPRRTAWNPLGEAAPPGE LYRRTLDSDEERRPRAPDWSHMRGITSSDGESS LCVFSKHPTOJELTGHTYLNGVPHWHIGDWFSGKAVGLUAHL SGMVLNAYVTHLHABYNRQKDIYLAKRAQAWELAQPTHHTSKK ADVVLLCGDLÄMHEEDLGCCLLKEWTGLHDAYLETTDFKSSESG VAMPURNCVYSQGELKPFPGVAIDYVLYKAVSGFYISCKSFET TTGFDFHRGTPISDHEALMATLFWSSTGOLVLKAGAFYLFHVQEVNG LYRAQABLQHVLGRAREAQDLGPBPQLYALLLLAGGGGCABAALLLWTPSVGLVLKAGAFYLFHVQEVNG LYRAQABLQHVLGRAREAQDLGPBPQLYALLLLAGGGGCGDRTKQ PMSSPTMKPRNSLRIRINIACKGIFYLSKHRADRMRRLGDFL NQSSFDLALLEEVMSEQDFQYLGRLSFTYPAAHHFRGGITGSG CLVFSKHPTOSLITCHTYLNGYPMHHIGDWFSGKAVGLUAHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQPTHHTSKK ADVVLLCGDLMHPEDLGCCLLKEWTGLHDAYLETTDFKSSEEG NTWPRNCYVSQGELKFTPSAAHHFRGGITGSG CLVFSKHPTOSLITCHTYLNGFYPMHHIGDWFSGKAVGLUAHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQPTHHTSKX ADVVLLCGDLMHPEDLGCCLLKEWTGLHDAYLETTDFKSSEEG NTWPRNCYVSQGELKFFFFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTLSDHRALMATLFVRHSPGQUVLWAGAFYLFHVQEVNG SGMVLNAYVTHLHAEYNRQKDTYLAHRVAQAWELAQPTHHTSKX ADVVLLCGDLMHPEDLGCCLLKEWTGLHDAYLETTDFKGSEEG NTWPRNCYVSQGELKFFFFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTLSDHRALMATLFVRHSPCQUVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRARBAQDLGPBPQLYALLLLALLLAGGGGGGAALLLWTBSGCGCGGSAKPGEECHCLWF EAVLSPDPALTHSTHSLTMSHATHATUSDCDISCKGMTERTHSIN LHHFSNSULFETINGGRGHFCDVYVRHGMMRAQRCULAGG PFPODKLLLGYSDIETISVSVOGSVQKLIDPMYSGULRVSQSRA LQLITAASILQIKTVIDECTRIVSONVGDVFFGIQDSQOTTRAG PFPODKLLLGYSDIETISVSVOGSVQKLIDPMYSGULRVSQSRA LQLITAASILQIKTVIDGTTNITVSONREDDFDNTTRIRRSQOMGRUL STPPSTTHCRKQOP GTVOTOTOMINITAKREMEDDFDDFTGQDURGOPUT LLERRSEECTEDTDQAGEPTDQAAEAPABEGGGPTNOLETGASPE CQSFGPGAARDS	6960	387	2068	
PCSDPERKPFRPNSESSGSGEASSDVPGPPARMYGASRITTHE KEENPRAK_SKAVEBSSDEERQRDLPAQRGEESSBEEEKGYKGK TRKKPVVKQAPGKASVSRKQAREESSBEEBKSABPVQRTAKKVEGN KGTKSLKESEQSSEEI LAQKKEQREEEVSEEEKGEBKADKK PRTESNGRKSABREBSCKQKSQARLIGDSDSEEQKRAASGS DDSGRDRPPVQRKSEDRTQLKGGKRLGGSDSEEDSCKGRPTA KGGSRWARLIGSTSGEESDLERSVESSBAGGPPGREKNRSSKKS SRKGRTRSSSSSDGSPEAKGGKAGSGRRGEDHPAWMEKRYTR ACGAHRNYKKLLGSCGSHKERLS ILRAELBALGMKGTFSLGKCR ALKEQREBAZVSALDVANI IGSGGRETAMPLIGBAPPGE LYRRTLDSDEERPPAPPDWSHRRGI ISSDCESN RPWSSPPMPMPFSGLIK IFNIACWGI PYLEKHEADDMRRIGDPL NGESPDLALLEEVWSBQDFQYLRQKLSPTYPAAHHFRGGI IGSG LCVFSKHPIQLTCHTITILNSTYPMIHHGDWFSGKVGLDVIHL SGMVLNAYVTHHABYNRQKDIYLAHVAQAWBLAQFTHHTSKK ADVVLLCGDLMHHEDDJGCCLLKEWTGHHDAYLETTDFKGSESG NTMVPKNCVSQGELKPFPFGVAIDVLKAVSGFYISCKSFFT TTGFDFHRGTPLSDHEALMATLFVFHSPPQONPSSTHGP\AERS PL/MCVCLKAALDGSLGLGMA\QARWMA\TFA\SYVIGLGL\LL LALLCULAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELCHVLGRARRAQDLAPBPQLYALL\LGQQEGDRTKSQ PMSSTPMFMPFSGLRIF INNLCKGIF LYKHRADDMRRLGDFL NOSSPDLALLEEVWSEQDFQYLRQKLSFTYPAAHHFRGGI IGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVHL SGWLBARVYTHLHABYNRQXDIYLBKRADGMFSGKAVGLLVHL SGWLBARVYTHLHABYNRQXDIYLBKRADGMFSGKAVGLLVHL SGWLBARVTHLHABYNRQXDIYLBKRADGMFSGKAVGLLVHL SGWLBARVYTHLHABYNRQXDIYLBKRADGMFSGKAVGLLVHL SGWLBARVYTHLHABYNRQXDIYLBKRADGMFSGKAVGLLVHL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFTDFKGSEEG NTMVPRNCVYSQGELKFPFFGWIIDVLYKAVSGFYISCKSFFT TTGFDFHRGTPLSDHRALMATLFVRHSPQONSSTHGP\AES PL/MCVCLKEALDGSLGLGMA\QAAWMA\TPA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFTDFKGSEEG NTWYPRNCVYSQGLKGLGMA\QAAWMA\TPA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFTDFKGSEEG PKYPELIKLLKKFFTLARGNQASEERETJCHGGSGSAFTEGLOFLUN LHAFNSULVETJNEQNRGHFCDVYVYLTKONSGSTHGPLOBGQDTPRG PFPQDKLLLGYSDLETJNEGNRGHFCDVYVTHGSMRADAGOTCHAAGS PFPQDKLLLGYSDLETJNEGNRGHFCDVYVTHGSMRADAGDCTLAAGS PFPQDKLLLGYSDLETJNEGNRGHFCDVYVTHGSMRADAGDCTLAAGS PFPQDKLLLGYSDLETJNEGNRGHFCDVYVTHGSMGNEGDVDYYGORNOGGE RSFYSGAVVSHHETTALGDPRDHMEDPSWTTRHRRSQOMBRYL STPPETTHCRKOPP PWIQTOTUGNITATRHRRSQOMBRYL STPPETTHCRKOPP PWIQTOTUGNITATRHRRSGOMBTYL STPPETTHCRKOPP PWIQTOTUGNITATH]	2000	
KEENPRRA SKAVEESSDEERQRDLPAQRGESSSEEEKGYKGK TRKKPVVKQAPGKASVSRKQAREESEBSBEPVQRTAKKVEGN KGTKSLKESEQSSEEE I LAQKKGQREEVEBEKEEDEKGDKK PRTKSINGRKSAREERSCKQKSQAKRLLGDSDSEEBQKEAASG DDSGRDREPPVQRKSESDRTDLKGKGSSESDEEDGKGAPTA KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTKSSSSSSSOGSPEAKGGKAGSGRAGGDPQGERKNRSSKKS SRKGRTKSSSSSSSOGSPEAKGGKAGSGRAGGBPQAGEKNRSSKKS SRKGRTKSSSSSSSOGSPEAKGGKAGSGRAGGBPQAGTHSTSLGKCR ALGEQREEAAEVASLDVANI ISGSGEPRRTTAMPLGEAAPPGE LYRRTLDSDEERPRAPPDMSHNRGI ISGSGEPRRTTAMPLGEAAPPGE LYRRTLDSDEERPRAPPDMSHNRGI ISGSGEPRRTTAMPLGEAAPPGE LYRRTLDSDEERPRAPPDMSHNRGI ISGSGEPRRTAMPLGEALPGE NQESFPIALLEEVMSEODFGYLRKLSPTYPAAHHFRSGI IGSG LCVFSKHPLQELTCHITYTLMCYPTYMTHHODWFSGKAVGLULVHL SGMVLNAYVTHLHASYNRQKDI VLAHRVAQAWELAQFIHTTSKK ADVULLCOLLNHIPBULGCCLLKEWGHAAVALLOGLINHPSKSESG NTMVPRNCYVSQQELKPFPFGVRIDYVLYKAVSGFYLSCKSFET TTGFDPHRGTFISDHEALMATLFVRRSSPCJORPSSTHGP\ARES NTMVPRNCYVSQQELKPFPFGVRIDYVLYKAVSGFYLSCKSFET TTGFDPHRGTFISDHEALMATLFVRRSPCJOLALL\LQGGDGPRKSG LVFRAQAGCHVLUGRARRAQDLGFPLAKGAFFLFHVQBVNG LYRAQAGCHVLUGRARRAQDLGFPLAYLATHFNGGI IGSG LCVFSKHPJGELTGHITYTILNCYSFYNTHHODWFSGKAVGLLVHH SGMVLNAYVTHLHASYNRQKDI VLAHRVAQAWELAQFI HHTISKK ADVULLCGELINHPSUDGCCLLKEWGHAAVLFPKGSEIG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYLSCKSFET TTGFDPHRGTFILSDHEALMATLFVRRSPCJORPSSTHGP\ARES NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYLSCKSFET TTGFDPHRGTFILSDHEALMATLFVRRSPCJORPSSTHGP\ARES NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYLSCKSFET TTGFDPHRGTFILSDHEALMATLFVRRSPCJORPSSTHGP\ARES NTMVPKNCYVSQQELKPFPFGVRIDYVVLYKAVSGFYLSCKSFET TTGFDPHRGTFILSDHEALMATLFVRRSPCJORGSCRDFKSCS NTMVPKNCYVSQQELKPFPFGVRIDYVVLYKAVSGFYLSCKSFET TTGFDHRGTFILSDHEALMATLFVRRSPCJOLGCSCRDKRSC SPFPQDKLLLGYSDIE ISPSVVSQSVQKLIDEMYSGVLRVSQSSR LYRQAGAGBAAILLMTPSSVGLVLALL\LGGGGGDRTKSC PFFCDKLLLGYSDIE ISPSVVSQVSVQKLIDEMYSGVLRVSQSSR LYRQAGAGBAGFTLINSTHSTTNSHAHTGSSDCCILSCKMTERHHSIN LHFRSSVLFETLRSGURRSHCDVTVTRIGSSMLRAGSGER FSFSGAVVSHHETALGLPRAVROPVFPGIQDSGDTPRG TPSSGTSGSSSTSGSTAGPAGDVTTVRIGSSMLRAGCSCBR LQLITAASILQIKTVIDECTRIVSQNVGSVGKLIDEMYSGURRSCSSR RSFYSGAVVSHHETALGLPRADAAPAEGGPQTTNQLETGASSPE EQQFGPAAR			1.1	
TRKKPVVKQAPGKASVSRKQARESSESSABPUQRTAKKVEGN KGTKSLKESBQESEEI LAQKKEQREEVBEEEKEBDEEKGDKK PRTESNORRKSARERSCKQKSQAKRLLGDSDSEEGKEAASSG DDSGRDEPPVQRKSEDRTDLKGGKRLGGSSBDEEDGKGEPTA KGSRKMARLGSTSGEBSDLEERUSEAGGFQGERKNRSSKKS SRKGRTRSSSSSSDGSPEAKGGKAGSGRGEDHPAVMRLKRYIR ACGAHRNYKKLLGSCCSHKERLSI LRAELBALGMKGTSSLGKCR ALKEQKEEAAEVASLDVANI ISGSGRPRRTAMPLGEAAPPGE LYRRTLDSDEERPRPAPPDMSHNRGI ISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRIFINLOWGIPYLSKHRADRRRLGDFL NGESPDLALLEEVMSEQDFQYLRGKLSPTYPAAHHFRSGI IGSG LCVFSKHPIQELTQHIYTLINGYPYMIHHGDWF3GKAVGLLUJHL SGMYLINAYVTHLHABYNRQKDIYLAWQAGWLAQFHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEBG NTMYPRKNCYVSQQELKFPFFGVRIDYVLKAVGGFYLSCKSFT TTGFDPHGRTPLSDHEALMATLEYHRSPFQONFSSTREP\AERS PL/MCVCLKEALDGSLGIGMA\QARWAAYTFA\SVVIGLGL\LL LALGULAAGGGAGEAAILLWTSSPFQONFSSTREP\AERS PL/MCVLLKAGHALGAGEAAILLWTSSPFQONFSSTREP\AERS PL/MCVLLKAGHALGAGEAAILLWTSSPFQONFSSTREP\AERS PL/MCVLLAGGGAGEAAILLWTSSPFQONFSSTREP\GFT SGRPSSTMKPNFSLRLRIFRLNOWGIPYLSKRADRRRRIGDEL NGSSFDLALLEEVWSEQDFQYLRGKLSPTYPAAHHFRSGI IGSG LCVFSKHPIQELTQHIYTLNGYPYNLHHGDWFSGKAVGLUJHL SGMVLNAYVTHLHAEYNRQKDIYLAKAGFYLFRVGSEBG NTMYPKNCYVSQQELKFPFFGVRIDYVLVKAGFYLSCKSFFT TTGFDPHGTPLSDHEADHMTSPQONFSSTREP\AERS PL/MCVCLKEALDGSLGLGMA\QARWAA\TPA\SYVIGLGL\LL SGMVLNAYVTHLHAEYNRQKDIYLAKAGFYLSCKSFFT TTGFDPHGRTPLSDHEALMATLEYRPQOMPSGKAVGLUJHL LALLCVLAAGGGAGEAAILLWTFSVGLVLMAGAFYLFRVGSEBG NTMYPKNCYVSQQELKFPFFGVRIDYVLVKAGFYLSCKSFFT TTGFDPHGRTPLSDHEALMATLEYRPPKGSEBG NTMYPKNCYVSQQELKFPFFGVRIDYVLVKAGFYLSCKSFT TTGFDPHGRTPLSDHEALMATLEYRPQOMPSTYLGCKSFTL LYRQAELQHVLIGRARRRQDLGFPPQLYALLL\LLQQGBGDTTKRQ PL/MCVCLKEALDGSLGIGMA\QARWA\TPA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTFSVGLVLMAGAFYLFHVGSVGG NTMYPKNCYVSQQELKFPFFGVRIDYVLVKAGFYLSCKSFT TTGFDPHGRTPLSDHAATLATHAGNORMAFYLFHVGSVGG PFFQDKLLLGYSDLEIPSVVSVQSVQKLLDMAGFYLFHVGSVG LYRQAEACHVLGRARRRQDQLGPPCVTVR HGSMLRAQRCVLAAGS PFFQDKLLLGYSDLEIPSVVSVQSVQKLLDGGODTPRG TPESGTSQQSDTESGYLQHPQHSVDRIYSALYACSMQNGGGE RSFYSGAVVSHETALGLPRAHMEDPSSITTHHERSQQMERTL STPESTTHCRKQRRYVIIGTUCKNIKI KQEMEDDYVTYQGQRVQ ILERNSEECTEDTDQAAGTSSPKGESFDSCVSSIGTEPDSV EQQFGPAAR				
KGTKSLKESSØSERELIAQKKEQREEVEEREKEEDEKGDEK PRTRNNGRRKSAREERSCKQKSQAKRLLGDSDEEBQKEAASG DDSGROREPPVQRKSEDRTQLKGGKLIGSSSBDEEDGKGEPTA KGSRKMARLGSTSGESDLEREVSDEEAGGGPGERKRSSKKS SRKGTRTKSSSSSDESPAKKGGKRGENDEAMBLKRYTR ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCR ALKEQREEAAEVASLDVANIISGSGRPRRTHAWPLGEAAPGE LYRRTLDSDEERPRPAPPDMSHMPGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLERIFININCKGIPFUSKHRADRMBRLGDFL NORSFPDLALLEEWBEODFOYLRGKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLMGYPYMIHHGDWFSGKAVGLLVLHL SGMYLNAYYTHLHARYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVULLCOJLNHHPBDLGCCLLKWPPPQANBELAQFIHHTSKK ADVULLCOJLNHHPBDLGCCLLKWPPPQONBSTHGPYAGERS NTMYPKNCYVSQQELKPPPFGVRIDVYLVKAVSGFYISCKSFBT TTGFDPHGROFILSDBLAMATLFVRIPQOMPSSTHGPYAGERS NTMYPKNCYVSQQELKPPPFGVRIDVYLVKAVSGFYISCKSFBT TTGFDPHGROFILSDBLAMATLFVRIPQOMPSSTHGPYAGERS NDESPDLALLEEUWBEQDFQVLRGKLSPTYPAAHHFRSGIIGSG LYRRQAELCHVLGRRRRAQDLGFPLAYLLLQGGGGDBTKEG PL/MCVLKBALDGSLGIGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTESVGLVUMAGAFYLFHVQEWG LYRRQAELCHVLGRRRRAQDLGFPLYNLLHDDWFSGKAVGLUVLHL SGMYLNAYYTHLHBEYNRQKDIYLAERVAQAWELAQFIHTTSKK ADVULLCGDLNHHPBDLGCCLLKWGLHDHATLETRPFKGSEGS NTMYPKNCYVSQQELKPPPFGVRIDYVLKKAVSGFYISCKSFBT TTGFDPHRGTPLSDHEALMATLFVRHSPPQNPSSTHGP\ABRS PL/MCVCLKBALDGSLGIGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVUMAGAFYLFHVQEWG LYRRQAEACHAUGHANALFTARSDCDLTLKGMGTFCTHFVGSWG ADVULLCGDLNHHPBDLGCCLLKWAGAFYLFHVQEWG LYRRQAEACHAUGHANALFTARSDCDLTLKGMGTFCTHFVGSWG NTMYPKNCYVSQQELKPPPFGVRIDYVLKKAVSGFYISCKSFBT TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\ABRS PL/MCVCLKBALDGSLGIGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVUMAGAFYLFHVQEWG LYRRQAEACHAUGHANALFTARSDCDLTSCKSMTERHHSIN LHFSSNSQLEHTHGSGNGTHGTFCTVTVR HIGSMLRAQGCULANGSG NTMYPKNCYVSQQELKPPPFGVRIDYVTVR HIGSMLRAQGCULANGS PFFCDKLLLGYSDIEISGVGNGGHGTCVTVTR HIGSMLRAQGCULANGSG PFFCDKLLLGYSDIEISGVGNGGHGTCVTVTR HIGSMLRAQGCULANGSG RSFYSGAVVSHETALGLPRHMEDPSWITTHESSNCGURSTL STPESTTHCRKQRFRYRIGTIVCNITY GEMBEDPOTYGQGNC LIERNSEECTEDTDQAEGTSSEPKGESDGSCSSSIGTEPBOV LQUFGDAARDSQAEPTOPEQAAABAEGGPQTTNQLETGGLSSPE CQGFGAARDSQAEPTOPEQAAABAEGGPQTTNQLETGGLS				
DRGRDREPPVQRKSDATCLIGGDSSEEGKEPTA BOSGRDREPPVQRKSEDRTQLKGGKASGSEDEDEGGKEPTA KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQERKNRSSKKS SRKGRTESSSSSDGSPEAKGGKASGSRGBDHPAVMRLKRYTR ACGARMYKKLLGSCCSHKERLSI LRAELEALGMKGTPSLGKCR ALKEQREEAAEVASLDVANI ISGSGRPRRTAMMPLGEAAPPGE LYRRTLDSDEERPRAPPDWSHMRGI ISDGESN 6961 340 1646 RPMSSPJMKPNFSLRIR IFNLKWGIPVLSKHRADRWRRLGDFL NGESPDLALLEEWSSQDFQYLRQKLSPTYPAAHHFRSGI IGSG LCVFSKHPLQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVHLHABYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKENTGLHDAYLETRDFKGSEEG NTMVPRNCYVSQQELKPPFPGGYSLVLWRAGFYLSKCKFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQNNFSSTHGP\AERS PL/MCVCLKBALDGSLGJGMA\QARWMA\TFA\SYVIGLL\LL LLLCVLAAGGGGGGATALLLMPSGULVHWAGAYPLHVDKVSK LYRAQABLCHVLGRAREAQDLGPBPQLVALL\LGQQEGDRTKSQ LYRAQABLGHVLGRAREAQDLGPBPQLVALL\LGQQEGDRTKSQ LYRAQABLGHVLGRAREAQDLGPBPQLVALL\LGQQEGDRTKSQ LYRAQABLGHVLGRAREAQDLGPBPGLYALL\LGQQEGDRTKSQ LCVPSKHPIQELTQHIYTLNGYPMIHHGDWFSGKAVGLLVLHL SGMVLNAYVHLHAEVNROKOLFARVRAGVASHALAGFIHHTSKK ADVVLLCGDLNHHPEDLGCCLLKEWTGLHDAYLETRDPKGSEEG NTMVPKNCYVSQQELKPPFFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNBSTHGP\AERS NTMVPKNCYVSQQELKPPFFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQNDSSTHGP\AERS NTMVPKNCYVSQQELKPPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQNDSSTHGP\AERS PL/MCVCLKRALDGSLGJGMA\QARWMA\TPA\SYVIGLL\LL LLLCVLAAGGGAGGAAILLWTPSVQUVLWAGAFYLFHVQEVNG LYRAQAELGHVLGRAREAQDLGPBPQLYALL\LGQQEGDRTKRQ RYPSQLHKLLGYSDIETPSVVSVQSVQKLIDDMYSGVROVLENGLENG LYRAQAELGHVLGYSDIETPSVVSVQSVQKLIDDMYSGVROVLAAGS PFFQDKLLLGYSDIETPSVVSVQSVQKLIDDMYSGVROVLAAGS PFFQDKLLLGYSDIETPSVVSVQSVQKULDDMYSGVROVLAAGS PFFQDKLLLGYSDIETPSVVSVQSVQKULDDMYSGVROVLAAGS PFFQDKLLLGYSDIETPSVVSVQSVQSVKLIDDMYSGVROVRSGEA RSFYSGAVVSHHETALGDPRDHHMEDPSVTRIHERSQCMERU STPTETTHCRKQPPRVTQTTUVGNHILGQMEDTVYTGQMPDTYGGGYRU ILERNSESECTBOTDQABGTESEPKGSFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEADAGGGPQTNQLETGASSPE EQQFGPGAARDSQAEPTQPEQAAEADAGGGPQTNQLETGASSPE	1			1
DDSGRREPPVQRKSEDRTQLKGGKRLGGSSEDEEDGKGEPTA KGSRKMARLGSTSGESDLEREVSDSGGFQGGERTRASKKS SRKGRTKSSSSSSDGSPEAKGGKAGSGRGEDHPAVMRLKRYIR ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSIGKCR ALKEQREAAEVASLDVANIIGGGRPRRTTAWNPLGEAAPPGE LYRRTLDSDEERPRPAPPDWSHMRGIISSDCESN 6961 340 1646 RPWSSPTMKPNFSLRIRISNLNCWGIPYLSKHRADRWRRLGDFL NGRSPDLALLEEVWSRDDPOYLRQKLSPTYPAAHHFRSGIIGGE LCVFSKHPIQELTQHIYTLNGYPYMIHHGWFSGKAVGLLVLHL SGMYLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKWTGHANAYTERDPKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDEHRGTPLSDHEALMATLFVRHSPPQONPSSTEGP\AEKS PL/MCVLKEALDGSIGLGMA\QARWA\TFA\SYVIGLGL\LL LALLCVLAAGGGGGRAA ILLWTPSVGLVLMAGAFYLFHVQEVNG LYRAQAELQHVLGRARRAQDLGPBPQLYALL\LQQGEDRTKEQ ROBSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRWRRLGDFL NQRSFTMKPNFSLRLRIFNLNCWGIPYLSKHRADRWRRLGDFL NGRSFDLALLEEVWSRQDPQYLAQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMYLNAYVHLHBEVNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPBELIGGCLLKBWTGHDAYLETRDPKGSEEG NTMVPKNCYVSQQELKPPFFGVGVJLVHXAGAFYLFHVQEVNG LCVFSKHPIQELTQHIYTLNGYPFWIHHGDWFSGKAVGLLVLHL SGMYLNAYVHLHBEVNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPBELIGGCLLKBWTGHDAYLETRDPKGSEEG NTMVPKNCYVSQQELKPPFFGVGVJLVHXAGYSTISCKSPST TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AEKS PL/MCVLKRADDGSLGIAMA\QARWA\TFA\SYVIGLL\LL LLLCVLAAGGGGGGAAILLHTPGGGSLAWAYTHENGWSEE PL/MCVLKRADDGSLGHAPHYGFUJLVHXAGYFTLFHVGSVGS NTMVPSKNCYSQGEAGPAILLHTPGGGSSAKPGEDCINF EAVLSPPPALIHSTHSLTMSHAHHTGSSDCDISCKGMTERTHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLVAGGS PFFQDKLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLVAGGS PFFGDKLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLVAGGS PFFGDKLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLVAGGSE RSYSGAVVSHETALGGPPRDHHEDPSWITRIHERSQCMERYL STTPETTHCRKQPRPRTQTLVGNIHIKQEMEDDYDYYGQQRQ ILBRNSESECTBDTDQABGTBSEPKGSFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAGGGPQTNQLETGASSPE EQQFGPGAARDSQAEPTQPEQAAEAPAGGGPQTNQLETGASSPE				
KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTKSSSSSSDSDSPAKGGKAGSGRGBHPAVMRLKYIR ACGAHRYKKLIGSCCSHKERIS ILRABLEALGMKGTPSIGKCR ALKEQREEAAEVASLDVANIISGSGPRRRTAWNPLGEAAPPGE LYRRTLDSDEERPRAPPDWSHMRGIISSDESN 6961 340 1646 RPWSSPJMKPNFSLEIRI FINLAGWGIPYLSKHRADRWRRIGDFL NQESPDLALLEEVWSRODFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVHLHABEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPISDHEALMATLFVKHSSPQONPSSTTGP\AERS PL/MCVCLKBALDGSLGJGMA\QARWMA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELGHVLGRARRAQDLSPBPQLYALL\LGQQEGDRTKRQ 6962 340 1646 RPWSSPTMKPNFSLRIRIFNLNCWGIFYLSKHRADRWRRIGDFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQEITQHIYTLNGYPYMIHHGDWFSGKAVGLLVHL SGMVLNAYVTHLHAEYNRQKDIYALAKAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFFFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPISDHEALMATLFVRHSPPQONPSSTTGP\AERS PL/MCVCLKEALDGSLGJGMA\QARWMA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLHTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELGHVLGRARRAQDLGPBFQLYALL\LQQQEGDRTKRQ CHYNSPDFALIHSTHSLTNSHAHATGSDCDISCKGMTERIHSIN LHNFSNSVLETLINEQRNRGHFCDVTVRHGSMLRAQRCVLAAGS PFFQDKLLLGYSDLEIPSVVSVQSVGLLDFMYSGSEAK LQILTAASILQIKTUDBCTRIVGSMLRAQRCVLAAGS PFFQDKLLLGYSDLEIPSVVSVQSVGLLDFMYSGSEAKPGLPCLNF TRESGTSGGSSDTESGYLQSHPQHSVDRIYSALVACSMONGSGE RSFYSGAVVSHHETALGLPRDHHMEDDFSWTRTIHERSQQRRYL STTPETTHCRKQPRPVRIQTLVGNHIKQBMEDDTYYYGQGRV ILERNESEECTBDTDQARGTESEPKGSFDSGVSSSIGTBPDSV EQQFGPGAARDSQAEPTQPEQAAEAPASGGPCTNQLETGASSPE RSNEVEMDSTVITUSNSBDKSVLQQPSVNTSIGQPLFSTQLYLR	1			
SRKGRTESSSSSDGSPEAKGGKAGSGRRGEDHPAWRLKRYIR ACGARRNYKILLGSCCSHKERLSILEABLEALGMKGTPSIGKCR ALKEQREEAAEVASLDVANIISGGRPRRETANPIGGEAAPPGE LYRRTLDSDEERPRPAPPOWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNINCWGIPYLSKHRADRMRRLGDFL NQESFDLALLEEWWSRQDFYJLRKKLSPTYPAAHHRRSGIIGGG LCVFSKHPIQELTQHIYTLMGYPYHHHHGWFGGKAWGLUVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTQLHDAYLETRDFKGSEGG NTMYPRKCYVSQQELKFFPFGVRIDYVLYKAVSGFYISCKSFFT TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSIGLGMA\QARWMA\TFA\SYVIGLI\LL LALLCULAAGGGAGEAAILLWTESVCIJLWWAGAFYLFHVQEVNG LYRQAELGHVHGRARRAQDLGPBPQLYALL\LGQQEGDRTKSQ 6962 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL NQESFDLALLEEVWSRQDFQYLARKLSPTYPAAHHRRSGIIGSG LCVFSKHPIQELTQHIYTLMGYPYNHHHGWFSGKAWGLVHHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKSSEGG NTMYPKNCYVSQQELKFFPFGVIDTVLYKAVSGFYISCKSFBT TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSIGLGMA\QARWMA\TYA\SYVIGLGL\LL LALLCULAAGGGGGAGAAILLWTESVGLIVUNAGAFYLFHVQEVNG LYRAQASLGHVLGRARRAQDLGPEPQLYALL\LGQQGGDRTKSQ LYRAQASLGHVLGRARRAQDLGPEPQLYALL\LGQQGGDRTKSQ LYRAQASLGHVLGRARRAQDLGPEPQLYALL\LGQQGGDRTKSQ LYRAQASLGHVLGRARRAQDLGFENEITPGGGSSAKFGLPCLNF EAVLSPDPALIHSTHSLITNSHAHTGSSDCDISCKGMTERHSIN LHNFSNSVLETLMEQRNRGHFCDUTVRIHSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFFGIQDSGQDTFRG TPBSGTSGQSDTESGYLQSHPGHDSVDRTYGLDRSQCDTPRG TPBSGTSGQSDTESGYLQSHPGHSVDRTYSALYACSMQNGSGE RSFYSGAVVSHETTALGLPRDHMEDPSWITRIHERSQMERYL STTPETTHCKKQPRFNITIVUNNIHIKQBMEDDYDYYGQQRVQ ILERNESEECTEDTDQAGGTESEPKGESPDSGSSSIGTEPDSV LERNESEECTEDTDQAGGTESEPKGESPDSGSSSIGTEPDSV LERNESEECTEDTDQAGGPQTTNQLETGASSPE RSNEVEMDSTVITVSNSKSVLQQFSVNTSIGQPLPTGLTCRSPE RSNEVEMDSTVITVSNSKSVLQQFSVNTSIGQPLSTGLYRL	1			
ACGARRNYKKLIGSCCSHKERLSILRAELEALGMKGTPSIGKCR ALKEQREEAAEVASLDVANTISGSGRPRRTAMNPIGEAAPPGE LYRRTLDSDEERPRAPPDWSHMRGISSDESN 6961 340 1646 RPWSSPTMKPNFSLRIFINLNCWGIPYLSKHRADRMRRLGDFL NQESFDLALLEEVWSRQDFQYLRQKLSPTYPAAHHRSGIGGS LCVPSKHPIGELTQHIYTLNGYPYMIHGDWFSGKAVGLUVHL SGMVLNAYVTHLHAEYNRQKDIYLAKVASGFYISCKSFBT TYGFDPHRGTPLSDHEALMATLFVRHSPQONPSSTHGP\AERS PL/MCVCLKEALDGSIGLGMA\QARWA\TFA\SYVIGLGL\LL LALLCVLAAGGAGAAALLWTBVSGLVHRADRWRRLGDFL LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LGQQEGDRTKEQ 6962 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRWRRLGDFL LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LGQQEGDRTKEQ LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMYLNAYVTHLHAEYNRQKDIYLARHVAQAWBLAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKSSEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFBT TTGFDPHRGTPLSDHEALMATLFVRRSPPQNPSSTHGP\AERS PL/MCVCLKEALDGSIGLGMA\QARWMA\TPA\SYVIGLGL\LL LALLCVLAAGGGAGAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRARRAQDLGPEPQLYALL\LGQQEGDRTKEQ 6963 374 2618 RVFPLILKLIKKPKTABNOKASEENBITQPGGSAKYGGLOLL LALLCVLAAGGGAGAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRARRAQDLGPEPQLYALL\LGQQEGDRTKEQ FPFQDKLLLGSYSDIETSSVSVSVQKVLDPMSSGLTHSIN LHNFSNSVLETIMEQRNRGHFCDVTVTHGSMLRAQRCVLAAGS PFFGDKLLLGSYSDIETSGVSVQKVLTDFMSSGLTRGQGAF TPESGTTSGQSDTESGYLASHFTNSGARAGNGSGE RSFYSGAVVSHHTALGLPRDHMEDPSWITRIHERSQCMERYL STTPETTHCKQPRPRIGTLVCNIHLKQEMEDDTYYTGQGRVQ ILERNESEECTENTDQAGGTGSSPKGESPDGGSSSIGTEPDSV EQQFGAARDSQAEPTQDEQAAEDAEGGPQTNQLETGASSPE RSKEVEMDSTVITVSNKSDKSVLQQPSVNTSIGQPLDFTQLYLR	1			
ALKEQREEAAEVASLDVANIISGSGPRRRTAWNPLGEAAPPGE LYRRTLDSDEERPRPAPDWSHMKCI ISSDGESN 6961 340 1646 RPWSSPTMKPMPSICHLRI TPNLNCWGIPYLSKURADPMRRLGDPL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVPSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLUVLHL SGMVLNAVVTHLHABYNGKDYLAHRVAQAWELAQPIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFBT TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGIGMA\QARWMA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LQQQEGDRTKEQ 6962 340 1646 RPWSSPTMKNNFSLRLRIFNLNCWGIPYLSKURADPMRRLGDFL LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LQQQEGDRTKEQ NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVPSKHPIGELTQHIYTLNGVGIPYLSKURADPMRRLGDFL SGMVLNAYVTHLHAEYNRGNTYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKBWTGLHDAYLETRDPKGSEEG NTMYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFBT TTGFDPHRGTPLSHHEAIMTLFVHNSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGIGMA\QARWWA\TFA\SYVIGLGL\L LALLCVLAAGGGAGEAAILLHTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LQQQEGDRTKEQ 6963 374 2618 RVTPLILKLLKKFKTAENQKASEENEITQPGGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQNRRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDEMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFFGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSRPQHSVDRIYSALVACSMQMSGSE RSFYSGAVVSHETALGLPHHMEDDSWITTHIRRSQOMERYL STTPETTHCRKQPRPRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEFKGESFDGSVSSIGTEPDSV EQQFPGGAARDSQAEPTAREGGPTNOLETGASSPE RQMFEVEMDSTVITTYSNSDKSVLQQPSVNTSIGQPLPSTQLYLR			•	
LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRIRIFNINCWGIPYLSKHRADRMRRLGDFL NOESPDLALLEEWNSEQDYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAMELAGFIHHTSKK ADVVLLCGDLMMHPEDLGCLLKEWTGLHDAYLETREDFKSEBG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTFLSDHEALMATLFVHSPPQOMPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWAYTAP\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LQQQEGDRTKSQ 6962 340 1646 RPWSSPTMKPNFSILRIRINCWGIFYLSKHRADRMRRLGDFL NQESFDLALLEEWNSEQDFQVLRQKLSPTYPAAHHFRSGIIGSG LCVPSKHPIGELTQHIYTINGYPYMIHHGDWFSGKAVGLLVHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGHDAYLETRDFKGSEBG NTMYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFFT TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLIGMA\QARWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LQQQBGDTKEQ PFFCDKLLLGLYSDLEIPSVSVGSVGKLIDFMYSGVLRVGSEBA EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHHFSNSVLETLMEQRNRGHCDVTVLHGSMLRAQRCVLAAGS PFFCDKLLLGYSDLEIPSVVSVGSVGKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFFGIQDSGQDTPRG TPESGTSGQSSDTESGYLGSHPQHSVDRIYSALYACSMONGSGE RSYFYGGAVVSHHETALGLPRDHMEDDSWITRIHRRSQOMERYL STTPETTHCRKQPRFVRIQTLVGNIHIKQEMEDDYDYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGAARDSQAEPPAEGGPOTNOLETGASSPE RSNEVEMDSTVITYSNSDKSVLQQPSVNTSIGQPLPSTQLYLR				
NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGI IGSG LCVPSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLMMHPEDLGCCLLKEWTGLHDAYLETTDFFGSEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL\MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LGQQEGRTKEQ 1YRAQAELQHVLGRAREAQDLGPBPQLYALL\LGQQEGRTKEQ NGESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGI IGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLARKAVAQAWBLAQFIHHTSKK ADVVLLCGDLNMHPEDLGCLLKEWTGLHDAYLETTDPKGSEEG NTMYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TPA\SYVIGLGL\LL LALLCVLAAGGGAGEALLLHTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LQQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LQQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LQQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LQQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHHFSNSVLETINEQRNGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGODTRG TPESGTSGQSSDTESGYLQSPPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGDPDHHMEDPSWTRIHERSQQMERYL STTPETTHCRQPRPVRIQTLVCNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFPSGSSSSIGTEPDSV EQQGFGPGARRDSQAEPTQPGQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				
LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAVYHLHAENYNGKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGHDAYLETRDFKGSEEG NTMYPKNCYVSQGELKPFPFGVRIDYVLYKAVSGFYISCKSFET TGFDPHRGTPLSDHEALMATLFVRHSPPQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWMA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LGQQEGDRTKEQ NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLUVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWBLAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKBWTGLHDAYLETRDFKGSEEG NTMYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPBPQLVALL\LGQQBGDRTKEQ LYRAQAELQHVLGRAREAQDLGPBPQLVALL\LGQQBGDRTKEQ LYRAQAELQHVLGRAREAQDLGPBPQLVALL\LGQQBGDRTKEQ EAVLSPDPALHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNGGHFCDVTVRINGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSGNVGDVFPGIQDSGQDTTRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQMERYL STTPBTTHCRKQPRPVRIQTIVGNIHIKQBMEDDYDYYGQQRVQ ILERNESEECTRDTDQAEGTESEPKGESFDSGVSSITGTEPDSV EQQFGPGGAARDSQAEPTQPEQAAEDAGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	6961	340	: 1646	į l
SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQPIHHTSKK ADVVILCGDLINHIPEDIGCCLIKEWTGLHDAYLETRDFKGSEGG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQDRSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRARRAQDLGPBPQLYALL\LGQQEGDRTKEQ 6962 340 1646 RPWSSPTMKPNFSLRLRIFMLNCWGIPYLSKHRADRWRRLGGFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVUHL SGMVLNAYVTHLHEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNNHPEDLGCCLLKEWTGHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLKKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TPA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVUGRAREAQDLGPBFQLVALL\LGQQEGDRTKEQ 6963 374 2618 RVTPLILKLLKRPKTAENQKASEENEITQPGGSSAKPGLPCLNF EAVLSPDPALHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSONVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPBTTHCRKQPRPVRIQTLVGNIHIKQBMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAETOPEGAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR		•	·	NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG
ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMYPKNCYVSQDELKPPFFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPGQDFSSTHGP\AERS PL/MCVCLKEALDGSLGIGMA\QARWWA\TFA\SYYIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LGQQEGDRTKEQ NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGBLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQMPSSTHGP\AERS PL/MCVCLKEALDGSLGIGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTNSHAHTGSSDCDISCKGMTERIHSIN LHHFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFFGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHETALGJPRDHMEDPSWITRIHERSQQMERYL STTPESTTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAAEAPARGGPOTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR		,		
NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVVHRSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LGQQEGDRTKEQ NQESFDLALLEEVWSQDPFQYLRQKLSPTYPAAHFRSGIIGSG LCVPSKHPTQELTQHIYTLNGYPYNIHHGDWFSGKAVGLLVHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDPKGSEEG NTMVPKCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRARQDLGPPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTMSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFGDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIVSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				
TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGI\LL LALLCVLAAGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELCHVLGRAREAQDLGPBPQLYALL\LGQQEGDRYKEQ LYRAQAELCHVLGRAREAQDLGPBPQLYALL\LGQQEGDRYKEQ RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVPSKHPIQELTCHIYTUNGYPYNIHHGDWFSGKAVGLUVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGI\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELCHVLGRAREAQDLGPEPQLYALL\LGQQEGDRYKEQ LYRAQAELCHVLGRAREAQDLGPEPQLYALL\LGQQEGDRYKEQ EAVLSPDPALIHSTHSLTMSHAHTGSSDCDISCKGMTERIHSIN LHHFSNSVLETLWEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSGNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL SITPETTHCRKQPRPVRIQTLVCNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGAARDSQAEPTQEEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR		i		
PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVIAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPPQLYALL\LGQQEGDRTKEQ 1 1646 RPWSSPTMKPNFSLRIRIFNLNCWGIFYLSKHRADRMRRLGDFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMYLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKBWTGLHDAYLETRDFKGSEEG NTMYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ 6963 374 2618 RVTPLILKLKKPKTAENQKASEENETTQPGGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETILNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVSDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPREVRIQTLTUGNIHIKQBMEDDYDYYGQQRVQ ILERNESEECTEDDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPARGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR			:	
LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LGQQEGDRTKEQ 8962 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVPSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVUHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLMMHPEDLGCCLLKBWTGLHDAYLETRDFKGSEEG NTMYPKNCYVSQGLKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TPA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALHSTHSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETILNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFGDKLLLGYSDIEIBSVVSVQSVQKLIDEMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFFGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQCMERYL STYPETHCRKQPRPVRIQTLVGNIHIKQEMEDDYYYGQMEVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGFPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	'			
LYRAQAELQHVLGRAREAQDLGPBPQLYALL\LGQQEGDRTKEQ 8962 340 1646 RPWSSPTMKPNFSLRLFIFNLNCWGTPYLSKHRADRMRRIGDFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGTIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLMMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGIGMA\QARWWA\TFA\SYVIGIGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ 6963 374 2618 RVTPLILKLKKPKTAENQKASEENEITQPGGSSAKPGLPCLNF EAVLSPPPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFFGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQMSSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPBTTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILBERNESECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	1.			PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL
6962 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRIGDFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQABELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKBWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLVKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQDNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAPYLFHVQEVNG LYRAQAELQHVUGRAREAQDLGPEPQLYALL\LGQQEEDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETINEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSWQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQCMERYL STTPBTTHCRKQPRPVRIQTLVGNIHIKQEMEDDDYYGQQRVQ ILBENESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	-		1	
NQESFDLALLEEVMSEQDFQYLRQKLSPTYPAAHHFRSGIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWBLAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ 6963 374 2618 RVTPIILKLLKKPKTAENQKASEENEITQPGGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILEENESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				
LCVFSKHPIQELTQHITTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDPKGSEEG NTMVPKNCYVSQQELKFPFFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TPA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ 6963 374 2618 RVTPLILKLKKPKTAENQKASEENEITQPGGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGBVFFGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	6962	340	1646	
SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSQQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHIMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	1			
ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDPKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				
NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				
TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				1
PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLITNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	,			
LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ 6963 374 2618 RVTPLILKLLKKPKTAENQKASEENEITQPGGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPBTTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				
LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ 6963 374 2618 RVTPLILKLLKKPKTAENQKASEENEITQPGGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPBTTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
8963 374 2618 RVTPLILKLLKKPKTAENQKASEENEITQPGGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPBTTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				
EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPBTTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	6963	374	62-	
LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPBTTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	0703	3/4	2618	, , , , , , , , , , , , , , , , , , , ,
PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPBTTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				
LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPBTTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				· -
TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPBTTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR			*	
RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPBTTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	, ,			
STTPBTTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				
ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				1
EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				
RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				i
QTETLTSNLRMPLTLTSNTQVIGTAGNTYLPALFTTQPAGSGPK	[1
	L		<u> </u>	QTETETSNERMPLTETSNTQVIGTAGNTYEPAEFTTQPAGSGPK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1 10.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 .	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	504	\=possible nucleotide insertion)
			PFLFSLPOPLAGOOTOFVTVSQPGLSTFTAQLPAPQPLASSAGH
1			STASGOGEKKPYECTLCNKTFTAKONYVKHMFVHTGEKPHQCSI
·	ļ		CWRSFSLKDYLIK\HMVTHTGVRAYQCSICNKRFTQKSSLNVHM
1		1	RLHRGEKSYECYICKKKFSHKTLLERHVALHSASNGTPPAGTPP
			GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQFNDHMRMHVSDG
6964	1	178	SGRPFFFFFSNTDVYFIKKVTNRWTAGSSYKMTRMKSIGKILLL
""	_		QIFIG\NCSMFVLVI
6965	757	208	NVFIEPRIQGFMKTSAHPGQKHPDFSMGLLFPLLAALEVCSCGS
1	, , , ,]	SGSLGYNLPONH\GLLGRNTLVLLGOMRRISPFLCLKDRSDFRF
1			PQEKVEVSQLQKA\QAMSFLYDVLQQVFNFSHKALL\CCMEHDL
1		İ	PGPTPHFTSSAAGTPGDLLGAGDGRRRSWGQWVIEGSTLALRRY
1			FOESISTLE
6966	820	1867	IITALGVRGMPGCPCPGCGMAGPRLLFLTALALELLGRAGGSQP
,		1	ALRSRGTATACRLDNKESESWGALLSGERLDTWICSLLGSLMVG
1 .			LSGVFPLLVIPLEMGTMLRSEAGAWRLKQLLSFALGGLLGNVFL
1			HLLPEAWAYTCSASPGGEGQSLQQQQQLGLWVIAGILTFLALEK
			/HVPGQQGGDQPGPQQRPHCCCRRAQWRPLSGPAGCRARPRCR
i	•	[GP\DIKVSGYLNLLANTIDNFTHGLAVAASFLVSKKIGLLTTMA.
	1		ILLHEIPHEVGDFAILLRAGFDRWSAAKLQLSTALGGLLGAGFA
1			ICTOSPKGVEETAAWVLPFTSGGFLYIALVNVLPDLLEEEDPW
6967	162	633	GFLPFKYWILDLSASSRMETDCNPMELSSMSGFEEGSELNGFEG
	i i		TDMKDMRLEAEAVVNDVLFAVNNMFVSKSLRCADDVAYINVETK
]			ERNRYCLELTEAGLKVVGYAFDQVDDHLQTPYHETVYSLLDTL\
1 .		ļ	SPAYREAFGKR\LLQRLEALKRDGQS
6968	1 :	2265	RGGGGGRGCPGARERERPGEPERTMEAAAGGRGCFQPHPGLQKT
			LEQFHLSSMSSLGGPAAFSARWAQEAYKKESAKEAGAAAVPAPV
1	Ì		PAATEPPPVLHLPAIQPPPPVLPGPFFMPSDRSTERCETVLEGE
1.		ĺ	TISCFVVGGEKRLCLPQILNSVLRDFSLQQINAVCDELHIYCSR
			CTADQLEILKVMGILPFSAPSCGLITKTDAERLCNALLYGGAYP
:			PPCKKELAASLALGLELSERSVRVYHE\CFGKCKGL\LVPELYS
			SPSAACIQCLD\CRLMYPPHKFVVHSHKALENRTCHWGF\DSA\
1 :			NWRAYILLSQDYTGKEEQARLGR\CLDDVKEKFDYGNKYKRRVP
· .	` .		RVSSEPPASIRPKTDDTSSQSPAPSEKDKPSSWLRTLAGSSNKS
1	ĺ	1	LGCVHPRQRLSAFRPWSPAVSASEKELSPHLPALIRDSFYSYKS
1 (FETAVAPNVALAPPAQQKVVSSPPCAAAVSRAPEPLATCTQPRK
1 .			RKLTVDTPGAPETLAPVAAPEEDKDSEAEVEVESREEFTSSLSS
		1	LSSPSFTSSSSAKDLGSPGARALPSAVPDAAAPADAPSGLEAEL
1 .			EHLRQALEGGLDTKEAKEKFLHEVVKMRVKQEEKLSAALQAKRS
1			LHQELEFLRVAKKEKLREATEAKRNLRKEIERLRAENEKKMKEA
			NESRLRLKRELEQARQARVCDKGCEAGRLRAKYSAQIEDLQVKL
			QHAEADREQLRADLLREREAREHLEK\VVK\ELQEQLWPRARPE
			AAGSEG\AAELEP
6969	1855	118	AGTMHGRLKVKTSEEQAEAKRLEREQKLKLYQSATQAVFQKRQA
			GELDESVLELTSQILGANPDFATLWNCRREVLQQLETQKSPEEL
1			AALVKAELGFLESCLRVNPKSYGTWHHRCWLLGRLPEPNWTREL
	i e	I	ELCARFLEVDERNFHCWDYRRFVATQAAVPPAEELAFTDSLITR
ł		1	
			NFSNYSSWHYRSCLLPQLHPQPDSGPQGRLPEDVLLKELELVQN
			AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF
			AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP
			AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE
			AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKELQELEPENKWCL\LTIILLM
			AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKELQELEPENKWCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS
			AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKELQELEPENKWCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL
			AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKELQELEPENKWCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL
			AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKELQELEPENKWCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL
			AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKELQELEPENKWCL\LTIILLM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL

	·		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
·	sequence	•	\=possible nucleotide insertion)
6970	3	1528	SFPPLLSSPSAVGEGKVAVAAPCPGRSECARAKMAYIOLEPLNE
		2320	GFLSRISGLLLCRWTCRHCCOKCYESSCCOSSEDEVEILGPFPA
}			QTPPWLMASRSSDKDGDSVHTASEVPLTPRTNSPDGRRSSSDTS
	•		KSTYSLTRRISSLESRRPSSPLIDIKPIEFGVLSAKKEPIOPSV
i			LRRTYNPDDYFRKFEPHLYSLDSNSDDVDSLTDEEILSKYOLGM
ſ	[~ ***
			LHFSTQYDLLHNHLTVRVIEARDLPPPISHDGSRQDMAHSNPYV
1			KICLLPDQKNSKQTGVKRKTQKPVFEERYTFEIPFLEAQRRTLL
1	[LTVVDFDKFSRHCVIGKVSVPLCEVDLVKGGHWWKALIPSSQNE
1		1	VELGELLLSLNYLPSAGRLNVDVIRAKQLLQTDVSQGSDPFVKI
			QLVHGLKLVKTKKTSFLRGTIDPFYNESFSFKVPQEELENASLV
Ì	ł		FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRRMLNTHRT
			AVEQWHSLRSRAECDRVSPASLEVT
6971	37	3702	ACFYVPGSRSFKLIPRHGLVNMGRSGKLPSGVSAKLKRWKKGHS
1		,	SDSNPAICRHRQAARSRFFSRPSGRSDLTVDAVKLHNELQSGSL
1]		RLGKSEAPETPMEEEAELVLTEKSSGTFLSGLSDCTNVTFSKVQ
			RFWESNSAAHKEICAVLAAVTEVIRSQGGKETETEYFAALIRKA
	· .		AQHGVCSVLKGSEFMFEKAPAHHPAAISTAKFCIQEIEKSGGSK
1			EATTTLHMLTLLKDLLPCFPEGLVKSCSETLLRVMTLSHVLVTA
1			CAMQAFHSLFHARPGLSTLSAELNAQIITALYDYVPSENDLOPL
	1		LAWLKVMEKAHINLVRLQWDLGLGHLPRFFGTAVTCLLSPHSQV
	1		LTAATQSLKEILKECVAPHMADIGSVTSSASGPAQSVAKMFRAV
1	·	,	EEGLTYKFHAAWSSVLQLLCVFFEACGRQAHPVMRKCLQSLCDL
			RLSPHFPHTAALDOAVGAAVTSMGPEVVLQAVPLEIDGSEETLD
ì	ĺ		FPRSWLLPVIRDHVQETRLGFFTTYFLPLANTLKSKAMDLAQAG
	1		<u>-</u>
			STVESKIYDTLQWQMWTLLPGFCTRPTDVAISFKGLARTLGMAI
			SERPDLRVTVCQALRTLITKGCQAEADRAEVSRFAKNFLPILFN
1	ł		LYGQPVAAGDTPAPRRAVLETIRTYLTITDTQLVNSLLEKASEK
į.			VLDPASSDFTRLSVLDLVVALAPCADEAAISKLYSTIRPYLESK
· ·			AHGVQKKAYRVLEEVCASPQGPGALFVQSHLEDLKKTLLDSLRS
1	1		TSSPAKRPRLKCLLHIVRKLSAEHKEFITALIPEVILCTKEVSV
ł			GARKNAFALLVEMGHAFLRFGSNQEEALQCYLVLIYPGLVGAVT
1			MVSCSILALTHLLFEFKGLMGTSTVEQLLENVCLLLASRTRDVV
1	;		KSALGFIKVAVTVMDVAHLAKHVQLVMEAIGKLSDDMRRHFRMK
1	į į		LRNLFT\KFIPK\FGILTWGKKAVGPKEYHRVLVNIRKABARAK
			RHRALSQAAVEEEEEEEEEEEPAQGKGDSIEEILADSEDBEDNE
			EEERSRGKEQRKLARQRSRAWLKEGGGDEPLNFLDPKVAQRVLA
		•	TQPGPGRGRKKDHSFKVSADGRLIIREEADGNKMEEEEGAKGED
İ	1		EEMADPMEDVIIRNKKHQKLKHQKEAEEEELEIPPQYQAGGSGI
	,		HRPVAKKAMPGAEYKAKKAKGDVKKKGRPDPYAYIPLNRSKLNR
ļ			RKKMKLQGQFKGLVKAAQRGSQVGHKNRRKDRRP
6972	2179	973	PGGAILLPLWRRTRPREATVPRGAAQRGRARSAEGRIPSSQSPS
			PAEAGGATRSPPPRPPRPARPPGPSAPPLLRSDAGPGATVSAAA
1	[AAATERARRGATMGAQLSTLGHMVLFPVWFLYSLLMKLFORSTP
			AITLESPDIKYPLRLIDREIISHDTRRFRFALPSPOHILGLPVG
			OHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKDTHPK
			FPAGGKMSOYLESMOIGDTIEFRGPSGLLVYOGKGKFAIRPDKK
			SNPIIRTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLF
1			
			ANOTEKDILLRPELEELRNKHSARFKLWYTLDRAPEAWDYGOG\
			FVNEEMIRDHLPPPE\EEPLVLMCGPPPMIQYACLPNL\DHVGH
			PTERCFVF
6973	1	1964	LQPRCAHRGLRAQKCGRPAPGVDAMVLCPVIGKLLHKRVVLASA
ľ			SPRRQEILSNAGLRFEVVPSKFKEKLDKASFATPYGYAMETAKQ
			KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVDKQDAY
]]		RMLSRFE/SGREHSVFTGVAIVHCSSKDHQLDTRVSEFYEETKV
			KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFL
			NVVGFPLNHFCKOLVKLYYPPRPEDLRRSVKHDSIPAADTFEDL

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
:	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	poqueiico	\=possible nucleotide insertion)
 	bequence		SDVEGGGSEPTORDAGSRDEKAEAGEAGQATAEAECHRTRETLP
	٠.		PFPTRLLELIEGFMLSKGLLTACKLKVFDLLKDEAPOKAADIAS
1 /			
			KVDASACGMERLLDICAAMGLLEKTEQGYSNTETANVYLASDGE
1			YSLHGFIMHNNDLTWNLFTYLEFAIREGTNQHHRALGKKAEDLF
{			QDAYYQSPETRLRFMRAMHGMTKLTACQVATAFNLSRFSSACDV
			GGCTGALARELAREYPRMQVTVFDLPDIIELAAHFQPPGPQAVQ IHFAAGDFFRDPLPSAELYVLCRILHDWPDDKVHKLLSRVAESC
1			KPGAGLLLVETLLDEEKRVAQRALMQSLNMLVQTEGKERSLGEY
6974	3082	2172	QCLLELHGFHQVQVVHLGGVLDAIL\PPKWPPEAQAACSL
65/4	3052	21/2	RSCAAFASFASRPPLELFAPPGSHRSPPGRGVATSAQCALSVRK
1 1			LLAARPGLGTKYQATMVYKTLFALCILTAGWRVQSLPTSAPLSV
			SLPTNIVPPTTIWTSSPONTDADTASPSNGTHNNSVLPVTASAP
			TSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVH
			LTTTLEEHSLGTPEAGVAATLSQSAAEPPTLISPQAPASSPSSL
1 '	·		STSPPEVFSASVTTNHSSTVTSTQPTGAPTAPESPTEESSSDHT
6975	2	500	PTSHATAEPVPQEKTPPTTVSGKVMCELIDMET\PPPFPG
69/3	2	500	RPRPTVHCCKWALKLETAMETLINVFHAHSGKEGDKYKLSKKEL
]			KELLQTELSGFLDVKELML*ATEALKTFEEA*KSPIIQCSSSRS
1			SLPPAPQPPPYL+LSAVPFPIHLPLPLPPQAQKDVDAVDKVMK
6976	1216	970	BLDENGDGEVDFQEYVVLVAALTVACNNFFWENS
03/6	1215	. 970	GCQL*VAYGTTENSPVTFAHFPEDTVEQKAESVGRIMPHTEARI
1			MNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKW
			YWTGDVATMNEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHTH
			PKVQEVQVVGVKDDRMGEEICACIRLKDGBETTVEEIKAFCKGK
	1		ISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL*IKQQ
6977	1298	588	ACPGRLA
6977.	1298	588	SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R
•		: ·	ANKKSKHHVNGNRTVEPFPEGTQMAVFGMGCFWGAERKFWVLKG
1	,	•	VYSTQVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYQPEHMSFE
		:	ELLKVFWENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS KENYQKVLSEHGFGPITTDIREGQTFYYAEDYHQQYLSKNPNGY
	· · · · · ·	\$ ·	CGLGGTGVSCPVGIKK
6978:	3	242	SFPFRDSRRCGCCKGSSLRHTAVAMVKLSKEAKORLOOLFKGSO
05/0	3	242	
6979	3917	1146	FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG
1 ,00,00	3347	7740	DEARVRGEAVAAAILSRCRHWSGPPPFPPSPPDRKGLRGTEPWE AGPGSGATPGARAMDVRRLKVNBLREELORRGLDTRGLKTELAE
	•	,	l
	• • •		RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRONOFYDTOVIKOE
[İ	•	NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP
]]			DROOFOSRKRPYEENRGRGYFEHREDRRGRSPOPPAEEDEDDFD
j l			DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG
1 1	ſ		VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTOL
1			GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN
1 I			i I
[DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIOHLPLSERIRGTVGPKSKAECEILMMV
			GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR
[NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR
[RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL
]			EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP
[PPEKRFDNRGGGGFRGRGGGGGGGGTQRYENRGPPGGNRGGFQNRGG
			GSGGGGYYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA
] [PQQQPPPQQPPPPQQPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTF0PSYSQPPYNQGGYSQ
	ŀ		
			GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY
6980	1	420	

WO 01/53312

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1.	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
			CWTLRWPPLCSLHALHVFHCLFSSRLGTPVSPRLAMDPNCSCEA
			GGSCACAGSCKCKKCKCTSCKKSCCSCCPLGCAKCAQGCICKGA
6981			SEKCSCCA
6361	10	1054	PGRGFRRASLRPAFAARGVFQGGLGQAKQARTRACAALPTPHPS
			APRLLEPQGVFSLFPPPPGPWPNMILTKAQYDEIAQCLVSVPPT
1	ł		RQSLRKLKQRFPSQSQATLLSIFSQEYQKHIKRTHAKHHTSEAI
1			ESYYQRYLNGVVKNGAAPVLLDLANEVDYAPSLMARLILERFLQ
			EHEETPPSKSIINSMLRDPSQIPDGVLANQVYQCIVNDCCYGPL
1	ľ		VDCIKHAIGHEHEVLLRDLLLEKNLSFLDEDQLRAKGYDKTPDF ILQVPVAVEGHIIHWIESKASFGDECSHHAYLHDQFWSYWNRFG
I			PGLVIYWYGFIQELDCNRERGILLKACFPTNIVTLCHSIA
6982	153	1285	FPQQDCSAPAAPGLAGSEPRRLRAYRRRQRARGLKRVAWLAPP
			PSLLQGLQGWAQAPVDGTLGPEDSRASSPMIQNSRPSLLQPQDV
,	Y		GDTVETLMLHPVIKAFLCGSISGTCSTLLFQPLDLLKTRLQTLQ
	· · ·		PSDHGSRRVGMLAVLLKVVRTESLLGLWKGMSPSIVRCVPGVGI
			YFGTLYSLKQYFLRGHPPTALESVMLGVGSRSVAGVCMSPITVI
		,	KTRYESGKYGYESIYAALRSIYHSEGHRGLFSGLTATLLRDAPF
			SGIYLMFYNQTKNIVPHDQVDATLIPITNFSCGIFAGILASLVT
			QPADVIKTHMQLYPLKFQWIGQAVTLIFKDYGLRGFFQGGIPRA
6983			LRRTLMAAMAWTVYEEMMAKMGLKS
6963	82	773	EMSFLQDPSFFTMGMWSIGAGALGAAALALLLANTDVFLSKPQK
			AALEYLEDIDLKTLEKEPRTFKAKELWEKNGAVIMAVRRPGCFL
			CREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQPYFKGE
1			IFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLE
1	*	:	GEGFILGGVFVVGSGKQGILLEHREKEFGDKVNLLSVLEAAKMI KPQTLASEKK
6984	1845	1282	GGRSAYSLPAGSLPRVPATAAAKMASGVQVADEVCRIFYDMKVR
1			KCSTPEBIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTIT
-			DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELA
1 .1		*	PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLG
			GSLIVAFEGCPV
6985	1887	1324	RRTAGIYPCFPKPGRTRHALCSVVLLLLTGQLAFDDFQESCAMM
1	,		WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRALY
1 1		,	YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLK
		:	IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFK
6986	643	1250	LSGENGDEVKKE
		1350	YHLYFKMGDPNSRKKQALNRLRAQLRKKKESLADQFDFKMYIAF
1			VFKEKKKKSALFEVSEVIPVMTNNYEENILKGVRDSSYSLESSL
]			ELLQKDVVQLHAPRYQSMRRDVIGCTQEMDFILWPRNDIEKIVC LLFSRWKESDEPFRPVQAKFEFHHGDYEKQFLHVLSRKDKTGIV
			VNNPNQSVFLFIDRQHLQTPKNKATIFKLCSICLYLPQEQLTHW
1	1		AVGTIEDHLRPYMPE
6987	1623	341	LEAAEKASRAFKESQRQTDSKNYETENWSPQKSQRRYDMYNTAC
		-	PLGEIEVGLYTIQILQLTPFFHKENELSKKHMVQFLSGKWTIPP
1 1	l		DPRNECYLALSKFTSHLKNLQSDLKRCFDFFIDYMVLLKMRYTQ
]			KEIAEIMLSKKVSRCFRKYTELFCHLDPCLLQSKESQLLQEENC
	1		RKKLEALRADRFAGLLEYLNPNYKDATTMESIVNEYAFLLOONS
1	1		KKPMTNEKQNSILANIILSCLKPNSKLIQPLTTLKKQLREVLOF
	į.		VGLSHQYPGPYFLACLLFWPENQELDQDSKLIEKYVSSLNRSFR
	. [GQYKRMCRSKQASTLFYLGKRKGLNSIVHKAKIEQYFDKAQNTN
}	}		SLWHSGDVWKKNEVKDLLRRLTGQAEGKLISVEYGTEEKIKIPV
6000			ISVYSGPLRSGRNIERVSFYLGFSIEGPPGL
6988	3	689	TQLLRRPAVFVGSAASGIRSGLWSASSGHWCAPAAGRAHAPVPR
	1		LVRGLGAASTAAPQDAQTGPQPMPRADCIMRHLPYFCRGQVVRG
			FGRGSKQLGIPTANFPEQVVDNLPADISTGIYYGWASVGSGDVH
			KMVVSIGWNPYYKNTKKSMETHIMHTFKEDFYGEILNVAIVGYL

0.00	Predicted	T name 22 = 4 = 2	I have a sid compart containing
SEQ		Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine.
NO:	location		
		corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first	I .	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	amino acid	
,	residue of	residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	1	sequence	Codon, /=possible nucleotide deletion,
	sequence	ļ 	\=possible nucleotide insertion)
1			RPEKNFDSLESLISAIQGDIBEAKKRLELPEHLKIKEDNFFQVS
			KSKIMNGH
6989	2	1118	LMPSDRPLSPSTHASAGSHCHAPPTTARRAFPIPFGSKSNMATL
ł			KDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLADEL
1			ALVDVIEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNVTANSKLV
1	ì	ľ	IITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKLLIV
i			SNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV
1	i		HPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDK
			EQWKEVHKQVVESAYEVIKLKGYTSWAIGLSVADLAESIMKNLR
1	1	1	RVHPVSTMIKGLYGIKDDVFLSVPCILGQNGISDLVKVTLTSEE
6990	710	250	EARLKKSADTLWGIQKELQF
טעעס	719	258	THASGMASVVLALRTRTAVTSLLSPTPATALAVRYASKKSGGSS
1	1		KNLGGKSSGRRQGIKKMEGHYVHAGNIIATQRHFRWHPGAHVGV
	[GKNKCLYALEEGIVRYTKEVYVPHPRNTEAVDLITRLPKGAVLY
6991	169	451	KTFVHVVPAKPEGTFKLVAML RRSSDFHNPGFLSRPVSLRENIHHOVICSTKNKRRNPKKIAYLL
6331	103	451	
]		SSLLMTNLNPNESTENQPVDAYWAFTLDQEFLTYACVEGTGCLF CGRHVH
6992	944		<u></u>
0332	344	510	RQAPGCSSLALRQVRQVYCGLVRAPQVQTRPLSSRFVERRGALY
1			RSPMNQENPPPYPGPGPTAPYPPYPPQPMGPGPMGGPYPPPQGY
ł			PYQGYPQYGWQGGPQEPPKTTVYVVEDQRRDELGPSTCLTACWT
6993	1	374	ALCCCCLWDMLT OWCVTCPQHNARQGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG
6333	1 ·	3/4	DRVWIKNWNVASLCPLWKGPQTVVLSPPTAVKVEGIPAWIHHSH
			VKPAARETWEARPSPDNPFRVTLKKTTSPAPVTPGS
6994	346	1100	QWPEKDPVMAASSISSPWGKHVFKAILMVLVALILLHSALAQSR
بورون	240	1100	RDFAPPGQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES
ľ			SSQVLWAISSAISVAFFALSGIAAQLLNALGLAGDYLAQGLKLS
			PGQVQTFLLWGAGALVVYWLLSLLLGLVLALLGRILWGLKLVIF
		• ••	LAGFVALMRSVPDPSTRALLLLALLILYALLSRLTGSRASGAQL
			BAKVRGLERQVEELRWRQRRAAKGARSVEEE
6995	144	1346	GSVAVGLSGIMAAQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL
	}		LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMMHECYQIWAQL
		· ·	BHEAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHOCLSS
1 .			EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG
		•	GIVRDGEKVVEINPGLLVTVKTTSRSYQAKSLVITAGPWTNOLL
	.		RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH
			HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL
1			SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI
1			GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG
			KAHL
6996	543	1942	ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE
1			MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR
			EESRAVFLORKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN
1			YENFLKVGEKAGAKCKQFFTAKVFAKLLHTDSYGRISIMQFFNY
1			VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILELIPTLPQL
			DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD
1			LLELRDEELSKESQETNWFSAPSALRVYGQYLNLDKDHNGMLSK
			EBLSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN
]			RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD
į l			PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL
}	J	•	NGFWTYENREALVANDSENSADLDDT
6997	370	1104	AMBLTIFILRLAIYILTFPLYLLNFLGLWSWICKKWFPYFLVRF
	-		TVIYNEQMASKKRELFSNLQEFAGPSGKLSLLEVGCGTGANFKF
1	İ		YPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAAGENMH
<u> </u>			

	Dradietes	I Described	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
Ι.	residue of		
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
 	sequence	·	\-possible nucleotide insertion)
İ		ļ. ·	QVADGSVDVVVCTLVLCSVKNQERILREVCRVLRPGGAFYFMEH
l]		VAAECSTWNYFWQQVLDPAWHLLFDGCNLTRESWKALERASFSK
6998	2	616	LKLQHIQAPLSWELVRPHIYGYAVK
0998	2	810	FVSRALLRVRSRRHPAEERAAPGRPEDAPIECPGATNCPEPLWC
	1		SHLPVPYAPPTMESRGKSASSPKPDTKVPQVTTEAKVPPAADGK
ļ			APLTKPSKKEAPAEKQQPPAAPTTAPAKKTSAKADPALLNNHSN
İ	İ	į	LKPAPTVPSSPDATPEPKGPGDGAEEDEAASGGPGGRGPWSCEN
6999	1	3.563	FNPLLVAGGVAVAAIALILGVAFLVRKK
6999	14	1591	GRAGACSRRDTAMSIEIESSDVIRLIMQYLKENSLHRALATLQE
			ETTVSLNTVDSIESFVADINSGHWDTVLQAIQSLKLPDKTLIDL
1	1		YEQVVLELIELRELGAARSLLRQTDPMIMLKQTQPERYIHLENL
	·	1	LARSYFDPREAYPDGSSKEKRRAAIAQALAGEVSVVPPSRLMAL
] ·			LGQALKWQQHQGLLPPGMTIDLFRGKAAVKDVEEEKFPTQLSRH
		· .	IKFGQKSHVECARFSPDGQYLVTGSVDGFIEVWNFTTGKIRKDL
		·	KYQAQDNFMMMDDAVLCMCFSRDTEMLATGAQDGKIKVWKIQSG
Į.			QCLRRFERAHSKGVTCLSFSKDSSQILSASFDQTIRIHGLKSGK
			TLKEFRGHSSFVNEATFTQDGHYIISASSDGTVKIWNMKTTECS
ſ	[NTFKSLGSTAGTDITVNSVILLPKNPEHFVVCNRSNTVVIMNMQ
			GQIVRSFSSGKREGGDFVCCALSPRGEWIYCVGEDFVLYCFSTV
7000	2	. 027	TGKLERTLTVHEKDVIGIAHHPHQNLIATYSBDGLLKLWKP
7000	. 2	827	GPGVVFLELMESEGPPESERSEFFSQREEENBEEEAQEPEETGP
			KNPLLQPALTGDVEGLQKIFEDPENPHHEQAMQLLLEEDIVGRN
1			LLYAACMAGQSDVIRALAKYGVNLNEKTTRGYTLLHCAAAWGRL
1	·		ETLKALVELDVDI EALNFREERARDVAARYSQTECVEFLDWADA
		١ .	RLTLKKYIAKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEWL
	;		ETHTEASINELFEQRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH DOKRSODDTSN
7001	2056	844	RRCLIIAFLKGCFIFIYFIFIFETEFLSCCPGWSAVAQSRLIAN
7001	2030	0.44	FASQVQAIFILPKDSQVGPDVKSEAAPKRALYESVFGSGEICGP
			TSPKRLCIRPSEPVDAVVVVSVKHDPLPLLPEANGHRSTNSPTI
	·		VSPAIVSPTQDSRPNMSRPLITRSPASPLNNQGIPTPAQLTKSN
rt-		· · ·	APVHIDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKO
			HYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQL
	,		OPMLLEMERWKODRETGRFSRPCECLVVRVAPDLGERITLSGDK
1			SLIEEVFPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQ
	, ,		VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI
	: .	1	RIKQEPLD
L		t .	
7002	1043	498	
7002	1043	498	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP
7002	1043	498	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS
7002	1043	498	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV
7002	1043	498	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA
			PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC
7002	1043	498 61	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP
			PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA
			PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP
			PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE
			PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM
7003	818	61	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGAEQLLPNFCPSLEG
			PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGAEQLLPNFCPSLEG FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK
7003	818	61	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGAEQLLPNFCPSLEG FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG/YYCRVRPLGFPDQECCIEVINNTTVQLHTPE
7003	818	61	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRWWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGAEQLLPNFCPSLEG FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG/YYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH
7003	818	61	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGAEQLLPNFCPSLEG FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG/YYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF
7003	818	61	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG/YYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ
7003	818	61	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG/YYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQEFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL
7003	818	61	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG/YYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ

		·		
Si	EQ	Predicted	Predicted end	Amino acid segment containing signal peptide
lı	D D	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No	0:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
"		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1 .		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	: .			
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence		\=possible nucleotide insertion)
				QEKEQITISQLSLVDLAGSERTNRTRAEGNRLREAGNINQSLMT
1	•			LRTCMDVLRENOMYGTNKMVPYRDSKLTHLFKNYFDGEGKVRMI
		•		VCVNPKAEDYEENLOVMRFAEVTOEVEVARPVDKAICGLTPGRR
-			-	YRNQPRGP\IGNEPLVTDVVLQSFPPLPSCEILDINDEQTLPRL
1				IEALEKRHNLROMMIDEFNKOSNAFKALLOEFDNAVLSKENHMO
				GKLNEKEKMISGOKLEIERLEKKNKTLEYKIEILEKTTTIYEBD
				<u>**</u>
ļ		1		KRNLQQELETQNQKLQRQFSDKRRLEARLQGMVTETTMKWEKEC
i				ERRVAAKQLEMONKLWVKDEKLKQLKAIVTEPKTEKPERPSRER
L				DREKVTQRSVSPSPVPVSYL
70	005	63	876	RNMALYQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEEL
				WAAQVKRLASMAQKEPRTIKISLPGGQKIDAVAWNTTPYQLARQ
1				ISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAV
				FWHSSTHVLGAAAEQFLGAVLCRGPSTEYGFYHDFFLGKERTIR
.	100			GSELPVLERICOELTAAARPFRRLEASRDQLRQLFKDNPFKLHL
1				IEEKVTGPTATVYGCGTLVDLCQGPHLRHTGQIGGLKLLSNSSS
1		,		LWRSSG
770	06	22	898	NAFGRHSTAVKMAAAAWLQVLPVILLLLGAHPSPLSFFSAGPAT
٧٠ ا	,06		050	VAAADRSKWHIPIPSGKNYFSFGKILFRNTTIFLKFDGEPCDLS
				LNITWYLKSADCYNEIYNFKAEEVELYLEKLKEKRGLSGKYQTS
				SKLFQNCSELFKTQTFSGDFMHRLPLLGEKQEAKENGTNLTFIG.
ı			,	DKTAMHEPLQTWQDAPYIFIVHIGISSSKESSKENSLSNLFTMT
1		:	,	VEVKGPYEYLTLEDYPLMIFFMVMCIVYVLFGVLWLAWSACYWR
				DLLRIQFWIGAVIFLGMLEKAVFYAGFQ
70	07	2 .	1001	AMTVSGPGTPEPRPATPGASSVEQLRKEGNELFKCGDYGGALAA
j				YTQALGLDATPQDQAVLHRNRAACHLKLEDYDKAETEASKAIEK
		•	•	DGGDVKALYRRSQALEKLGRLDQAVLDLQRCVSLEPKNKVFQEA
i	•			LRNIGGOIOEKVRYMSSTDAKVEOMFQILLDPEEKGTEKKOKAS
				QNLVVLAREDAGAEKI FRSNGVQLLQRLLDMGETDLMLAALRTL
		•	•	VGICSEHOSRTVATLSILGTRRVVSILGVESQAVSLAACHLLQV
.]	: '	÷	* * .	MFDALKEGVKKGFRGKEGAIIVGENKQVWGLLDVTVMEGMGLSQ
				PGQFFGDQTCSCRLFGIRFGDIILL
70	008	70	1478	CRSALGHERPPPAHLPAGGRRLQTCPRSCRWLGRPPSGLPPGPR
1 ′	,00	/"	14/0	SPPPLAGPGOKMVOKKPAELQGFHRSFKGONPFELAFSLDQPDH
	,	·	· .	1
1	:			GDSDFGLQCSARPDMPASQPIDIPDAKKRGKKKKRGRATDSFSG
Į			•	RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH
				IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG
	•			SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE
.	٠	•		NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS
1				AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG
1				RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA
i				KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR
1				WDSHFLLPPHPCRIHVRPGGLVRTVTVNB
. 70	109	1	626	ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG
1		[-		RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA
1		•		LRLVACAOSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH
1				WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL
1		,		1
	-			GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE
70	10	79	571	SHTRRAVVPETLLSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT
1		!		GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC
				VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS
1				HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG
70	11	3	994	RIQTLPNQNQSQTQPLLKTPPAVLQPIAPQTTFGVQTQPQPQSL
				LQAQISAASITPLLQTQPQPLLQQPQQKAGLLQPPVRIVSQPQP
				ARRLDPPSRFSGRNDRGDQVPNRKDDRSRERERERRRSRERSPQ
				RKRSRERSPRRERERSPRRVRRVVPRYTVQFSKFSLDCPSCDMM
				ELRRRYQNLYIPSDFFDAQFTWVDAFPLSRPFQLGNYCNFYVMH
		L		The Manage and a partie of the partie of the parties of the partie

	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			REVESLEKNMAILDPPDADHLYSAKVMLMASPSMEDLYHKSCAL
		•	AEDPQELRDGFQHPARLVKFLVGMKGKDEAMAIGGHWSPSLDGP
			DPEKDPSVLIKT\AIRCCKALTG
7012	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
ì	· .		AAAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
ł			VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME
)			TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER
			NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFOSRLPH
			DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL
	1		TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL
}	1		PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
			ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKOKCP
1		•	LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP
1	}	•	VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV
			NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
* * * * *		•	YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE
			FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG
			LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL
			PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
			FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
1		•	IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
ł			RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE
Į			HTIRNYPATYHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
<u> </u>	·		AQQSPSM
7013	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
			AAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
1			VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME
.			TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER
		.	NAKAEKEKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH
	ļ ;		DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL
ł	·	· 	TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL
	1	•	PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
	:		ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP
	:	• 	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP
	: *		ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV
			ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV 'NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
	: 		ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV 'NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE
	: 		ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV 'NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG
			ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV 'NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL
			ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV 'NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
			ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV 'NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
			ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV 'NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
		•	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE
			ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV 'NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
7014	3	3950	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV 'NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
7014	3	3950	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITFGPSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE
7014	3	3950	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV NLKEKIKELHQQYKEASEVKPPRDITAEFLVRSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEABEPD
7014	3	3950	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEABEPD CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM
7014	3	3950	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGB HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEABEPD CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM PLATDSPTSDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP
7014	3	3950	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEABEPD CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM PLATDSPTSDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS
7014	3	3950	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEABEPD CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM PLATDSPTSDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG
7014	3	3950	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEABEPD CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM PLATDSPTSDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG PQAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP
7014	3	3950	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEABEPD CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM PLATDSPTSDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG
7014	3	3950	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEABEPD CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM PLATDSPTSDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP HSEQYPDLLPLBARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG PQAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR
7014	3	3950	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEABEPD CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM PLATDSPTSDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG PQAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR

Г	SEQ	Predicted	Predicted end	Amino agid cogment containing signal and it
	ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		·location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence		\=possible nucleotide insertion)
				MELQQLREMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAKVIE
-		•		BLLQTERDYIRDLEMCIERIMVPMQQAQVPNIDFEGLFGNMQMV
		•		IKVSKQLLAALEISDAVGPVFLGHRDELEGTYKIYCQNHDEAIA
		•		LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFLIKP
ı				VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVNINE
				YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSHLKH
ŀ				LTGFAPQIKDEVFEETEKNFRMQERLIKSFIRDLSLYLQHIRES
ı				ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNFKER
1				TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAEKLK
1				DKKTLEELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCVHGY
				ABAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSRVLQ
				QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYMLQSE
.		- -		ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVIKKK
				DPMGSQNRWLIDNGVTKGFVYSSFLKPYNPRRSHSDASVGSHSS
				TESEHGSSSPRFPRQNSGSTLTFNPN\S\MAVSFTSGSCQKQPQ DASPPPKEWDQGTLSASLNPSNSESSPSRCPSDPDSTSQPRSGD
				SADVARDVKQPTATPRSYRNFRHPEIVGYSVPGRNGQSQDLVKG
				CARTAQAPEDRSTEPDGSEAEGNQVYFAVYTFKARNPNELSVSA
1		•		NQKLKILEFKDVTGNTEWWLAEVNGKKGYVPSNYIRKTEYT
H	7015	1842	513	RQAWHE\VAAPSWRGARLVQSVLRVWQVGPHVARERVIPFSSLL
				GFQRRCVSCVAGSAFSGPRLASASRSNGQGSALDHFLGFSQPDS
		•		SVTPCVPAVSMNRDEQDVLLVHHPDMPENSRVLRVVLLGAPNAG
1		•		KSTLSNQLLGRKVFPVSRKVHTTRCQALGVITEKETQVILLDTP
				GIISPGKQKRHHLELSLLEDPWKSMESADLVVVLVDVSDKWTRN
1				QLSPQLLRCLTKYSQIPSVLVMNKVDCLKQKSVLLELTAALTEG
		`		VVNGKKLKMRQAFHSHPGTHCPSPAVKDPNTQSVGNPQRIGWPH
	İ			FKEIFMLSALSQEDVKTLKQYLLTQAQPGPWEYHSAVLTSQTPE
	1	.		EICANIIREKLLEHLPQEVPYNVQQKTAVWEEGPGGELVIQQKL
		. ')		LVPKESYVKLLIGPKGHVISQIAQEAGHDLMDIFLCDVDIRLSV
-	7016	167	2513	KLLK
		107		ILNAPKPPPPRDSVEAVAAKRDTGGGSWGTGMDVSGQETDWRST AFRQKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEYLS
	ļ			LVARLIIHFRDIHNKKSQASVSDPMNALQSLTGGPAAGAGIGM
1	.			PPRGPGQSLGGMGSLGAMGQPMSLSGQPPPGTSGMAPHSMAVVS
		:		TATPQTQLQQQVAAAAAAATARSSSSSSRRYSSSSSSSNSKQ
1	ļ			FQAQQSAMQQ\QFQA\VVQQQQQL\QQQQQQQQHLIKLHHQNQQ
				Q1QQQQQLQR1AQLQLQQQQQQQQQQQQQQQQALQAQPP1QQP
1	. }		•	PMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQ
	- 1		ł	LPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQP
ı				QVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTP
	1	ļ	ļ	QSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPF
	İ	l	1	\QSPVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQY
				LDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSKMKSLLDILTDP
				SKRCPLKTLQKCEIALEKLKNDMAVPTPPPPPPVPPTKQQYLCQP
1	ł	1		LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR
		1		RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC
1		1		KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV
-	7017	1	1785	HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA
		*	1/85	INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL FAFLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFLLDR
	ļ			FAFLAHTQKEAYAPKIFFEASRPPWFTPRSQQDCSEYLRFLLDR LHEEEKILKVQASHKPSEILECSETSLOEVASKAAVLTETPRTS
1	1			DGEKTLIEKMFGGKLRTHIRCLNCRSTSQKAEAFTDLSLAFWPS
				YSLEYMSCPDCSQSPSIQDGGLMQASVPGPSEEPVVYNPTTAAF
				ICDSLVNEKTIGSPPNEFYCSENTSVPNESNKILVNKDVPQKPG
		1	ĺ	GETTPSVTDLLNYFLAPEILTGDNQYYCENCASLQNAEKTMQIT
L	- 1			EEPEYLILTLLRFSYDQKYHVRRKILDNVSLPLVLELPVKRITS
_				

SEQ Predicted beginning nucleotide location nucleotide location corresponding to first amino acid segment containing sign (A=Alanine, C=Cysteine, D=Asparti Glutamic Acid, F=Phenylalanine, GH=Histidine, I=Isoleucine, K=Lysi L=Leucine, M=Methionine, N=Aspara P=Proline, Q=Glutamine, R=Arginin amino acid residue of amino acid sequence Seq	c Acid, E= =Glycine, ne, gine, e, wn, *=Stop tion, SCTKLVPYLLS QSEALALASSQ VTFTSFQSVQK WINGDPPLQKE FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence No: nucleotide location corresponding to first amino acid residue of amino acid sequence No: nucleotide location corresponding to first amino acid residue of amino acid sequence No: nucleotide location corresponding to first amino acid residue of amino acid sequence No: nucleotide location corresponding to first amino acid semino acid residue of amino acid sequence No: nucleotide location corresponding to first amino acid semino acid residue of amino acid sequence No: nucleotide location corresponding to first amino acid semino acid residue, N=Histidine, I=Isoleucine, K=Lysi L=Leucine, M=Methionine, N=Aspara P=Proline, Q=Glutamine, R=Arginin S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unkno Codon, /=possible nucleotide dele lepossible nucleotide insertion) FSSLSESWSVDVDFTDLSENLAKKLKPSGTDEA SVVVHSGISSESGHYYSYARNITSTDSSYQMYH SHLLGRDSPSAVFEQDLENKEMSKEWFLFNDSR ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGL LMDAITKDNKLYLQEQELNARARALQAASASCS PGSCGPTGGGGGGGGFTTVGRLVF 7018 484 1066 SLVFRGNTWSGEAGHHCSALFNLAAYHQLFVGT PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQN GMKARMEKELLEMRPFRSSFQVQLASNPVLDAW DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIR QASSKGSAAGGGGAGEQA	=Glycine, ne, gine, e, wn, *=Stop tion, SCTKLVPYLLS QSEALALASSQ VTFTSFQSVQK WINGDPPLQKE FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
location corresponding to first to first amino acid residue of amino acid sequence P=Proline, Q=Glutamine, X=Arginin Codon, /=possible nucleotide dele codon, /=possible nucleot	ne, gine, e, wn, *=Stop tion, SCTKLVPYLLS QSEALALASSQ VTFTSFQSVQK WINGDPPLQKE FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
corresponding to first to first amino acid residue of amino acid sequence sequence Test amino acid residue of amino acid sequence sequence Test amino acid residue of amino acid sequence Test amin	gine, e, wn, *=Stop tion, SCTKLVPYLLS QSEALALASSQ VTFTSFQSVQK WINGDPPLQKE FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
to first amino acid residue of amino acid residue of amino acid sequence Se	e, wn, *=Stop tion, SCTKLVPYLLS QSEALALASSQ VTFTSFQSVQK WINGDPPLQKE FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
amino acid residue of residue of residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unkno Codon, /=possible nucleotide dele \(=possible nucleotide insertion \) FSSLSESWSVDVDFTDLSENLAKKLKPSGTDEA SVVVHSGISSESGHYYSYARNITSTDSSYQMYH SHLLGRDSPSAVFEQDLENKEMSKEWFLFNDSR ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGL LMDAITKDNKLYLQEQELNARARALQAASASCS PGSCGPTGGGGGGGFNTVGRLVF 7018 484 1066 SLVFRGNTWSGEAGHHCSALFNLAAYHQLFVGT PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQN GMKARMEKELLEMRPFRSSFQVQLASNPVLDAW DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIR QASSKGSAAGGGGAGEQA	wn, *=Stop tion, SCTKLVPYLLS QSEALALASSQ VTFTSFQSVQK WINGDPPLQKE FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
residue of amino acid sequence Codon, /=possible nucleotide dele sequence =possible nucleotide insertion)	tion, SCTKLVPYLLS QSEALALASSQ VTFTSFQSVQK WINGDPPLQKE FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
residue of amino acid sequence W=Tryptophan, Y=Tyrosine, X=Unkno Codon, /=possible nucleotide dele \ =possible nucleotide insertion) FSSLSESWSVDVDFTDLSENLAKKLKPSGTDEA SVVVHSGISSESGHYYSYARNITSTDSSYQMYH SHLLGRDSPSAVFEQDLENKEMSKEWFLFNDSR ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGL LMDAITKDNKLYLQEQELNARARALQAASASCS PGSCGPTGGGGGGGFNTVGRLVF 7018 484 1066 SLVFRGNTWSGEAGHHCSALFNLAAYHQLFVGT PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQN GMKARMEKELLEMRPFRSSFQVQLASNPVLDAW DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIR QASSKGSAAGGGGAGEQA	tion, SCTKLVPYLLS QSEALALASSQ VTFTSFQSVQK WINGDPPLQKE FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
amino acid sequence Codon, /=possible nucleotide dele =possible nucleotide insertion)	tion, SCTKLVPYLLS QSEALALASSQ VTFTSFQSVQK WINGDPPLQKE FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
sequence =possible nucleotide insertion	SCTKLVPYLLS QSEALALASSQ VTFTSFQSVQK WINGDPPLQKE FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
FSSLSESWSVDVDFTDLSENLAKKLKPSGTDEA SVVVHSGISSESGHYYSYARNITSTDSSYQMYH SHLLGRDSPSAVFEQDLENKEMSKEWFLFNDSR ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGL LMDAITKDNKLYLQEQELNARARALQAASASCS PGSCGPTGGGGGGGFNTVGRLVF 7018 484 1066 SLVFRGNTWSGEAGHHCSALFNLAAYHQLFVGT PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQN GMKARMEKELLEMRPFRSSFQVQLASNPVLDAW DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIR QASSKGSAAGGGGAGEQA	QSEALALASSQ VTFTSFQSVQK WINGDPPLQKE FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
SVVVHSGISSESGHYYSYARNITSTDSSYQMYH SHLLGRDSPSAVFEQDLENKEMSKEWFLFNDSR ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGL LMDAITKDNKLYLQEQELNARARALQAASASCS PGSCGPTGGGGGGGFNTVGRLVF 7018 484 1066 SLVFRGNTWSGEAGHHCSALFNLAAYHQLFVGT PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQN GMKARMEKELLEMRPFRSSFQVQLASNPVLDAW DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIR QASSKGSAAGGGGAGEQA	QSEALALASSQ VTFTSFQSVQK WINGDPPLQKE FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
SHLLGRDS PSAVFEQDLENKEMSKEWFLFNDSR ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGL LMDAITKDNKLYLQEQELNARARALQAASASCS PGSCGPTGGGGGGGFNTVGRLVF 7018 484 1066 SLVFRGNTWSGEAGHHCSALFNLAAYHQLFVGT PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQN GMKARMEKELLEMRPFRSSFQVQLASNPVLDAW DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIR QASSKGSAAGGGGAGEQA	VTFTSFQSVQK WINGDPPLQKE FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGL LMDAITKDNKLYLQEQELNARARALQAASASCS PGSCGPTGGGGGGGFNTVGRLVF 7018 484 1066 SLVFRGNTWSGEAGHHCSALFNLAAYHQLFVGT PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQN GMKARMEKELLEMRPFRSSFQVQLASNPVLDAW DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIR QASSKGSAAGGGGAGEQA	WINGDPPLQKE FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
LMDAITKDNKLYLQEQELNARARALQAASASCS PGSCGPTGGGGGGGFNTVGRLVF 7018 484 1066 SLVFRGNTWSGEAGHHCSALFNLAAYHQLFVGT PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQN GMKARMEKELLEMRPFRSSFQVQLASNPVLDAW DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIR QASSKGSAAGGGGAGEQA	FRPNGFDDNDP ERIRAPEIIFQ VFLTGGNTMYP
PGSCGPTGGGGGGGFNTVGRLVF 7018 484 1066 SLVFRGNTWSGEAGHHCSALFNLAAYHQLFVGT PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQN GMKARMEKELLEMRPFRSSFQVQLASNPVLDAW DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIR QASSKGSAAGGGGAGEQA	ERIRAPEIIFQ VFLTGGNTMYP
7018 484 1066 SLVFRGNTWSGEAGHHCSALFNLAAYHQLFVGT PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQN GMKARMEKELLEMRPFRSSFQVQLASNPVLDAW DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIR QASSKGSAAGGGGAGEQA	VFLTGGNTMYP
PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQN GMKARMEKELLEMRPFRSSFQVQLASNPVLDAW DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIR QASSKGSAAGGGGAGEQA	VFLTGGNTMYP
GMKARMEKELLEMRPFRSSFQVQLASNPVLDAW DDNEVWITRKEYBEKGGEYLKEHCASNIYVPIR QASSKGSAAGGGGAGEQA	
DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIR QASSKGSAAGGGGAGEQA	
QASSKGSAAGGGGAGEQA	
	LPKQASRSSDA
7019 1048 335 APGGFLVTMVFPAPSPPWMLGCCSHEVTAGPPT	
, , , , , , , , , , , , , , , , , , ,	
RMRHIPLAPGSDWRDLPNIEVRLSDGTMARKLR	
SSGALRGVCSCVEAGKACDPAARQFNTLIPWCL	
GLYGRLEWDGFFSTTVTNPEPMGKQGRVLHPEQ	
SQGFPDTYRLFGNILDKHRQVGNAVPPPLAKAI	GLBIKLCMLAK
ARESASAKIKEEEAAKD	
7020 1 2154 FADSKRKSVLLDKIKNLQVALTSKQQSLETAMS	FVARNTFKRVR
NGFLMRKVAVFFSNTPTRASPQLREAVLKLSDA	GITPLFLTRQE
DRQLINALQINNTAVGHALVLPAGRDLTDFLEN	VLTCHVCLDIC
. NIDPSCGFGSWRPSFRDRRAAGSDVDIDMAFIL	DSAETTTLFQF
NEMKKYIAYLVRQLDMSPDPKASQHFARVAVVQ	HAPSESVDNAS
MPPVKVEFSLTDYGSKEKLVDFLSRGMTQLQGT	RALGSAIEYTI
ENVFESAPNPRDLKIVVLMLTGEVPEOOLEEAO	RVILOAKCKGY
FFVVLGIGRKVNIKEVYTFASBPNDVFFKLVDK	STELNEEPLMR
FGRLLPSFVSSENAFYLSPDIRKQCDWFQGDQP	TKNLVKFGHKO
VNVPNNVTSSPTSNPVTTTTKPVTTTTK	
INOPSVKPAAAKPVAAKPVATKTATVRP	-
PVAAKPAAVRPPAAAAAKPVATKPEVPRPQAAK	
MVKMSREVQVFEITENSAKLHWERPEPPGPYFY	
LVLKQNLTVTDRVIGGLLAGQTYHVAVVCYLRS	
TKKSOPPPPOPARSASSSTINLMVSTEPLALTE	
TCRDFILKWYYDPNTKSCARFWYGGCGGNENKF	
PVLAKPGVISVMGT	000.0000.00
7021 2 338 VNAVSFFPNGYAFATGSDDATCRLFDLRADQEL	T.T.VSUDMITTO
ITSVAFSKSGRLLLAGYDDFNCNVWDTLKGDRA	
CLGVTDDGMAVATGSWDSFLRIWN	~ A THOUTHURY A
7022 2 856 VYIGSFWSHPLLIPDNRKLFEAEEODLFRDIOS	T.DDNIA T DVI N
DLIKRARLAKVHAYIISSLKKEMPSVFGKDNKK	
GRIEREHQISPGDFFNLKRMQDQLQAQDFSKFQ	
DMLAHDIAQLMVLVRQEESQRPIQMVKGGAFEG	
EGAGEGIDDAEWVVARDKPMYDEIFYTLSPVDG	
VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALA	MHLIKVKLEGH
ELPNELPAHLLPPSKRKVAE	
7023 2 748 AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLV	
WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRV	
TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFS	-
VAGYITYLSIDSALFVETLGFLAVLTEAMLGVP	
EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSV	CGLLQVLVDLA
ILGQAYAFARHPQKPAPHAVHPTGTKAL	
7024 1207 190 RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPE	RGLGPSDGWLV
SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLL	TRSPTAWHRLS
QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGG	QGQPQGPGLRT
RLLITGLFGAGLGGAWLALRAEKERLQQQKRTE	ALRQAAVGQGD
FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDI	
VRQLEAEPGLPPVQPVFITVDPERDDVEAMARY	

C 000	1 5 1 1 1	Y 22	
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
. .	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
J	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ. ·	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence		\=possible nucleotide insertion)
			TGSTKQVAQASHSYRVYYNAGPKDEDQDYIVDHSIAIYLLNPDG
			LFTDYYGRSRSAEQISDSVRRHMAAFRSVLS
7025	232	832	ERNSPIGNNENL*K\HSLDCLCFRGDWEGNTQFQTLQDNQEECF
		+	KQVIRTCEKRPTFNQHTVFNLHQRLNTGDKLNEFKELGKAFISG
	,	·	SDHTQHQLIHTSEKFCGDKECGNTFLPDSEVIQYQTVHTVKKTY
1			ECKECGKSFSLRSSLTGHKRIHTGEKPFKCKDCGKAFRFHSQLS
<u> </u>		J	VHKRIHTGEKSYECKECGKAFSCG
7026	328	1146	NPNPSIGDIKDIKKAAKSMLDPAHKSHFHPVTPSLVFLCFIFDG
1			LHQALLSVGVSKRSNTVVGNENEERGTPYASRFKDMPNFIALEK
1	[SSVLRHCCDLLIGVAAGSSDKICTSSLQVQRRFKAMMASIGRLS
			HGESADLLISCNAESAIGWISSRPWVGELMFTFLFGDFESPLHK
ľ	ĺ	ĺ	LRKSS*LPRKHR*QPINAVRMFLDQCMDGSIALRAIVSEIPVFE
			EKKNNG*KGIGEIF*VWGCTLPPHYWGAVTTNVPKLSNSGKLLG
			QDEQPHIFG
7027	43	954	GRRLQQQQRPEDAEDGAEGGGKRGEAGWEGGYPEIVKENKLFEH
ļ	ŀ		YYQELKIVPEGEWGQFMDALREPLPATLRITGYKSHAKEILHCL
			KNKYFKELEDLEMDGQKVEVPQPLSWYPEBLAWHTNLSRKILRK
			SPHLEKFHQFLVSETESGNISRQEAVSMIPPLLLNVRPHHKILD
·			MCAAPGSKTTQLIEMLHADMNVPFPEGFVIANDVDNKRCYLLVH
			QAKRLSSPCIMVVNHDASSIPRLQIDVDGRKEILFYDRILCDVP
	•	4	CSGDGTMRKNIDVWKKWTTLNSLQLHGLQLRIATRGAEQL
7028	189	608	SRPPPEPEPGTMVEKGSDSSSEKGGVPGTPSTQSLGSRNFIRNS
, , , ,	-05	300	
	:		KKMQSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALQR
			EILLQGRLYLSENWICFYSNIFRWETTISIQLKEVTCLKKEKTA KLIPNAIO
7029	1343	40	VLESNTEAKQATGTSSKLRHGTGQEKGREGPRCPSGLAQLRLWG
, , ,	1313	40	/PCPHAGRETGPRASAPIPGS*GHGWHW*RKDGRGERSEGPSAL
			SPHSPSLLNMQQAPTHVGPGMGSQRPRSSVVPEQVGVGSQLSRE
		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RWRA*RSLPGAAASERTEMTKERSP/RPCQGYDSSNWFTQPGKK
			TRKRNSRRNTMVSRGGGCLLYPLQSIMPE*QLR*GAHASPPTOG
• 1		,	R*GKGGPRSPLTKASGTTHIPTFFFGSIP/RPTRDSGPGTDNS\
٠,			AAPGQKRGHREA*QGPEPV/WGRVTTHLQGPAG*TKPLGS\RNW
			VPGPAEGEQGEGAGLEGRP*PLKGCRSTLTFSPQLSIPMVGKKP
			PEGTTASFFP\RSCHSE*RKPPPSCPHAPALSLPHPLPLPLPL
			PLOT DOLOGOPHICA DOCUMENT CONTROL CONTROL OF THE PROPERTY OF T
	;		PLPLPGAGT*HSARSGRPGQSETGSLCHNCHHCPPHCPKCSPGG
7030	2	521	<u> </u>
	-	JOL	FVCFSAPGSGGGKRRVNMELSAVGERVFAAEALLKRRIRKGRM
			EYLVKWKGWSQKYSTWEPEENILDARLLAAFEEREREMELYGPK
			KRGPKPKTFLLKAQAKAKAKTYEFRSDSARGIRIPYPGRSPQDL
j		•	ASTSRAREGLRN\RVCPRQRAAPAPAP\PRRGPSGPGPRPG*G
7031	960	FA	PGLHFPGPGGPSKHGFVPASEQHQHQQHLPRRGPSGPGPRPG
, , , ,	200	59	HCSVPGAEWPRKPPAQICPQLTSRPHLSSPRSLSPGCGHSPGPG
	Į		/CKPS/RHCDELHEGPSRTAALPCGKPQPKHGVEECG/PCPCLA
1	ļ		PRRLTEPPALTVSPVGRAAPSGAL*PSGRACSACSHRLAPEAAL
]	j		SAAAPRPSLGSGQNASGLPAASLPPQDSSQPHKTVPSPARSVPP
			LGAQARAAPPRLWCPRALVSG*EASPEAVSVAAGPPVPGPTPST
]			SGSTASHSRRGC*SPR*TPAPPRRDHGRSAAFEVLTAAASAQPC
7022		· · · · · · · · · · · · · · · · · · ·	ASQGGPRPTGAGRTPSPLGLPFSRGPPAASARPFCRHPSL
7032	1393	2104	RRPGRTEPVEPPPVPPPPRASNSKSRCR*RNLHLAPL*QSPLRK
ļ	1		SRQIGTSSLPFGRSAGERPRPAATFCLSRGGSSPVFL*PSSSSL
	l		EPWMKRQFGRLHSLFWKSWQKMNSFLLTPKLDTSLMSGWRYRQR
į		!	LPRLHTFLKKSLQMASELAPPLPTPAPLASSLPPPPGPPPLLPV
ł		1	PLA*LSRSGILVPPNSGFSLSC\PLGDH*GSSGEVRGSCGSPPP
		1	HHCWVLPPPP*LLLPPR

Degianing Cocation Corresponding Cocation Corresponding Cocation Corresponding Cofirst Samino acid Cofirst	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide				
Mo:	, –			(A=Alanine C-Cysteins D-Assartis Asid R				
Cocation Corresponding Cofirst amino acid maino	NO:			Glutamic Acid F-Dhenylalaning C-Clusing				
corresponding to first smino acid residue of amino acid residue of amino acid sequence squence		1		H=Histidine I-Isolevaine V-Ivaine				
to first amino acid residue of amino acid residue of amino acid amino acid sequence Servine, T-Mireonine, V-Voline, amino acid sequence W-Tryptophan, Y-Tyrcosine, X-Unknown, *-stop Codon, /-possible nuclectide deletion LMMPSSCPWRTGALOFPENSSKALEGETSSVPGESSWITTRISSP AAAPSAPTTPAAADPTSPASSWALEGETSSVPGESSWITTRISSP GCATRIWKTMMERPEDLERRYGESAPGIPALIPSAAPGGSAPG AAAPSAPTTPAAADPTSPASSWALEGETSSVPGESSWITTRISSP GCATRIWKTMMERPEDLERRYGESAPGIPALIPSAAPGGSAPGAPA AAAPSAPTTPAAADPTSPASSWALEGETSSVPGESSWITTRISSP GCATRIWKTMMERPEDLERRYGESAPGIPALIPSAAPGGSAPGAPA AAAPSAPTTPAAADPTSPASSWALEGETSVPGESSWITTRISSP GCATRIWKTMMERPEDLERRYGESAPGIPALIPSAAPGGSAPGAPA AAAPSAPTTPAAADPTSPASSWALEGETSVPGESSWITTRISSP GCATRIWKTMMERPEDLERRYGESAPGIPALIPSAAPGGSAPGAPATAPAAPTAPAAPGAPTAPAAPGAPATAPAAPTAPAAPGAPATAPAAPATAPAAPATAPAAPATAPAAPATAPAAPATAPAAPA	: .			LeLeucine M-Methionine M-Agnaragine				
amino acid residue of amino acid aequence Septime	1			D-Proline O-Clutomine D. Ameirica				
residue of amino acid sequence	:		7					
amino acid sequence Codon,	· I							
Sequence A-possible nucleotide insertion		I		Codon /-noggible nuglectide deletion				
LIMMESS PRETOLICISES NAS PAGE PRETOLICISES NO PROBREMITETS SUPERAMENTAL CONTRO		I.	bedrese	\-nossible nucleotide deletion,				
GCATRIWATMENERPERISSMESSADISDALBISARDSORS ARAPSAPTTPARAMONICAS CONCRIC SWISA ARAPSAPTTPARAMONICAS CONCRIC SWISA SUSTCPTSRIBGRAMETA (SWIPALLICS WILL SESTARSATORA) SUSTCPTSRIBGRAMETA (SWIPALLICS WILL SESTARSATORA) SUSTCPTSRIBGRAMETA (SWIPALLICS WILL SESTARSATORA) SUSTCPTSRIBGRAMETA (SWIPALLICS WILL SESTARSATORA) RISE FOR CONCRICTION OF THE PROPERTY O		1 1	 	IMMPSSCOWDTCAL COCDA COCTA COCTACO COCTACA PTCMPYGTVNLLHGVRPGSTPVTCTAGIGTPT VIGERTALSI TGDPVEDVARVALMRILMESRSDIGLVORMHDVLTSKRVALOBA IGARVDSYPFILVKAAILLGOVKRAMPHEVINTARTRYTTFDDM TILWQCHYKGTVSRPVTGSLEAVMPGLGSIGIDIDDAARHTINNY TURKOPGGLEFTVNLOGATURKKEGVEVERUHDVLTSKRVALOBG IGARVDSYPFILVKAAILLGOVKRAMPHEVINTARTRYTTFDDM TILWQCHYKGTVSRPVTGSLEAVMPGLGSIGIDIDDAARHTINNY TURKOPGGLEFTVNLOGATURKEKEGVEVELDMERFYSLKFERSKAUTVAAT GDPTLLEIGRDAVESIEKI SKVECGFATI KOLEDHKLDNRMSF FILASTVKAVILIFDDTVFI HINNSTFDAVITTYGSCILGAGGYI FINTSAHPIDPAALHCCORLKEECKEVEDLAMBETYSLKFERSKY KRYTHADSSILALGAQVFLDSS*FLONFFI FIFTKILATYKKLLLAI IKK K TOSS 92 1942 BOTSSMPFILIFIGALCALLFOCHGAPPERGSAPDPAHYERS FORTSCHALLGOVFLDSS*FLONFFI FIFTKILATYKKLLLAI IKK K K RMMYHANDSSILALGAQVFLOSS*FLONFFI FIFTKILATYKKLLLAI IKK K K TURLYGGGGEFTVI FOGTVVEKKEGVPLOGSUPDIDVINASVPETHUR RVVGGLISAHLISKAGVEVERAGPCGGLIRMBERAKKLIPA FOTFTCMPYGTVALLHGVHRGETTVTCTAGIGFT FUFFATLSCH TURLYGGGGLEFTVI FOGTVVEKKEGVPLREBARKKLIPA FOTFTCMPYGTVALLHGVHRGETTVTCTAGIGFT FUFFATLSCH TURLYGYGGLIBFTVI FOGTVVEKKEGVPLREBLIESAMVLINAF GOPPILLEIGRDAVSSILKS SKVECGFATI KOLEDHKLDRINGSTP TORTSCHALLGOVTVEKKEGVPLREFT SCHARCHKOP RVMSGPGGLEFTVI FOGTVVEKKEGVPLREFT SLKRREKGVF RVMSGPGGLEFTVI FOGTVVEKKEGVPLREFT SLKRERGFR GOPPILLEIGRDAVSSILKS SKVECGFATI KOLEDHKLDRINGSF FAATTWALVILLEDDTNP IRRNGSTDAVI TYPKGCLLAGGGYI FYTTAAUPI LIDABALLGCORLIKERCYGELTRINGKVPLLLESCH GOPPILLEIGRDAVSSILKS SKVECGFATI KOLEDHKDAVRH GOPPITARE PARAGCGGCPC PAQCHHGRPGOVSPLEREPHTTURFLIPP PPPPPPPPPPPPPPPPPPPPPPPPPPPPPTRPPTTURFLIPP PPPPPPPPPPPPPPPPPPPPRPRREGG 7037 442 761 CLAFLESCGTILLILLAGRGGRANALRGPGRN* LPGEGFSIPT RNM* BRKAGCGGPC PAQCHHGRPGOVSPLEREPHTTURFLIPP PPPPPPPPPPPPPPPPRPRREGG 7048 1		•	<u> </u>	
WDWRPPLQVSSPAPSSSCRASCWILLESIT*SSTARSATATAS SSSTCPTSRSSCRAATY SEMARA FLICEVEY LISRERALQDPR P034								
SSSTCPISRSDRGAMATY SEMGAPILICSUPLISREALODPR NPSP-GUGGSGSCHRALLAGE PVACSUP 1942 EDTSSMPFELLI PLGILLCALLPOHHGAGGPGGSADDRAHYRERU KAMPYHANDSULRAM PPOBLER PLUTCCHITMOSPSITLIDALD TLLATLLYPOILCNUSE PQRUVEVLQDSVDPDI DVINASVPETNI RVUGGLISAHLISKKAGUEVEAGWPCSSPLIBMAEBARKALDPA PQTPTOMPHOTVINLIGWOPEDFTVOTCAGICTUPEAPTISSI TGDEVEEDVARVALMRILESSESI OLUVANILIDVITGKWADDAG IGAGVDSYPETVUKGAI LLQOKKIAMMELESHEKA RKYTEPDDM YLWOYMKGTTSMPUPGSLEAVMPOLGSLIGDINNAMFFINYY TUWGGGGLPPYNITGGGTUPKERSEVLPEHESAMILYRAT GDPTLLELGEDAVESI EKI SKUECGPATIKDLENDKINDREMSP FLARTVKUNLILIPOPINYI INNNSSTPDAUTSEGDILGAGGYI PNTEAHPIDPAALHCCQRIKSEQMEVEDLAMBEYSILKSERSKFQ KNTYSSGPWEPPARPOTLIPS PENHODABERKOKVPLILSOPS QPTSKLALLGQVFLDSS * PLDNFFIFIFIRINYIKLLIATIKK K K TO35 92 1942 EDTSSMPFRLIIPLGILCALLPQHHGAPGPDKSAPDDAHYRERV KAMPYHAYDSILENAP PPDELRPLTCOGHDTWGGSFSLTITDALD TLLATLYFKYLILIONUSPERGWVEVLQDSWPDIDVINASVPETNI RVVGGLISAHLISKKAGUEVEAGWPCGSGPLIRMBERABKKLIPA FQTPTOMPYGTVALLHGWINGEFTYTCTAGICTIVEPATIGSI TGDEVEEDVARVALMBILBERSDIGISVANHIDVITGKWAQDAG IGAGVDSYFEVILLIGUNISPETPTUTCAGICTIVEPATIGSI TODEVEEDVARVALMBILBERSDIGISVANHIDVITGKWAQDAG IGAGVDSYFEVILKGAILLGOKALAMPLESHKRITYTEPDDW YLWOYMKGITVSMPVOGLERAYWPGLOSLIGDINNAMFFINNY TUWGPGGLPFYNTLOGOTYVERKRGVPLEPERFYSIKKRSKEPQ QPTTSKLALLGUPFINN FGGTYTVERRGBYPLEPERFYSIKKRSKEPQ QPTSKLALLGUPPINN FGGTYTVERRGBYPLEPERFYSIKKRSKEPQ QPTSKLALLGUPPINN FGGTYTVERRGBYPLEPERFYSIKKRSKEPQ RNTVSSGWBEPARPGTIFSPENHOQAREKERARKKULDENG GPPTLLELGEDAVESIEKISKVECOPATIKOLRIDAHDENGTYSL TYMOPGGLPSPTNINGGGTYTERRGBYPLEPERFYSIKKRSKEPQ QPTSKLALLGUPPINN FILDERFITTIRINYNKLLLACSGP QPTSKLALLGUPPINN FGGTYTURKLILATIKK 7036 442 761 CLAFLFSCFGITINHLAPSGRLRWAURGPGRN*LPGEGPSIPT RNM*ERKAGCSGPC/PAQGHGRPGSVSPLPPDHPTTLRPLPP PPPPPPPPPPPRPRRRG QWESKIBLGOGPC/PAQGHGRPGSVSPLPPDHPTTLRPLPP PPPPPPPPPPPPRPRRRG CLABLFSCGGTINHLAPSGRLRWAURGPGRN*LPGEGPSIPT RNM*ERKAGCSGPC/PAGGHERPGGANPLEDEPBPP TRIALPONALDERGARGERGANFANINARE*K LQEAASPABERGCSSKGTSTSRTG GAGAASDWSSGLRAADFPRWKRHISEGLARRENINANRE*K LQEAASPABERGCRSSKGTSTSRTG TO400 155 891 GAGAASDWSGLRAADFPRWKRHISEGLARRENINGARGARET			·	AAAPSAPITPAAAGPNIL*SRRIAEWCWPPSCSCCWGWC*SWSA				
7034 92 1942 EDTSSMPFELLP FIGILICALIC PHENAGEPUSAS DEPAHYPERV KAMFYHAYDS YLENAE PYPELR PLITCOCHTYMGS PSILIDALD TILVTLFYS (LIGNUSE PERVEYUL) ON SUPERVITA RVUGGLISAHLISKKA GVEVEROM PCSIPLIRMA BEAARKLIPA FOTPTOMPY GYVINLLIGWIND PERVEYUNGA UND TUERWA AGAD TOD PYPEDVARVALMELWESRSD I GLVGNIT IDVALTERWA AGAD TOD PYPELVIKA ALLO KIKAGEVER AGA WE TO SUPPLIE SAMILYRAT GOPTILLEGIS PADAVES LEIK SKOKCOFAT I KOLDONIK LIGHAM TERM YA AGAD TUMO ON THE SUPPLIES SAMILYRAT GOPTILLEGIS PADAVES LEIK SKOKCOFAT I KOLDONIK LIGHAM TERM YA AGAD TUMO ON THE SUPPLIES SAMILYRAT GOPTIS SEMILO AGAD SEMILO				WDWRRPPLQVSPAPSSSCRASCCWCLESIT*SSSTARSRATGAS				
Post		,		SSSICPISKSDRGAAWIP\SPMGAPLLPCSVPLISREEALQDPR				
RAMFTHAYDS TLERAF PFDEER PITCOGENUMGS PSITLIDALD TILLYLEY POLIGAN SE PROVIDED TO WAS VEGALISABLE SKARG VERMANDES PSITLIDALD TILLYLEY POLIGAN SE PROVIDED TO WAS VEGALISABLE SKARG VERMANDES PSITLIDALD TILLYLEY POLIGAN SE PROVIDED TO WAS VEGALISABLE SKARG VERMANDES PSITLIDALD TILLYLEY POLIGAN SE PROVIDED TO WAS VEGALISABLE SHARG VEGALISABLE SKARG VERMANDE THAY TO WAS VEGALISABLE SKARG VERMANDE THAY TO WAS VEGALISABLE SHARG VERMANDE THAY TO WAS VEGALISABLE SHARG VERMANDE THAY TO WAS VEGALISABLE SHARG VERMANDE THAY TO WAS VEGALISABLE SHARG VERMANDES OF PLANT IN THE VERMANDES PLANT IN THE VERMAND	7034	92	1040					
TILLYTLEYPOLIGINUSEFORWINGDSUPEDIDUNASYPETNI RVVGGILSAHLISKKAGVERAGMPCSGILFAMAEBRARKLLPA POTPFGMPYGTVNILHGVNRGETBVTCTAGIGTFIVEFATLSSL TGDPVPEDVARVALMRILMERSRDIGLVGMHIDVITGKVAVQDAG IGAGVDSYBEYLVKGALLLQDKKLMAMFLENKAIRNYTRPDDM YLMVQMYKGTVSMPVFGSLEAYWPGLGSLIGDIDNAMRFILMYY TVWKGFGGLPEFYNIPGGTTVEKREGYPELESAMYLYRAT GDPTLLELGRDAVSSIEKISKVEGGFATIKOLRDHKLDRKESSF FLAETVKYLYLLFIPPTNETHNAGSTFPALTYPGECTLGAGGYI PNTEAHPIDPAALICCQRLKEEGWEVEDLMREFYSLKRSRSKFO QPFTSKLAALLGQVFLIDSS*PEDNHDQARERKPAKGVELLSCPS QPFTSKLAALLGQVFLDSS*PEDNHTPTIFICHIANNKLLLAIIKK K 7035 92 1942 EDTSSMPFRLLIPLGLCALLPCHGAPGPDGSAPDPAHYRERV KAMFYHAYDSYLEMAPPFDELRPLTCGGDTWGSFSLTLIDALD TLLYTLFYROLIGNUSEGROVEVLOLOGDFUNASYPETNI RVVGGLSAHLLSKKAGVSVERGMPCSGFLLRMAEBAARKLLPA PCTPTGMPYGTVNILHGVNPGETFVTCTAGIGTFYPATLSSI TGDPVEEDVARVALMRLMESKSDIGSVGMHIDVLTGKWAQDAG IGAGVDSYPEYLVKGAILLQDXKLMAMFLEINKAIRNYTRPDDW YLWVQMYKGTSMPVEVLOSSERYWEVLGDSUIDNAMRFFLNYY TVWKQFGGLPBFYNIPGGTTVEKREGYPLRELIESAMYLKRAT GDPTLLELGRADVSSERSTSKYWEGGAPLIDNAMRFFLNYY TVWKQFGGLPBFYNIPGGTTVEKREGYPLRELIESAMYLKRAT GDPTLLELGRADVSSERSTSKYWEGGAPLIDNAMRFFLNYY TVWKGFGGLPBFYNIPGGTTVEKREGYPLRELIESAMYLKRAT GDPTLELGRADVSSERSTSKYWEGGAPLIDNAMRFFLNYY TVWKGFGGLPBFYNIPGGTTVEKREGYPLRELIESAMYLKRAT GDPTLISCHGANVSSIERSTSWYGGGAPTLEDHAMRFLNYY TVWKGFGGLPBFYNIPGGTTVEKREGYPLRELIESAMYLKRAT GDPTLISCHGANVSSIERSTSWYGGGAPTLEDHAMRTFLNYY TVWKGFGGLPBFYNIPGGTTVEKREGYPLRELIESAMYLKRAT GDPTLISCHGANVSSIERSTSWYGGGAPTLEIDAMRTFLNYY TVWKGFGGLPBFYNIPGGTTVEKREGYPLREEGFBIPT FRATHEIDPAALLCCQURLEEGWEVEDLIMREFYSLKRSRSKFO QAPTSKLALLGQVFLDBS*PLDNAFTFIFILLANNKLLLALLEGPS QPFTSKLALLGQVFLDBS*PLDNAFTFIFILLANNKLLLALLEGPS QPFTSKLALLGQVFLDBS*PLDNAFTFIFILLANNKLLLALLEGPS QPFTSKLALLGQVFLDBS*PLDNAFTFIFILANNKLLLALLEGPS QPFTSKLALLGQVFLDBS*PLDNAFTFIFILANNKLLLALLEGPS QPFTSKLALLGQVFLDBS*PLDNAFTFIFILANTKLLBCPS QPFTSKLALLGQVFLDBS*PLDNAFTFIFITRLPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	7034	32	1942					
RVUGGLISAHLISKKAGVEVEGBPLERMAERARKILIPA FOTPTGMPYGTVINLIHGVURGETPUTCTGTFIVERATIGSI. TGDPVFEDVARVALMRIMESRSDIGLVGMHIDVITGKWVAQDAG IGAGVDSYPFYLVKGAILLQKKLMAMFLERNAIDTSTRDW YLHVQWYKGTVSMPVTQSLEAYWBGLQSLIGDIDNAMRTPILMYY TVWKQFGGLPEYNIPQGTTVEKKEGYPLRELIESAMYLTAAT GDPTLELEGRADVESIEKISKUGGGPATKOLROHKULDNRMESF FLASTVKYLYLLFPDTNFIHNGSTFDAVITPYGECILGAGGYI FNTEAHEIDPAALHCCQRIKEEGGWPEVBHFYSIKRESRSKFQ KNTVSSGPWEPPARPFTLFSPENHIDQARERKPSIKRESRSKFQ KNTVSSGPWEPPARPFTLFSPENHIDQARERKPSIKRESRSKFQ KNTVSSGPWEPPARPFTLFSPENHIDQARERKPSIKRESRSKFQ KNTVSSGPWEPPARPFTLFSPENHIDQARERKPSIKRESRSKFQ KNTVSSGPWEPPARPFTLFSPENHIDQARERKPSIKRESRSKFQ KNTVSSGPWEPPARPFTLFSPENHIDQARERKSLALLAILKIK K 7035 92 1942 EDTSSMPFILLIPIGLICALLPQHHGAPGPDSSAPDPAHYRERV KAMFYHAYDSYLENAPPFDEURPITGHDWGSFSITTIDALD TILLYTLFYRQIIGMVSEFGRVUEVLQDSVDFDIDVNSFFTNIT RVVGGLISAHLISKKAGVERAGMPGGGPLIRMAEBAARKILPA FQTPTGMPYGTVNLIHGVSPEGRVUEVLQDSVDFDIDVNSFFTNIT RVVGGLISAHLISKKAGVERAGMPGGGPLIRMAEBAARKILPA FQTPTGMPYGTVNLIHGVSPEGRVUERAGNGFTHANSFFTDAVITSFTDDM YLWVGMYLSAHLISKKAGVERAGMPGGGPLIRMAEBAARKILPA FQTPTGMPYGTVNLIHGVSPEGRVUERAGNITHTREPDH YLWVGMYLSAHLISKKAGVERAGMPGGFULMAEBAARKILPA GDPTILLELGRAVBYLTSMPTGTDHUTTKWAQDAG IGAGVDSYPETIVKGAILLGOKKUMMPLEVINKAIRNTYRFDDM YLWVGMYLSHERSBDGLUVRINKAIRNTYRFDDM YLWVGMYLSHERSBDGLUVRINKAIRNTYRFDDM YLWVGMYLSHERSBDGLUVRINGSTBANDHUTTREPDP FPTSKLALLGQVFUEDSFFTIFFFFFFFTDADARRRPARGVPILLSCPS QPFTSKLALLGQVFUEDSFFFFFFFFFFFFFFTDADARRRPARGVPILLSCPS QPFTSKLALLGQVFUEDSFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF								
POTPTGMPYGTVNLLHGWNPGETPUTCTAGIGTFI VEPATLSSI TGDPVPEDVARVAINALMESRSDIGLUKONHIDULTCKWYAQDAG IGAGVGSYPFYLVKGA ILLQDKKLMAMPLEYNKA IRNYTRPDDW YLHVQMYKGTVSMPVPGSLEAYWPGLGSLIGDIDIDAMSTFINYT TVMKOPGGLPEYNIP PGGYTVEKRAGYSLRPELI ESAMYLYRAT GDPTLLELGRDAVESIERI SKVECGFATIKOLDGAGGYI FNTEAHPIDPAALHCCORLKEEGWBVEDLMREFYSLKSSRSKFO KNTVSSGPWEPPARRPTH FINNOSTFDAVITPYGECILGAGGYI PNTEAHPIDPAALHCCORLKEEGWBVEDLMREFYSLKSSRSKFO KNTVSSGPWEPPARRPTT FPERHHDOSFPARKAGKVPLLSCPS OPFTSKLALLGQVFLDSS*PLDNFFIFIFIRNYNKLLLAIIKK K 7035 92 1942 EDTSSMPFRLLIPLGLCALLPOHGAPGPDGSAPDPAHYRERV KAMPYHAYDSYLENAPPFDBLRPLTTOCHDTWMGSFSITT.IDALD TLL\TLYPGPILGNVSEQRVVWFLOGDSVPFDIDVMASYFETNI RVVGGLLSAHLLISKKAGUFVEAGWPCVGOFLIRMAEFSITT.IDALD FOTFTGMPYGTVNLHAUGNGETPUT-GAIGTFI VEPATLSSL TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG IGAGVDSYFFILVKGAILLQDKHAMPLESYNKATAINTTREDDW YLWVQMYKGTUSMPVFYOSLEAYWPGLGSLIGDIDMAMRTFLNYY TVWKQFGGLPEFYNIPGGYTVEKREGYPLRFELISAMYLYRAT GDPTLELGROAVSSIEKI SKVECGPATIKOLEDHALDNRESF FLASTVKYLYLLIPDTTWFIHNNOSTFDAVITPYGGCILGAGGYI PNTEAHPIDPAALHCCORLKEEGWBYGHEFSYLLKSRSKFO KNTVSSGPMEPPARGTLFSPENHDQARERKPAKQKVPLLSCPS OPFTSKLALLGQVPLDSS*PLDNFFIFIFIFIRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFOIINHLAFSGRLRWAMLRGFGRN*LDGEGGPSIPT RNM*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHTTLRPLPP PPPPPPPPPPPPRRPRRRPG 7037 442 761 CLAPLFSCFOIINHLAFSGRLRWAMLRGFGRN*LDGEGGPSIPT RNM*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHTTLRPLPP PPPPPPPPPPPPRRPRRRPG 7038 155 891 GAGAASDMSGCRAADFFRKKHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAGKLQAKHDVYNRHEISPGHDGTVNDNQ LQEMAQLRKHGDEITLHKKGGELAQVILDINNOMGRORBM QMISEKILAGCLQTISDLETECLDLETKLCDLERANOTLKDEYDA LQITPTALEGKLRKTTEENQELVTRWAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTITSRTG WINEBAKIAGCLQTISDLETECLDLETKLCDLERANOTLKDEYDA LQITPTALEGKLRKTTEENQELVTRWAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTITSRTG WINEBAKIAGCLQTISDLETECLDLETKLCDLERANOTLKDEYDA LQITPTALEGKLRKTTEENQELVTRWAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTISTSRTG KTTPPRPHRCSSCHGEGGDNSSVLSGELPPAMGKTALFYHSGGSS				TDD/IDFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI				
TGDPVFEDVARVALMRUMESSSIGLVONHIDULTCKWVAQDAG IGAGVOSPYFLVKGAILLQDKKLMENWTA INNYTRPDOW YLWVQMYKGTVSMPVPQSLEAYWPGLQSLIGDIDNAMRTFINYY TVMKQFGGLPEFYNTPGGYTVEKREGYPLRFELLESMYLVRAT GDPTLLELGERDAVES IERI SKWCGFGATIKOLEDHKUNNKESF FLAETVKYLYLLFDPTMFIHNNGSTFDAVTTPYGECILGAGGYI FNTERHPIDPAALHCCORLKESGUMEGHBEYFSLKKSRSKFG KNTVSSGPWEPPBARPGTLF9ENHDQAERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFIRNYNKLLLATIKK K 7035 92 1942 EDTSMMFRLLTPLGLCALLPOHGAPGDDGSAPDPAHYRERV KAMFYHAYDSYLENAPPPBELRPLTCOHDTWGSFSLTLIDALD TILLYTLFYFGILGNVSEFQEVVEVLQDSVDFDIDVMASVFBTNT RVWGGLISAHLLSKKAGVENGAMPGELIMBEARKLLPA FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL IGAGVOSYFETLIKGAILLDKKLMAMFLENNAINNTTRFDDW YLWVQMYKGTVSMPVFGSLEAYWPGLQSLIGDIDNAMRTFLNYY TVMKOFGGLPFYNTPGGTYVEKREGPLIMBEEARKLLPA GDPTLLELGRDAVESIEKISKVECGPATIKOLEDHKLDNRMESF FLAETVKYLYLLFDPTNFIHNNGSTFDAVTTYGGECILGAGGYI TNTEAHPIDPAALHCCQRLEEQMEVBDLMREFYSLKRSRKFQ KNTVSSGPMEPPBARPGTLF9PENHDQABEKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFBTPLKTHYNKLLLAIIKK K 7036 442 761 CLAELFSCFGIINLHLAPSGRLRWAWLEGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPPPPPPPPPRPPRRRPG 7037 442 761 CLAELFSCFGIINLHLAPSGRLRWAWLEGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	1 .			KVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA				
IGAGVDSYPEYLVKGAILLQDKKLMAMFLEYNKAIRNTTREDDW YLWVQWKGTVSMPVPGLSAYMPGLGSLIGDIDNAMRTFLNYY TVWKQFGGLPEYNIPGGYTVEKREGYPLRPELIESAWYLVRAT GDPTLLELGRDAVESIEKISKVECGFATIKOLADKLDNAMRSF FLAETUKYLYLLFDTFININGSTEDAVITPYGECILGAGGYI FNTEXHPIDPAALHCCQRLKEEGWEVEDLMREFYSLKSGSKFG KNTVSSGPWBPPARPGTLFPENHDDARERKPAKQKVPLLSCPS OPFTSKLALLGQVFLDSS*PLDNFFIFIFRLNYNKLLLATIKK K 7035 92 1942 EDTSSMPFRLLTPLGLLCALLPCHGAPGPDGSAPDPAHYRERV KAMFYHAYDSYLENAPPDBLERPLTCDGHDTWGSFSLTILDALD TILATLEYPGILGNUSPGRVVEVLQDSVDPDIDVNASVPETNI RVVGGLLSAHLLSKKAGVEVEAGWFCSGPLLRNAEEAARKLLPA FCTPTGMPYGTVULHGVNGGETPVTCTAGIGFTYUFFATLSSL TGDPVFBDVARVALMRUSESSDIGLGVAMHDULTIGKWAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEENKAIRNTTRFDDW YLWVGMKGTVSMPVPGSLEAYMPGLGJUDIDNAMRTPLNYY TVWKQFGGLPEFYNIPGGYTVEKREGYPLRPELIESAWYLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKOLEDHLIDNAMRTPLNYY TVWKQFGGLPEFYNIPGGYTVEKREGYPLRPELIESAWYLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKOLEDHLIDNAMRTPLNYY TVWKQFGGLPEFYNIPGGYTVEKREGYPLRPELIESAWYLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKOLENGAGGYI FNTEXHPIDPAALHCCQRLEEGWEVBELMREFYSIKRSSKFO KNTVSSGDMEPPAARPGTLFSPENHOASKPAKAKVELLGCPS OPFTSKLAILLGQVPLDSS*PLDNFFIPIFIRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNN*ERKAGCSGPC/PAQCHHGRPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPPPPPPPPPPPPPPPPPP				FOTFIGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL				
TLWVQMYKGTVSMPVPGSLEXTWPGLQSLIGDIDNAMSTFINTY TVWKGFGQLPEFYNIPGETLESAPYLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF FLAETVKYLYLLFDPTHFIHNNGSTFDAVITPYGGCILGAGGYI FNTEAHIPIDPAALHCCQRLKESGWEVHERFYSLKRSKSKFQ KNTVSSGPWEPPARFGTLF9FBWHDQARERKPAKQKVPLLSCPS OPFTSKLALLGQVFLDSS*PLDNFFIFIFILNYNKLLLAIIKK K POSSMPFRLLIPGLLCALLPQHHGAPGPDGSAPDPAYRERV KAMYTHAYDSYLENAPFPDBLRPLTCOHDTWGSFSLTLIDALD TILLYTLFYRGILGNUSFGRUVEVLQDSVDPDIDVJASVFBTNI RVVGGLISAHLLSKGKGVEVAGWPGSGPLIRMBERARKLIPA FOTFTCMPYGTVNLHGWINGEFDFVTCTAGIGTFIVEFATLSSL TGDPVPEDVARVALMRLWESRSDIGLVGMNABERARKLIPA FOTFTCMPYGTVNLHGWINGEFDFVTCTAGIGTFIVEFATLSSL TGDPVPEDVARVALMRLWESRSDIGLVGMNABERARKLIPA FOTFTCMPYGTVNLHGWINGEFDFVTCTAGIGTFIVEFATLSSL TGDPVPEDVARVALMRLWESRSDIGLVGMNABERTLINYT TVMKQFGGLPFFINIPGGTYVEKREVJERELISGAMYLIFAT GDPTLLELGRDAVESIEKISKVECGFATIKDLEDHKLDNRMESF FLAETVKYLYLLFDFTURFINNGSTFAUTPVEGCILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSKFQ KNITVSSGPMEPPARFGTLFSPENHUQARERKPAKQKVELISCPS QPFTSKLALLGQVFLOSS*PLDNRTPTLTPYGGCILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSKFQ KNITVSSGPMEPPARFGTLFSPENHUQARERKPAKQKVELISCPS QPFTSKLALLGQVFLOSS*PLDNRTPTGFGCILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSKFQ KNITVSSGPMEPPARFGTNSPPLDRHPTTLRPLPP PPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	1			TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG				
TWKCFGGLEFYNTEQGTVEKREGYELFELTESAMYLYRAT GDPTLELIGRADAYELGRADAYELGRATIKDLEDHKLDNRMESF FLAETVKYLYLLFDPTNFIHNNGSTFDAVITYGECIGAGGYI ENTEAHPIDPAALHCCQELKEECKEVEDLMERFYSLKSSRSKFC KNTVSSGPWEPPARFOTTJESPENDQARERKPAGKVEVLISCES OPFTSKLALLGQVFLDSS*PLDNFFIFIFIRLNYKLLLAIIKK K 7035 92 1942 EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYREV KAMPYHAYDSYLENAPPPDELRPLTCCHHOVGSTSLTLIDALD TIL\TLYFGILLNOWSEFGRVVEVLOSVDFDIDVNASVPETNI RVVGGLLSAHLISKKAGVEVERGWPCGGPLLRMAEEAARKLIPA FOTPTGMPYGTVNLLHGWNPGETEVTCTAGIGTFIVEFATLSSL TGDPVFEDVARVALWRLWESRSDIGLVGNHIDVLTGKWVAQDAG IGAGVDSYFFYLVKGAILLJOKKLMANFLEYNKAIRNTTRFDDW YLWVQMKGTVSMPVFGSLEAYWEYGSLEGVIDNAMTFILNYY TVWKOFGGLEFYNTPQGYTVEKREGYPLRPELIESAMYLYPAT GDPTLLELIGRDAVESIEKISKVECGPATIKDLEDHKLDNRMESF FLAETVKYLYLLEPDTNFIRNNGSTFDAVITPYGECILGAGGYI FNTEAHBIDDAALHCCQRLKEEQWEVEDLMREFYSLKSSRSKFQ KNTVSSGPWEPPARFOTLFSPENDQARERKPAKGKYPLLSCES OPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPRPRRRRG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPPPRRRRRG 7038 155 891 GAGAASDMSSGLRAADFFRWKRHISEQLERRDRLQROAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKBUPVNHEISGHGTWNDMQ LQEMAQLRIKHGBELTELHKKRGELAQ\RVIDLNNQMGRKDREM QMEBAKIABCLQTISDLETTEGLDLRTKLCDLERRNOTLKDEVDA LQITTALBGKLKRKTEENGGLVTRMAKKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG GAGAASDMSSGLRAADPFPWKRHISEQLRRRDRLQROAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNHEISGCHFGTWNDMQ LQEMAGLRIKHGBELTELHKKRGELAQ\RVIDLNNQMGRKDREM QMEBAKIABCLQTISDLETTEGLDLRTKLCDLERRNOTLKDEVDA LQITTALBGKLKRKTEENGGLVTRMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 7640 7650 76740 76740 76740 7675 FRIFTERPRPRRGSSEGHGSDNSSVLSGELPPAMGKTALFYHSGGSS			- "	TGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW				
GDPTLLELGRDAYESIEKISKVECGFATIKDLEDKLINNMESF FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI NNTESHHIDPAALHCQRLKSEQKEVEDLMREFYSLKRSRSKFQ KNTVSSGPWBPPARPGTLFSENHDQAREKREAKGKVVELLSCES QPFTSKLALLGQVFLDSS*PLDNFFIFIFIRINYNKLLLAIIKK K 7035 92 1942 EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV KMMYHAYDSYLENAFPFDELRPLTCGHDTMGSTSLTLIDALD TILLYTLFYFGILGNUSEFGRUVEVLQDSVDFDIDVNASVPFTNI RVVGGLLSAHLLSKKAGVEVEAGEGSPLLRMAEEAARKLLPA FQTPTGMPYGTVNLLHGUNGETFUVCTAGIGTFIVGFATLSSL TGDPVFEDVARVALMELMESRSDLGLWGMHIDLVTGKWAQDAG IGAGVDSYFFILVKGAILLQDKKLMAMFLEFYNAKIANTRFDDW YLWVQMYKGTUSMPVFQSLEAYMFGLQSLIGDIDNAMKTPLNYY TVWKQFGGLPFFYNIPGGYTVKERGGYPLRPELIESAMVLYRAT GDPTLLELGRDAVESIEKISKVEGFATIKDLRDHKLDNRMESF FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGFCILGAGGYI FNTEAHPIDPAALHCCQNLKEEQMEDMREFYSLKSRSKFQ KNTVSSGPWBPDARPGTLPSPENHDQAREKPAKQKVPLLSCPS QPFTSKLALLGGVFLDSS*PLDNFFIFIFIRINYNKLLLAIIKK K 7036 442 761 CLAFLFSCFQIINLHLAPSGRLRWAMLRGPGRN*LPGEGPSIFT RNW*BRAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPPPPRPRNRRG 7037 442 761 CLAFLFSCFQIINLHLAPSGRLRWAMLRGPGRN*LPGEGPSIFT RNW*BRAGCSGPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPPPPPPRPRNRRG 7038 155 891 GAGAASDMSSGLRAADFFRWRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISGHGTNNDMQ LQEMAGLRIKHGBELTELHKKRGELAQ\RVIDLINNQMGRKDRM QMERALAECLQTISDLETECLDLRTKLCDLERANGLIKADE*KR LQEAASPAABRACRSSKGTSTSTRTG 7039 155 891 GAGAASDMSSGLRAADFFRWRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDMQ LQEMAGLRIKHGBELTELHKKRGELAQ\RVIDLINNQMGRKDRM QMERALAECLQTISDLETECLDLRTKLCDLERANGLKDEVDA LQITFTALBGKLRKTTEENOGLVTRMMAEKAQEANRLNARE*KR LQEAASPAABRACRSSKGTSTSRTG 7040 34 789 KTTPFRFRFRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	i			YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY				
FLAETVKYLYLLEDPTNPIHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAAHCCQRLKSEQMEVEDLMREFYSLKRSRSKFQ KNTVSSGPWBPPARPGTLFSPENIDQARERKPAKKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFIRLNYKKLLLAIIKK K 7035 92 1942 EDTSSMPFRLIIFLGLCALLPQHHGAPGEDGSAPDPAHYRERV KAMFYHAYDSYLENAFPFDELRPLTCOGHDTWGSFSLTIDALD TILLYLFYFQILGNVSEPGRVVEVLQDSVDFDIDVNASVFETNI RVVGGLLSAHLLSKKAGVEVEAGMPCSGPLIKNAEEAARKLIPA FQTFTGMPYGTVALLHGUNPGETFVTCTAGIGFFIVETPATLSSI. TGDPVFEDVARVALMKLMESRSDIGLVGNHIDVLTGKWVAQDAG IGAGVDSYFFYLVKGAILLGVKLMANFJERVKAIRNYTRFDDW YLWVQMYKGTVSMPVFQSLEAYMPGLOSLIGIDIDNAMFTFLNYY TVWKQFGGLBFYNTPQGYTVEKREGFYLFRKAIRNYTRFDDW YLWVQMYKGTVSMPVFQSLEAYMPGLOSLIGIDIDNAMFTFLNYY TVWKQFGGLBFYNTPQGYTVEKREGFYLFRKAIRNYTRFDDW YLWVGMYKGTVSMPVFQSLEXISVEGPATIKDLRDUKLDNIMESF FLAETVKYLYLLJEDPTNPIHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQMEVEDLMREFYSLKRSRSKFQ KNTVSSGPMEPPARPGTLFSPENIDQARERKPAKGKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFTIFIFLRNYNKLLIAIIKK K 7036 442 761 CLAFLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGGGPSIFT RNM*BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPRPRRRRG 7037 442 761 CLAFLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGGGPSIFT RNM*BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPRPRRRRG 7038 155 831 GAGAASDMSSGLRAADFFRKKHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHGSTNNDNQ LQMAGKIAECLQTISDLETECLDLRTKLCDLERRNQTLKDETDA LQTTTTALBCKLRKTTEENOGLVTRWABKAQEANRLNARE*KR LQBAAGPAAERACRSSKGTSTSRTG QMEAKIAECLQTISDLETECLHCLRTRLCDLERRNQTLKDETDA LQTTTALBCKLRKTTEENOGLVTRWABKAQEANRLNARE*KR LQBAAGPAAERACRSSKGTSTSRTG QMEAKIAECLQTISDLETECLHLCDLERRNQTLKDEDBA LQTTTALBCKLRKTTEENOGLVTRWABKAQEANRLNARE*KR LQBAAGPAAERACRSSKGTSTSRTG 7040 34 7640 TRIPPRPRRFRCSSCHGSDNSSVLSGELPPAMGKTALFYHSGGSS			·					
FINTERHPI DPAALHCCQRLKEEGWEVEDLMREFYSLKRESKERG KNTVSGGWEP PARPGTLFS PENHDQAREKKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS P LDNFFI FIFLKINYNKLLLAI IKK K TO35 92 1942 EDTSSMPFRLIFIGLLCALLPOHHGAPGPDSSAPDPAHYRERY KAMFYHAYDSYLENAPPFDELRPLTCDGHDTWGSFSLTLIDALD TILLYTLFYFGILGNVSEFGRVVEVLQDSVDFDIDVINASVETTII RVVGGLLSAHLLSKKAGVEVENGPCSGFLLRMAEBARKLLPA FQTFTGMPYGTVNLLHGVMFGSTPVTCTAGIGTFIVEFATLSSL TGDPYFEDVARVALMRLWESRSDIGLGVMNHIDVLTGKWVAQDAG IGAGVDSYFSYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW YLMVQMYKGTVSMPVFGSLEATWPGLGSLIGDIDNAWRTLNYY TVWKQFGGLDEFTNIPQGTTVEKREGYPLREDLIESAMYLYRAT GDPTLLELGRDAVESIEKISKVECGPATIKDLRDHKLDNRMESF FLAETVKYLYLLEDPTNIP HINNGSTFDAUTTPYGGGLGAGGYI FNTERHPIDPAALHCCQRLKERQWEVEDLMREFYSLKRSRSKFQ KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDGS*PLDNFFIFIPLRNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGSFIPT RNW*ERKAGCSQPC/PAQOHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPPPRRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGSFIPT RNW*ERKAGCSQPC/PAQOHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPPPRRRPG 7038 155 891 GAGAASDMSSGLRAADFFRKKHISEGLRRRDRLQRAFEETIL GYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHGBELTELHKKRGELAQ VRYDLDNNOMRCRDEM MNEKKIAECLGTISDLETEGLBRKLGDLERRNOTLKDEVDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG GAGASDMSSGLRAADFFRKKHISEGGRRRDRLQRAPFEIIL GYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ VRYDLDLNNOMRCNDEM MNEKKIAECLGTISDLETEGLDLETKLCDLERRNOTLKDEVDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG GAGASDMSSGLRAADFFRKRHISEGGRRRDRLORGAPFEIIL GYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ VRYDLDLNNOMRCNDEM MWBAKIAECLQTISDLETEGLDLETKLCDLERRNOTLKDEVDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG GAGASDMSSGLRAADFFRKRKDISEGLEPAMGKTALFYHSGGSS 7040 34 KITPPRPHRCSSGHGSDMSSVLSGELPPAMGKTALFYHSGGSS				GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF				
KNTYSSGPWEPARPGTLFSPENHDQARERKPAKQKVPLLSCPS OPFTSKLALLGQVFLDSS+PLDNFFIFIFLRINYNKLLLATIKK K	1	·		FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI				
OPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV KAMFYHAYDSYLENAPFPELRPLITCOHDTWGSFSLTLIDALD TILL\71EYFGJLGNVSEPGRVVEVLQDSVDFDIDVNASVPETNI RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEBAARKLIPA FQTPTGMPYGTVNLLHGVNPGETEVTCTAGIGTFIVEFATLSSL TGDPVFBUVARVALMRLWESRSDIGLGVGNHUDVLTGKWAQDAG LGAGVDSYFEVLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW YLWVQMYKGTVSMPVFQSLBAYMPGLQSLIGDIDMARTFLNYY TVWKQFGGLBFFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT GDPTILEIGRDAVESIEKISKVEGGPAITKOLRDHKLDNRMESF FLABTVXYLVJLHPDTMFRIMNGSTFDAVITDYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVBDLMREFYSLKRSRSKFQ KNTVSSGPWEPPARPGTIFSPENHIDQAREKKPAKGKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAFSGRLRWAWLRGPGRN*LPGEGFSIPT RNW*BRKAGCSQPC/PAQOHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPRPPRNRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGFSIPT RNW*ERKAGCSQPC/PAQOHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPRPRNRRPG 7038 155 891 GAGAASDMSSGLRADFFRWKRHISEGLRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEHDVPNRHEISPGHGTWNDNQ LQEMAQLRIKHQEBLTELHKKRGELAQLRVDLDNNQMQRKDREM MERKHAGCTISDLETEKLDLRTLCLDERANOTLKDEYDA LQITFTALEGKLRKTTENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPABRACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSVLSGELPPAMGKTALFYHSGGSS								
7035 1942 EDTSSMPFRLITPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV KAMFYHAYDSYLEMAFPFDELRPLTCDGHDTWGSFSLTLIDALD TILL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVPETNI RVVGGLLSAHLLSKKAGVEVEAGMPCSGPLLRMAEBAARKLLPA FQTPTGMPYGTVNLLHGVNPGETFVTCTAGIGTFIVEFATLSSL TGDEVFEDVARVALMRLWESRSDIGLWSNHIDVLTGKWAQDAG IGAGVDSYFELVLWGAILLDAKKLMAMFLEYNKAIRNYTRFDDW. YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRFFLHNY TVWKQFGGLFFFYNIPGGYTVERKEGFYLRPELIESAMVLYRAT GDPTLLELIGNDAVSSIEKISKVEGFATIKOLKDHKLDNEMESF FLABTVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAADHCCQRLKEEQGEVBLMREFYSLKERSKYRG KNTVSSGPWEPPARPGTIFSFSNHIDQARERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRNYNKLLLAIIKK K 7036 442 751 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGFSTPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPPPPPPPRRPRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGFGRN*LPGEGFSIPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPPPPRRPRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEETIL QYNKLLEKSDLHSVLAQKLQAEKHDVPRRHEISPGHGTWNDNQ LQEMAQLRIKHQBELTELHKKRGELAQ (RVIDLNNQMQRKDREM QMEAKIAECLQTISDLETECLDLRTKLCDLERANOTLKDEYDA LQITFTALEGKLRKTTEENGBLVTRMAEKAQEANRLNARE*KR LQEBASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRKKRHISEQLRRRDRLQRQAFEETIL QYNKLLEKSDLHSVLAQKLQAEKHDVPRRHEISPGHGTWNDNQ LQEMAQLRIKHQBELTELHKKRGELAQ (RVIDLNNQMQRKDREM QMEAKIAECLQTISDLETECLDLRTKLCDLERANOTLKDEYDA LQITFTALEGKLRKTTEENGELVTRWAEKAQEANRLNARE*KR LQEBASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRKKRHISEQLRRRDRLQRQAFEETIL QYNKLLEKSDLHSVLAQKLQAEKHDVPRRHEISPGHGTWNDNQ LQEMAQLRIKHQBELTELHKKRGELAQ (RVIDLNNQMQRKDREM QMEAKIAECLQTISDLETECLDLRTKLCDLERANQTIKDEYDA LQITFTALEGKLRKTTEENGELVTRWAEKAQEANRLNARE*KR LQEBASPAAERACRSSKGTSTSRTG 7040 34 7040 7040				KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS				
1942				QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK				
KAMFYHATDSYLENAF PFDELRPLTCOGHDTWGSFSLTLIDALD TIL\TLFYFQILGNUSEFQRVUSULQDSUDFDIDVASSVPETNI RVVUGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLIPA FQTPTGMSYGTVINLHGVMPGETPVTCTAGIGTFIVEFATLSSL TGDSYFEDVARVALMRLWSSSDIGLVGNHIDVLTGKWVAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYRKAIRNYTRFDDW YLWVQMYKGTVSMPVFQSGLEAVWPGLQSLIGDIDNAMRFPLNYX TVWKQFGGLPBFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT GDPTLLELGRDAVSSIEKISKVECGFATIKDLRDHKLDNRMESF FLABTVKYLYLLIFPDTNIP HINNGSTDADVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ KNTVSSGPWEPPARPGTLFSPENHDQAERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFIRINYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAFSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPPDPHPTTLRPLPP PPPPPPPPPPPRRRRPG 7037 442 761 CLAPLFSCFQIINLHLAFSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPPDPHPTTLRPLPP PPPPPPPPPPRRRRPG 7038 155 891 GAGAASDMSSGLRAADFFRWKHISEQLERRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHGBELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIABCLQTISDLETECLDLRRKLCDLERANQTLKDEVDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARB*KR 7039 155 891 GAGAASDMSSGLRAADFFRWKRHISEQLERRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHGBLIFELHKKRGELAQ\RVIDLNNNQMCRKDREM QMNEAKIABCLQTISDLETECLDLRRKLCDLERANQTLKDEVDA LQUFAGLRIKHGBELTELHKKRGELAQ\RVIDLNNNQMCRKDREM QMNEAKIABCLQTISDLETECLDLRRKLCDLERANQTLKDEVDA LQUFAGLRIKHGELETHKKRGELAQ\RVIDLNNNQMCRKDREM QMNEAKIABCLQTISDLETECLDLRRKLCDLERANQTLKDEVDA LQUFAGLRIKHGELETHKKRGELAQ\RVIDLNNNQMCRKDREM QMNEAKIABCLQTISDLETECLDLRRKLCDLERANQTLKDEVDA LQUFAGLRIKHGELETHKKRGELAQ\RVIDLNNNQMCRKDEM QMNEAKIABCLQTISDLETECLDLRRKLCDLERANQTLKDEVDA LQUFAGLRIKHGELETHKKRGELAQ\RVIDLNNNQMCRKDEM QMNEAKIABCLQTISDLETECLDLRRKLCDLERANQTLKDEVDA LQUFAGLRIKHGEEITHKRGELAQ\RVIDLNNNQMCRKDREM QMNEAKIABCLQTISDLETECLDLRRKCDLLRANQTLKDEVDA LQUFAGLRIKHGELETHLKRGELAQ\RVIDLNNNQMCRKDREM QMNEAKIABCLQTISDLETECLDLRRKGCLAQRACHNARE*KR LQEAASPABERACRSSKSTSTSTTG 7040 34 789 KTTPFRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS		<u> </u>	·	1 77				
TIL\TIFYEQILGNUSEFQRUVEVLQDSUDFDIDVASSVEETNI RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLIPA FQTPTGMPYGTVNLLHGVNPGETTPVTCTAGIGTFIVEFATLSSL TGDPVFEDVARVALMRLWESRSDIGLVGMHIDVLTGKWVAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYRKAINNYTRFDDW YLWVQMYKGTVSMPVFQSLEAVWPGLQSLIGDIDNAMRFHLNYY TVWKQFGGLPBFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF FLABTVKYLYLLFPDTINFIHNNGSTDADVITPYGECILGAGGYI PNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ KNTVSSGFWEPPARPGTLFSPENHDQAERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPPDPHPTTLRPLPP PPPPPPPPPPRPRRRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPPDPHPTTLRPLPP PPPPPPPPPPPRRRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKHISEQLERRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQBELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARF*KR LQEAASPAABERACRSSKGTSTSRTG GAGAASDMSSGLRAADFPRWKRHISEQLERRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQBELTELHKKRGELAQ\RVIDLNNNQMCRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQUTFTALEGKLRKTTEENQBLVTTRWMAEKAQEANRLNARF*KR LQEAASPAABERACRSSKGSTSTSRTG GAGAASDMSSGLRAADFPRWKRHISEQLTRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQBELTELHKKRGELAQ\RVIDLNNNQMCRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQUTFTALEGKLRKTTEENQBLVTTRWMAEKAQEANRLNARF*KR LQEAASPAABERACRSSKSTSTSRTG GAGAASDMSSGLRAADFPRWKRHISEQLTRRDRLQRQAFEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQBELTELHKKRGELAQ\RVIDLNNNQMCRCNEM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTTRWMAEKAQEANRLNARF*KR LQEAASPAABRACRSSKSTSTSRTG TG TOTAL	7035	92	1942					
RVVGGLLSAHLLSKKAGVEVEAGAPCSGPLIRMAEEAARKLLPA FQTPTGMPYGTVNLLHGVNPGETFVTCTAGIGTFIVEFATLSSL TGDPVFEDVARVALMRILWESRSDIGLVGNHIDVLTGKWYAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW. YLWVQMYKGTUSMPVPGSLEAYWFGLGSLIGDIDNAMRTFLMYY TVWKQFGGLPEFYNIP FQGYTVEKEGGYPLRFELI ESAMYLYRAT GDPTLLELGRDAVESIEKISKVECGPATIKDLRDHKLDNAMRESF FLABTVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREPYSLKRSRSKFQ KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKÇKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPRRPRNRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPRRPRNRRPG 7038 155 891 GAGAASDMSSGLRADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDSTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANQTLKDEVDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRADFPRWKRHISECLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHGEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMSEAKIABCLQTISDLETECLDLRTKLCDLERANQTLKDEVDA LQUMQLRIKHGEBLTELHKKRGELAQ\RVIDLNNQMGRKDREM QMSEAKIABCLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQEMAQLRIKHGEBLTELHKKRGELAQ\RVIDLNNQMGRKDREM QMSEAKIABCLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQEMAQLRIKHGEBLTELHKKRGELAQ\RVIDLNNQMGRKDREM QMSEAKIABCLUTISDLETECLDLRTKLCDLERANQTLKDEYDA LQEMAQLRIKHGEBUTTELMKRGELAQ\RVIDLNNQMGRKDREM QMSEAKIABCLUTISDLETECLDLRTKLCDLERANQTLKDEYDA LQEMAQLRIKHGEUTTERWABEKQGENRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	1		* **	KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD				
FOTPTGMPYGTVNILLHGVNPGETFVTCTAGIGTFIVEFATLSSL TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLENNKAIRNTTRFDDW- YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTPLNYY TVWKQFGGLBFFYNIPQGYTVEKREGYPLRFELIESAMYLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKOLDRUKLDNRMESF FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRILEEEGWEVBDLMMEFYSLKRSKFQQ KNTVSSGWEPPARPGTDF9PENEDQARERKPAKGKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNTNKLLIAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGFSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDEHPTTLRPLPP PPPPPPPPPPPRPRNRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGFSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDEHPTTLRPLPP PPPPPPPPPPPRRPRNRPG 7038 155 891 GAGAASDMSSGLRAADFFRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMIBAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEVDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG QYNKLLEKSDLHSVLAGKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHGEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMSAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEVDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHGEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG	ļ .	•		TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI				
TGDPVFEDVARVALMRLWESSBIGLUGNHIDVLTGKWAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNTRFDDW. YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMSTFLMYY TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT GDPTLLELGRDAVESIEKISKVECGPATIKDLRDHKLDNRMESF FLABTVKYLYLLFDPTNIPHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ KNTVSSGPMEPPARPGTLFSPENHDQAREKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPPPPRRFRFG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPPRRPPRNRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHGBELTELHKKRGELAQ\RVIDLNNQMGRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITPTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSGGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWDNQ LQEMAQLRIKHGBELTELHKKRGELAQ\RVIDLNNQMGRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAETACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS				RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA				
IGAGVDSYFEYLVKGA ILLQDKKLMAMFLEYNKA IRNYTRFDDW. YLWVQMYKGTVSMPVFGSLEAYWPGLGSLIGDIDNAMRTFLMYY TVWKQFGGLPEFTNI PQGYTVEKREGYPLRFELIESAMYLLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF FLABTVKYLYLLFDPTNFIHNNGSTFDAVTTPYGEC LIGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVBDLMREFYSLKRSKSKFG KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPRPRPRRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGFGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPRPRRRPG 7038 155 891 GAGAASDMSSGLRAADFFRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNHEISPGHDGTWNDNQ LQEMAQLRIKHQBELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANQTLKDEVDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSSRTG GAGAASDMSSGLRAADFFRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANQTLKDEVDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSSRTG QYNKLLEKSDLHSVLAQKLQAEKHDVPNHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANGTLKDEVDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANTLNARE*KR LQEAASPAAERACRSSKGTSTSSTG QYNKLLEKSDLHSVLAGKLOAEKHDVPNHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANGTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANTLNARE*KR LQEAASPAAERACRSSKGTSTSSTG QYNKLLEKSDLHSVLAGKLOAEKHDVPNHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANGTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSSTG				FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL				
IGAGVDSYFEYLVKGA ILLQDKKLMAMFLEYNKA IRNYTRFDDW. YLWVQMYKGTVSMPVFGSLEAYWPGLGSLIGDIDNAMRTFLMYY TVWKQFGGLPEFTNI PQGYTVEKREGYPLRFELIESAMYLLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF FLABTVKYLYLLFDPTNFIHNNGSTFDAVTTPYGEC LIGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVBDLMREFYSLKRSKSKFG KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPRPRPRRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGFGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPRPRRRPG 7038 155 891 GAGAASDMSSGLRAADFFRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNHEISPGHDGTWNDNQ LQEMAQLRIKHQBELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANQTLKDEVDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSSRTG GAGAASDMSSGLRAADFFRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANQTLKDEVDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSSRTG QYNKLLEKSDLHSVLAQKLQAEKHDVPNHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANGTLKDEVDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANTLNARE*KR LQEAASPAAERACRSSKGTSTSSTG QYNKLLEKSDLHSVLAGKLOAEKHDVPNHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANGTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANTLNARE*KR LQEAASPAAERACRSSKGTSTSSTG QYNKLLEKSDLHSVLAGKLOAEKHDVPNHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIABCLQTISDLETECLDLRTKLCDLERANGTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSSTG	1		_	TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG				
TLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY TVWKQFGGIPEFYNIPQGTVEKREGYPLRPBLIESAMYLYRAT GDPTLLELGRDAVESIEKISKVEGSPAITKDLRDHKLDNRMESF FLABTVKYLYLLEDPTNFIHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVBLMREFYSLKRSRSKFQ KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPRRPPRNRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPRRPPRNRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLGTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAABRACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLGTISDLETECLDLRTKLCDLERANQTLKDBYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAABRACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	1			IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW				
TVWKQFGGLPFFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT GDPTLLEGRDAVESIEKISKVECGFATIKOLRDHKLDNRKESF FLABTYKSYLVLIFDPTNPIHNNGSTFDAVITPYGGCILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVBDLMREFYSLKRSRSKFQ KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIPIFLRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGGGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPRPPRNRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGGGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPRPPRNRRPG 7038 155 891 GAGAASDMSGGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAKQKQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQBELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPCHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANGTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS				YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY				
GDPTLLELGRDAVESIEKISKVECGPATIKDLRDHKLDNRMESF FLABTVKYLYLLIFDPINPIHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCQRLKEEQWEVEDLMREFYSLKKRSRSKFQ KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIPIFLRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPRRPRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPPRPRRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQIFTFALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERAKSSKGTSTSRTG 7040 34 789 KITPPRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS				TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT				
FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPRRPPRRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPRRPPRRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHGBELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHGEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRPPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS								
FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPRRPPRRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPRRPPRRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHGBELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHGEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRPPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	1	,	:					
KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPRRPRRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPRRPRRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQBELTELHKKRGELAQ\RVIDLNNQWRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHBISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQWRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	j l							
QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K 7036 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPRRPRRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPRRPRRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	,							
K CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPRPPRNRPG		; ; <u> </u>		QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLATTKK				
RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPRRPPRNRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPRRPRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQURIKHQBELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS			• •					
RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPRRPRRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPRPRRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	7036	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSTPT				
PPPPPPPPRRPPRRRPG 7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPRRPPRNRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQBELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS				RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRDI.DP				
7037 442 761 CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPRPRNRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHGEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS			•					
RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP PPPPPPPPPPPPRRPRRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	7037	442	761					
PPPPPPPPPRRPPRNRRPG 7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQBELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	1							
7038 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQBELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	1							
QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	7038	155	891					
LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	1 1		-	OYNKLLEKSDLHSVI.AOKT.OARKHDUDNDHRT GDGUDGTENDMO				
QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	1			LOEMAOLRIKHORELTELHKKRGELAO\ DVIDI AMOMOREDEM				
LQITFTALEGKLRKTTEENQBLVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	į							
LQEAASPAAERACRSSKGTSTSRTG 7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	1							
7039 155 891 GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	1							
QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	7039	155	891					
LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	• • •		0)1					
QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	, ,	ļ						
LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAAERACRSSKGTSTSRTG 7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	1							
TO40 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS	į į	,						
7040 34 789 KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS				LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR				
KITTERKERKCSSGRGSDNSSVLSGELPPANGKTALF INSGGSS	7040	34	700					
GIESVMKDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKKRSN	.540	3-1	109					
				GIESVMKDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKKRSN				

			· · · · · · · · · · · · · · · · · · ·
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
]	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
6	sequence	Doguoneo	\=possible nucleotide insertion)
	boqueince		PGSORRRLIPALSLDTSSPVRKPPNSTGVRWVDGPLRSSPRGLG
1	٠,		EPFEIKVYEIDDVERLORRRGGASKEAMCFNAKLKILEHROORI
1			AEVRAKYEWLMKELEATKQYLMLDPNKWLSEFDLEQVWELDSLE
ł			YLEALECVTERLESRVNFCKAHLMMITCFDIT
7041	ļ	569	.l
7041	1	567	SGRVAMGRRAPAGGSLGRALMRHQTQRSRSHRHTDSWLHTSEL
ļ]	1	NDGYDWGRLNLQSVTEQSSLDDFLATAELAGTEFVAEKLNIKFV
			PAEARTGLLSFEBSQRIKKLHEENKQFLCIPRRPNWNQNTTPEE
			LKQAEKDNFLEWRRQL\VRLEEEQKLILTPFERNLDFWRQLWRV
			IERSDIVVQIVDA
7042	7	345	PIHMAAAALRADI\ISPLFPHIQGYLLLSASHG\ATSLHTKGAL
		[PLETVTMYTVIPKSKYVLVKPDTQYPYSENLDEFKRLAENSASN
		<u></u>	DDLLMAEVAISDYGDKLTLELREKY
7043	2	2170	ARGMAARDSDSEEDLVSYGTGLEPLEEGERPKKPIPLQDQTVRD
1			EKGRYKRFHGAFSGGFSAGYFNTVGSKEGWTPSTFVSSRQNRAD
		1 .	KSVLGPEDFMDEEDLSEFGIAPKAIVTTDDFASKTKDRIREKAR
	,		QLAAATAPIPGATLLDDLITPAKLSVGFELLRKMGWKEGQGVGP
			RVKRRPRRQKPDPGVKIYGCALPPGSSEGSEGEDDDYLPDNVTF
1			APKDVTPVDFTPKDNVHGLAYKGLDPHQALFGTSGEHFNLFSGG
		1	SERAGDLGEIGLNKGRKLGISGQAFGVGALEEEDDDIYATETLS
		•	KYDTVLKDEEPGDGLYGWTAPRQYKNQKESEKDLRYVGKILDGF
		,	SLASKPLSSKKIYPPPELPRDYRPVHYFRPMVAATSENSHLLQV
	* *** ;		LSESAGKATPDPGTHSKHQLNASKRAELLGETPIQGSATSVLEF
			LSQKDKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQPSPAAA
			AGHCSWNMALGGGTATLKASNFKPFAKDPEKQKRYDEFLVHMKQ
1			GQKDALERCLDPSMTEWERGRERDEFARAALLYASSHSTLSSRF
l .		•	THAKEEDDSDQVEVPRDQENDVGDKQSAVKMKMFGKLTRDTFEW
			HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLPETASLPTTQASSE
Ì] .	KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK
		ler for the second	QQSSPLVNKEEEHAPELSAN
7044	276	734	EVYLTDEFAKGRKVADLYELVQYAGNIIPRLYLLITVGVVYVKS
			FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG
,		,	EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR
			ERERQELRILVGTNLVRLSQV
7045	3	513	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP
: : !			KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK
':			DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE
[ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG
7046	3	513	LGFKMEALSRAGOEMSLAALKOHDPYITSIADLTGOVALYTFCP
	-		KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK
			DLEFOLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE
			ETRRSQQA/RSGQTESQPGOWLQRPQAHRHPGDAEQSQG
7047	103	486	QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN
''	200	-200	IMLIDVREIWEILEYOKIPESINVPLDEVGEALOMNPRDFKEKY
			NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER
7048	92	627	
1040	34	021	FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEBEEANY
			WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN
	,		RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA
			IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI
لحبيا			EKKW
7049	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL
			VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL
			NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT
			EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX
			ASSLWG
7050	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ſ	sequence	sequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
		• '	VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL
			NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT
			EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX
7051	119	076	ASSLWG
1 ,031	. 113	816	KKMNLAEICDNAKKGREYALLGNYDSSMVYYQGVMQQIQRHCQS
			VRDPAIKGKWQQVRQELLEEYEQVKSIVGTLESFKIDKPPDFPV
l			SCQDEPFRDPAVWPPPVPAEHRAPPQIRR/RQSRSKTSEERNGR
[1		SRSPGTCRPST\PISKSEKPSTSRDKDYRARGRDDKGRKNMQDG
1			ASDGEMPKFDGAGYDKDLVEALERDIVSRNPSIHWDDIADLEEA
7052	467		KKLLREAGVLPMWM
7052	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
7053	465		TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAARQGPRR
,053	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
7054	<u> </u>		TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAARQGPRR
7054	1	1036	GTSQRSRETDARRRSAGAEPTARLPWPAALEEWPSCPCEPLGFG
1		,	RRCRWDAMEYDEKLARFRQAHLNPFNKQSGPROHEOGPGEEVPD
			VTPEEALPELPPGEPEFRCPERVMDLGLSEDHFSRPVGLFLASD
1			VQQLRQAIBECKQVILELPEQSBKQKDAVVRLIHLRLKLOELKD
i			PNEDEPNIRVLLEHRFYKEKSKSVKQTCDKCNTIIWGLIOTWYT
		;	CTGCYYRCHSKCLNLISKPCVSSKVSHQAEYELNICPETGLDSO
1			DYRCAECRAPI/CS/DGVVPSEARQCDYTGOYYCSHCHWNDLAV
7055			IPARVVHNWDFEPRKVSRCSMRYLALMVSRPVLRLREIN
/055	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP
1		•	EYHYLHQMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAYLRG
1 .		<u>:</u>	SQKVPSRRTRRLLDKSRTFHITCGATICIFSGVHVAAHLVNALN
	[:	FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL
7056			M
/036	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP
		·	EYHYLHOMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAYLRG
	· 1	,	SQKVPSRRTRRLLDKSRTFHITCGATICIFSGVHVAAHLVNALN
			FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL
7057			<u>M</u>
/05/	1368	431	GIYLHVNEKIPRPTCIGDRQENDKENLNLENHRDQELLHASCQA
] .	:		SGEVPSQASLRGFFTEDEPGCFGEGENLPEALONIODEGTGEOL
] :		SPQERISEKQLGQHLPNPHSGEMSTMWLEEKRETSOKGOPRAPM
			AQKLPTCRECGKTFYRNSQLIFHQRTHTGETYFQCTICKKAFLR
		_	SSDFVKHQRTHTGEKPCKCDYCGKGFSDFSGLRHHEKIHTGEKP
	, [r	YKCPICEKSFIQRSNFNRHQRVHTGEKPYKCSHCGKSFSWSSSL
			DKHQRSHLGKKPFQ*PVTKLSFPISISQPSHKNTQLHQEELCLR
7058	 		GYPC
,058	1	469	FSGFGAVPDALGCRMSDLRITEAFLYMDYLCFRALCCKGPPPAR
			PEYDLVCIGLTGSGKTSLLSKLCSESPDNVVSTTGFSIKAVPFO
			NAILNVKELGGADNIRKYWSRYYQGSQGVIFVLDSASSEDDLEA
7050		<u> </u>	ARN*SCTQLLQHPQLCTLPFLILA
7059	1	1178	WPAFPRQPAAAAMDALLGTGPRRARGCLGAAGPTSSGRAARTPA
			APWARPSAWLECVCVVTFDLELGQALELVYPNDFRLTDKEKSSI
			CYLSFPDSHSGCLGDTQFSFRMRQCGGQRSPWHADDRHYNSRAP
			VALQREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL
	. 1		FQALLSLIAPEYFDKLAPCLBAVCSEIDQWPAPAPGQTLNLPVM
			GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF
			RCFRPVLTHMQTLWELMLLGEPLLVLAPSPDVSSEMVLALTSCL
	ŀ		QPLRFCCDFRPYFTIHDSEFKBFTTRTQAPPNVVLGVTNPFFIK
			TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP
7060	90	1670	SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ
			YRFEHLVTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEEMRAS
			Z-1

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
I NO:	nucleotide location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
.}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	-		LKTLHRMAEKVGADITVLREREVDYDSDMPRKITEVLVRKVPDN
		ļ	QQFLDLRVAVLGNVDSGKSTLLGVLTQGELDNGRGRARLNLFRH
			LHEIQSGRTSSISFEILGFNSKGEVHGINGTQWGQTLRMGW***
			RT*DGGRVWRLFEIV*MNALRGL*TSSAPLRKSMGNQLN*IKNG
			VKIKRQGHPGNGLGPGNSEGVGRAGRRH*GPWALGQVVNYSDSR
	1		TAEEICESSSKMITFIDLAGHHKYLHTTIFGLTSYCPDCALLLV
ļ			SANTGIAGTTREHLGLALALKVPFFIVVSKIDLCAKTTVERTVR
1	1	•	QLERVLKQPGCHKVPMLVTSEDDAVTAAQQFAQSPNVTPIFTLS
			SVSGESLDLLKVFLNILPPLTNSKEQEELMQQLTEFQVDEIYTV
7061	364	710	PEVGTVVGGTLSR*IDLLATLPTQPSPIYSKTSWPKGGDPGI ARMPSPLGPPCLPVMDPETTLEEPETARLRFRGFCYQEVAGPRE
7,301	304	/10	ALARLRELCCQWLQPEAHSKEQMLEMLVLEQFLGTLPPEIOAWV
			RGQRPGSPEEAAALVEGLQHDP*ARMPSPLGPPCLPVMDPETTL
7		1 1 1	EEPETARLRFRGFCYQEVAGPREALARLRELCCOWLOPEAHSKE
		•	QMLEMLVLEQFLGTLPPEIQAWVRGQRPGSPEEAAALVEGLOHD
1			PGQLLG
7062	71	744	AKAGTNLERLHWLSYFFCIPKHKLKSSQKDKVRQFMACTQAGER
1			TAIYCLTQNEWRLDEATDSFFQNPDSLHRESMRNAVDKKKLERL
1			YGRYKDPQDENKIGVDGIQQFCDDLSLDPASISVLVIAWKFRAA
İ	Ì	•	TQCEFSRKEFLDGMTELGCDSMEKLKALLPRLEQELKDTAKFKD
1			FYQFTFTFAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTFL
			менн
7063	2	562	LRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEDLKAFERR
			LTEYIHCLQPATGRWRMLLIVVSVCTATGAWNWLIDPETQKVSF
			FTSLWNHPFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLA BYNMSCDDTGKLILKPRPHVQ+QSSLIVMGLKIAFLRISDTAKS
· ·			HKGFLLRLDM .
7064	300	884	RDTGSDPSSTRRLCSTCCTGH*PAEPIASPHPSRGTCPPASSAS
		,	SRRTGCWTCPPESGHAOARRSRRASASRWGARGAVRSAVAARGC
			SSRAGRWLETPGRRRGPPACAAAAGRLRGPAP*AAPPTASVPAR
			CRCPAARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAP
			PLLTPLGAGRAGGSRANS
7065	1	555	ATTTHSARRSGRGAAAEAAASAAGGRQKGPDRKAWEGRRTTPGG
1 ;			RSQSEPKAPPPQKRSEAAFASMAHSPVAVQVPGMQNNIADPEEL
		.* .	FTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEABDEIEDI
	· ;		QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDLL
7066	256	(7)	RAGPFDEFQ
,,000	356	676	PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND
1]		VGVEVGGSGGCLEERTPP
7067	152	973	KENITMATEIGSPPRFFHMPRFOHOAPROLFYKRPDFAOOOAMO
1,	132	5/3	QLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ
			PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW
	J .		TPEGRRLVTGASSGEFTLWNGLTFNFETILOAHDSPVRAMTWSH
1	[NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP
			FSVVPIVMVKLFSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT
			HSPFCWAPF
7068	222	816	DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD
	[DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
			VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY
			GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL
			AELRIHENKVKKIQKDTFKKK
7069	1147	1765	FRDHRRYFYVNEQSGESQWEFPDGEEEEEESQAQENRDETLAKQ
			TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW
L			TLLQSNVPVLQPPLPLEMPPPPPPPPPPESPPPPPPPPPPPAPKMPPP

			<u>. </u>
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1 .	residue of		
1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			EKTKKGRKDKAKKSKTKMPSLVKKWQSIQRELDEEDNSSSSEED
	·	ł	RVSTAQKRIEEWKQQQLVSGMABRNANFEA
7070	1	547	DGTMEDSEAVQRATALIEQRLAQEEENEKLRGDARQKLPMDLLV
1 .	}	j ·	LEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIONLI
L	į.		ELRKKRKOKKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGK
	1	1	MKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG
1	j	} ·	ATVDFO
7071	2	921	
'0'1	4	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
}	1	}	VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY
		i	FQDPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV
	1		PESSLPPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV
1	1		PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT
1		,	SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ
1	l		IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
7072	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
ľ			VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIOY
1	i ·		FODPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV
1			PESSLPPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV
		1	
l	ĺ		PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT
			SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ
			IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
7073	50	504	LAHGSFGVSDFPAPAAAPAHTLTSFSGSLSPQFRKPLGRAPAMP
		j	LVRYRKVVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYSKI
	j .	·	VTLGKDEFHLHLVDTAGQDEYSILPYSFIIGVHGYVLVYSVTSL
			HSFQVIESLYQKLHEGHGK
7074	263	1003	VCPVLCSTRQEPGHSSLVTYFGKPTRRKEFLLGHCIAAGKMNIS
	İ		VDLETNYAELVLDVGRVTLGENSRKKMKDCKLRKKONERVSRAM
	i		CALLNSGGGVIKAEIENEDYSYTKDGIGLDLENSFSNILLFVPE
į	* /	** ***	YLDFMQNGNYFLIFVKSWSLNTSGLRITTLSSNLYKRDITSAKV
	·		MNATAALEFLKDMKKTRGRLYLRPELLAKRPRVDIQEENNMKAL
	;		AGVFFDRTELDRKEKLTFTESTHVEI
7075		1005	Y
1075	598	1005	NYINFFFRKEYPPHVQKVEINPVRLSRLQGVERIMKKTEESESQ
1	ľ		VEPEIKRKVQQKRHCSTYQPTPPLSPASKKCLTHLEDLQRNCRQ
			AITLNESTGPLLRTSIHQNSGGQKSQNTGLTTKKFYGNNVEKVP
			IDII
7076	. 279	1049	LQSESSNAAEGNEQRHEDEQRSKRGGWSKGRKRKKPLRDSNAPK
	,	,	SPLTGYVRFMNERREQLRAKRPEVPFPEITRMLGNEWSKLPPEE
			KQRYLDEADRDKERYMKELEQYQKTEAYKVFSRKTQDRQKGKSH
	,		RODAAROATHDHEKETEVKERSVFDIPIFTEEFLNHSKAREAEL
			ROLRKSNMEFEERNAALOKHVESMRTAVEKLEVDVIOERSRNTV
			LQQHLETLRQVLTSSFASMPLPEXGETPTVDTIDSYM
7077	3	1119	
1)	1113	SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVARQR
		*	ELKWLDMFSNWDKWLSRRFQKVKLRCRKGIPSSLRAKAWQYLSN
			SKELLEQNPRKFEELERAPGDPKWLDVIEKDLHRQFPFHEMFAA
j			RGGHGQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ
1			AFWCLVQICDKYLPGYYSAGLEAIQLDGEIFFALLRRASPLAHR
1			HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI
]			IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDF
[,		LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS
1			RAIHEERRROOPPLGPSSS
7078	483	767	
1	303	101	FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG
			VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE
-			SLPELY
7079	2	376	SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ
J	l i		MQARKKRRGIIEKRRRDRINSSLSELRRLVPTAFEKQGSSKLEK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
,	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	004	\=possible nucleotide insertion)
 			AEVLOMTVDHLKMLHATGGTGTHALLFQASFIQQIF
7080	200	595	VQLPLEAPCLSLLSCRDHSGGNRDLSRRHRDCRVYGSPODGIPY
1		3,3	LTHPLCHQDVVSVGRLQIRALATPGHTQGHLVYLLDGEPYKGPS
		[CLFSGDLLFLSGCGEFPRKREELGEEGETEVRAATVPWRALKP
7081	213	506	AVTEEEMILNSLSLCYHNKLILAPMVRVGTLPMRLLALDYGADI
			VYCEELIDLKMIQCKRVVNEVLSTVDFVAPDDRVVFRTCEREON
		·	RVVFOMGTS
7082	3	1137	APSRNTMLMAWCRGPVLLCLRQGLGTNSFLHGLGOEPFEGARSL
			CCRSSPRDLRDGEREHEAAQRKAPGAESCPSLPLSISDIGTGCL
			SSLENLRLPTLREESSPRELEDSSGDOGRCGPTHOGSEDPSMLS
1			OAQSATEVEERHVSPSCSTSRBRPFOAGELILAETGEGETKFKK
1			LFRLNNFGLLNSNWGAVPFGKIVGKFPGQILRSSFGKQYMLRRP
}			ALEDYVVLMKRGTAITFPKDINMILSMMDINPGDTVLEAGSGSG
: .	· !	,	GMSLFLSKAVGSQGRVISFEVRKDHHDLAKKNYKHWRDSWKLSH
:			VEEWPDNVDFIHKDISGATEDIKSLTFDAVALDMLNPHVTLPVF
			YPHLKHGGVCPVYVVNITQVIELLD
7083	115	541	RSNAVQLTRMEYAMKSLSLLYPKSLSRHVSVRTSVVTOOLLSEP
			SPKAPRARPCRVSTADRSVRKGIMAYSLEDLLLKVRDTLMLADK
1			PFFLVLEEDGTTVETEEYFQALAGDTVFMVLQKGQKWQPPSEQG
İ			TRHPLSLSHK
7084	3	522	NSVSVSSQSRFLASVPGTGVQRSAAADMAASTAAGKQRIPKVAK.
1		322	VKNKAPAEVQITAEQLLREAKERELELLPPPPQQKITDEEELND
			YKLRKRKTFEDNIRKNRTVISNWIKYAQWBESLKEIQRARSIYE
· ·			RALDVDYRNITLWLKYAEMEMKNRQVNHARNIWDRAITTL
7085	243	1499	RQLARLRRRGWRSPFGGAPMAHITINQYLOQVYEAIDSRDGASC
		2.25	AELVSFKHPHVANPRLQMASPEEKCQQVLEPPYDEMFAAHLRCT
1	•		YAVGNHDFIEAYKCQTVIVQSFLRAFQAHKEENWALPVMYAVAL
1			DLRVFANNADOOLVKKGKSKVGDMLEKAABLLMSCFRVCASDTR
· [AGIEDSKKWGMLFLVNQLFKIYFKINKLHLCKPLIRAIDSSNLK
	7		DDYSTAQRVTYKYYVGRKAMFDSDFKQAEEYLSFAFEHCHRSSO
l			KNKRMILIYLLPVKMLLGHMPTVELLKKYHLMQFAEVTRAVSEG.
1	٠, *		NLLLLHEALAKHEAFFIRCGIFLILEKLKIITYRNLFKKVYLLL
	,		KTHQLSLDAFLVALKFMQVEDVDIDEVQCILANLIYMGHVKGYI
"		•	SHQHQKLVVSKQNPFPPLSTGC
7086	256	525	ILAARMGKQNSKLRPEVMQDLLESTDFTEHEIQEWYKGFLRDCP
:	•		SGHLSMEEFKKIYGNFFPYGDASKFAEHVFRTFDANGDGTIDFR
1			EF
7087	166	723	LSGSSAGKVAAPCVPPSNHELVPITTENAPKNVVDKGEGASRGG
			NTRKSLEDNGSTRVTPSVQPHLQPIRNMSVSRTMEDSCELDLVY
1 1			VTERIIAVSFPSTANEENFRSNLREVAOMLKSKHGGNYLLFNLS
1 1			ERRPDITKLHAKVLEFGWPDLHTPALEKICSICKAMDTWLNAHP
			HRCRVLHNKG
7088	104	759	GTSAASPSSLLEMAGEITETGELYSSYVGLVYMFNLIVGTGALT
1 . [ſ		MPKAFATAGWLVSLVLLVFLGFMSFMTTTFVIEAMAAANAQLHW
.			KRMENLKEEEDDDSSTASDSDVLIRDNYERAEKRPILSVORRGS
	}		PNPFEITDRVEMGQMASMFFNKVGVNLFYFCIIVYLYGDLAIYA
1 1	İ		AAVPFSLMQVTCSATGNDSCGVEADTKYNDTDRCWGPLRRVD
7089	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
] [1		HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
	1	•	SPIHTSVQFQASYLPKPGAQLYQFRYVNROGQVCGQSPPFQFRE
[PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM
1 1	į	ĺ	QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS
			HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD
] {		1	RLRDTVKALTREQEKLLGQLKEVQADKEQSEAELQVAQQENHHL
1 .		ŀ	NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP
			Market and Market and

	(= 57 · 5		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
J	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
-	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	•		
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR
1	(LEVAEVNGKLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILK
1			LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREB
1		1	TELRSALRVLOKEKEOLOEEKOELLEYMRKLEARLEKVADEKWN
1			EDATTEDERAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETO
1			<u> </u>
	<u> </u>	ļ	ASLLLGLE
7090	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
		1	HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
ſ		ł.	SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE
1		1	PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM
1			QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS
1		1	HGEITEERDILSROOGDHVARILELEDDIOTISEKVLTKEVELD
[RLRDTVKALTREQEKLLGQLKEVQADKEQSEAELQVAQQENHHL
1			
1		1	NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP
1.			LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR
1	1	1	LEVAEVNGKLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILK
	Į.		LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREL
		į	TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
			EDATTEDEBAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETO
1	}		ASLLIGLE
7091	186	1076	EGMLTREHRCGRSEEQELEPWPSPKKARSGRWLRNGFKRKMEEP
1,031	100	10/8	, —
	· ·	•	EEPADSGQSLVPVYIYSPEYVSMCDSLAKIPKRASMVHSLIEAY
		ł.	ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDDHPD
		i	SIEYGLGYDCPATEGIFDYAAAIGGATITAAQCLIDGMCKVAIN
	Į.	ł ·	WSGGWHHAKKDEASGFCYLNDAVLGILRLRRKFERILYVDLDLH
	· ·	i	HGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVSDVGLGKGRY
	· ·	1	YSVNVPIQDGIQDEKYYQICERYEPPAPNPGL
7092	522	809	KOGINEDOEBSOKPRLGEGCEPISKROMKKLIKOKOWBEORELR
1.7052	322	1 803	
			KQKRKEKRKKLERQCQMEPNSDGHDRKRVRRDVVHSTLRLII
			DCSFDXLM
7093	454	655	NFGVSGVELAQQASMVRMSFVIAACQLVLGLLMTSLTESSIQNS
1			ECPQLCVCEIRPWFTPQSTYREA
7094	2	508	FVRSMHWGVGFASSRPCVVDLSWNQSISFFGWWAGSEBPFSFYG
j	. ,	I	DIIAFPLODYGGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHE
1		1	LLVIRKQOEIDSKDAIILHQFARPNNGVPSLSPFCLKMETYLRM
l	1		ADLPYONYFGGKLSAOGKMPWIEYNHEKVSGTEFII
7005	 	433	
7095	1	411	IASSLPKMASLLQSDRVLYLVQGEKKVRAPLSQLYFCRYCSELR
 -		!	SLECVSHEVDSHYCPSCLENMPSARAKLKKNRCANCFDCPGCMH
1	1	1	TLSTRATSISTQLPDDPAKTTMKKAYYLACGFCRWTSRDVGMAD
<u> </u>	L	1	KSVGE
7096	224	2067	ETRSLAVQEKPSQAGRRSSRISFAGALFLTRFLLQELLLNNFC
1		[SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR
1	1		APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE
			OREHYKLDWHRFNLKORLKDKPLLSALDFEKOSSTGDLSSISGS
1			
1			EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF
1			LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAAGHFA
1	1	1	GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN
ĺ			LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF
1	1	1	FGGKGAPLQRGDPRLWDIPLATRRPTFQELQRVLHKLTTLHVYE
1		1	EDPREAVRLHSPOTHWKTVREERKKPTEEEIRKICRDEKEALGO
1			NEESPKQGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR
1			RKRNKKEKSRDOEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL
1	1	1	
1			LDEAKAPGQPELWNALLAACRAGDVGVLKLQLAPSPADPRVLSL
L			LSAPLGSGGFTLLHAAAAAGRGSVVRLLLEAGADPTVQCQDH
7097	256	1228	IRTKSAATWEAWPQCGREGSRIITEPCEANAGSRQELQTERISS
			FLAAQGDQAFHSGLETNNSNSELPLRVGLKVAQGSPLMGGQVSA
		<u> </u>	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
4	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
-			SNSFSRLHCRNANEDWMSALCPRLWDVPLHHLSIPGSHDTMTYC
1			LNKKSPISHEESRLLQLLNKALPCITRPVVLKWSVTOALDVTEO
· .		·	LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTTALVEDTLTEISE
			WLERHPREVVILACRNFEGLSEDLHEYLVACIKNIFGDMLCPRG
			EVPTLRQLWSRGQQVIVSYEDESSLRRHHBLWPGVPYWWGNRVK
			TEALIRYLETMKSCGR
7098	82	956	SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYCVMRLOT
			EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHFHPSLEA
			LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLPSKPLLG
			LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFLGLWLVL
			LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAEGRTRGR
1 1			AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPVGCGCFF
	•		LGLALRLVYYHWLHPSCCWKPDPDQVD
7099	992	210	LFRLAPGFLRSLARQGYHQIWAFPFLPSGATATWPAASRSRSLA
1 1	·	,	ARSLPRSPARPGPNDALLGEHDFRGQGVRAQRFRFSEEPGPGAD
	<u> -</u>		GAVLEVHVPQIGAGVSLPGILAAKCGAEVILSDSSELPHCLEVC
}			ROSCOMNNLPHLOVVGLTWGHISWDLLALPPODIILASDVFFEP
1			EDFEDILATIYFLMHKNPKVQLWSTYQVRSADWSLEALLYKWDM
			KCVHIPLESFDADKEDIAESTLPGRHTVEMLVISFAKDSL
7100	205	671	ANGGFWEAAPGSEVSLPLWVPTASHSKTTALGIGSAPPPHLSVL
].	, .		FLFSFPPQLGDPLEAFPVFKKYDRNGLNVSIECKRVSGLEPATV
			DWAFDLTKTNMQTMYEQSEWGWKDREKREEMTDDRAWYLIAWEN
7101	2	F07	SSVPVAFSHFRFDVERGDEVLYW
1,101	. 4	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
		•	VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEITIPADVTP ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK
1			VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
7102	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
/===	_	505	VRILLYGEPRYGKTSLIMSLYSEEFPEEVPPRAEEITIPADVTP
			ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK
			VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
7103	119	438	GSQSSVAVNIRSGTDEESMDLMNGQASSVNIAATASEKSSSES
			LSDKGSELKKSFDAVVFDVLKVTPBEYAGQITLMDVPVFKAIOP
			DELSSCGWNKKEKYSSAP
7104	1670	795	RLWEHRSVSAGASGWGLSSPGCLLLHPSLPEEERVDILINNAGV
		•	MRCPHWTTEDGFEMQFGVNHLGEAWAGAAPWVQAILPRRPPKVL
		·	GF*V*VKSDLFIILNPGHFLLTNLLLDKLKASAPSRIINLSSLA
.			HVAGHIDFDDLNWQTRKYNTKAAYCQS\KLAIVLFTKELSRRLQ
1			GSGVTVNALHPGVARTELGRHTGIHGSTFLQHHN\WAHLLAAWS
ļ			KSPRSWPAPAQHNTLAVAEELA\VISGKYFDGLKQKAPAPEAED
			EEVARRLWAESARLVGLEAPSVREQPLPR
7105	765	143	GQMCRRPSPKSTSCLSMTCDLP/RGLQDPQCLALFRVAVDKHQA
1			LLKAAMSGQGVDRHLFALYIVSRFLHLQSPFLTQVHSEQWQLST
			SQIPVQQMHLFDVHNYPDYVSSGGGFGPADDHGYGVSYIFMGDG
	}		MITFHISSKKSSTKTDSHRLGQHIEDALLDVASLFQAGQHFKRR
1 7105			FRGSGKENSRHRCGFLSRQTGASKASMTSTDF
7106	14	1064	GLQAGHPHPRSASRIPEADTH\YSKLQRAFDSIVNKDHKRMFGT
	1		YFRVGFFGSKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGQCF
j l	1		GAEFVEVIKDSTPVDKTKLDPNKAYIQITFVEPYFDEYEMKDRV
] [TYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTTMHAF
	1		PYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPPD
			AKMLQMVLQGSVGATVNQGPLEVAQVFLAEIPADPKLYRHHNKL
			RLCFKEFIMRCGEAVEKNKRLITADQREYQQELKKNYNKLKENL
7107	1145	591	RPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS *I*WLQTGKKK
		271	"I "NITATOWV

		·	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
1	residue of	residue of amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1 2 4 4	sequence	sequence	\=possible nucleotide insertion)
7108	1	942	VKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSSTFYIAF
/200	-	342	FLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMOMGIIMVLK
1			QTWNNFMELGYPLIQNWWTRRKVRQEHGPERKISFPQWEKDYNL
1	1		QPMNAYGLFDEYLEMILQFGFTTIFVAAFPLAPLLALLNNIIEI
	'		RLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAFVI
1			AITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLSVFRIS
1			DFENRSEPESDGSEFSGTPLKYCRYRDYRDPPHSLVPYGYTLQF
	_		WALIVHW
7109	964	102	WDQRKRNSLVPGPAHGPAQEEPWEKKESLGAAQEALSIQLQPKE
	!		TQPFPKSEQVYLHFLSVVTEDGPEPKDKGSLPQPPITEVESQVF
			SEKLATDTSTFEATSEGTLELQQRNPKAERLRWSPAQEESFRQM
			VVIHKEIPTGKKDHECSECGKTFIYNSHLVVHQRVHSGEKPYKC
4			SDCGKTFKQSSNLGQHQRIHTGEKPFECNECGKAFRWGAHLVQH
	,	,	QRIHSGEKPYECNECGKAFSQSSYLSQHRRIHSGEKPFICKECG
7110	96	697	KAYGWCSELIRHRRVHARKEPSH RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKOMLTRASITFVLG
/110	,	657	SPSTKRRGQMLQPIIEGETAHFFEBIKEEEEDGVNLSSELGDML
1			KTAVQVQSSLKNSESDVEENQEKLALDLRLSSSRAASMPELLEO
			LWKARAEKKKLRKTLREFEEAFYOONGRNAOKEDRVPVLEEYRE
			YKKIKAKLRLLEVLISKODSSKSI
7111	2	414	GSGLYRGPTPGGQCIWKPNSMPPDHERNFGFTQFALELNELTAE
	·		LKRSLPSTDTRLRPDQRYLEEGNIQAAEAQKRRIEQLQRDRRKV
			MEENNIVHQARFFRRQTDSSGKEWWVTNNTYWRLRAEPGYGNMD
	L		GAVLW
7112	103	495	PRCFPVADRGRLIGGLPDVVTIMEGKTLNLTCTVFGNPDPEVIW
			FKNDQDIQLSEHFSVKVEQAKYVSMTIKGVTSEDSGKYSINIKN
70.00			KYGGEKIDVTVSVYKHGEKIPDMAPPQQAKPKLIPASASAAGQ
7113	1	824	KCLRQAWHEAPSSLAFTRWCSREERAEGGGNLHRSITRDPKPPG
			LRPSQRPMDDKKKKRSPKPCLAQPAQAPGTLRRVPVPTSHSGSL ALGLPHLPSPKQRAKFKRVGKEKCRPVLAGGGSGSAGTPLQHSF
	•		LTEVTDVYEMEGGLLNLLNDFHSGRLQAFGKECSFEQLEHVREM
			OEKLARLHFSLDVCGEEEDDEEEEDGVTEGLPREOKKTMADRNL
			DQLLSNLGSCLGALVPGGMRGGEGTYSQSHSWALGEKVGVHGSK
	·		SSGPLNLPRR
7114	3 .	1492	VWEVDEQIDHYKESQDKFLWQAAFIGKETLKDESGQECKICKKI
1 1			IYLNTDFVSVKQRLPKYYSWERCSKHHLNFLGQNRSYVRKKDDG
	:	:	CKAYWKVCLHYNLHKAQPAERFFDPNQRGKALHQKQALRKSQRS
		•	QTGEKLYKCTECGKVFIQKANLVVHQRTHTGEKPYECCECAKAF
			SQKSTLIAHQRTHTGEKPYECSECGKTFIQKSTLIKHQRTHTGE
			KPFVCDKCPKAFKSSYHLIRHEKTHIRQAFYKGIKCTTSSLIYQ
			RIHTSEKPQCSEHGKASDEKPSPTKHWRTHTKENIYECSKCGKS
			FRGKSHLSVHQRIHTGEKPYECSICGKTFSGKSHLSVHHRTHTG
			EKPYECRRCGKAFGEKSTLIVHQRMHTGEKPYKCNECGKAFSEK
		15	SPLIKHQRIHTGERPYECTDCKKAFSRKSTLIKHQRIHTGEKPY
			KCSECGKAFSVKSTLIVHHRTHTGEKPYECRDCGKAFSGKSTLI KHQRSHTGDKNL
7115	1	947	NAAHGYNWGLWCMYIIPPQDWLDRGDESAPIRTPAMIGCSFVVD
	^	, 341	REYFGDIGLLDPGMEVYGGENVKLGMRVWQCGGSMEVLPCSRVA
]	}		HIERTRKPYNNDIDYYAKRNALRAAEVWMDDFKSHVYMAWNIPM
			SNPGVDFGDVSERLALRORLKCRSFKWYLENVYPEMRVYNNTLT
			YGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSQLVRYSADGL
			LOLGPLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVARPTQRLWD
			FTQSGPIVSRATGRCLEVEMSKDANFGLRLVVQRCSGQKWMIRN
			WIKHARH
7116	866	95 .	RVRMRRNAEVIEEKLSMKSWAKFRPGEPWKGYPNIDPETDPYVT
			PGSVINNLSINTVREVDHLRDRNSGSSSSLNTTLPSTSAWSSIR

- 000	15 37		7		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide		
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=		
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,		
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,		
1 '	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,		
•	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,		
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,		
*	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop		
1	amino acid	sequence	Codon, /=possible nucleotide deletion,		
	sequence		\=possible nucleotide insertion)		
			ASNYNVPLSSTAQSTSARNSDSKLTWSPGSVTNTSLAHELWKVP		
	1		LPPKNITAPSRPPPGLTGQKPPLSTWDNSPLRIGGGWGNSDARY		
Ī			TPGSSWGESSSGRITNWLVLKNLTPQIDGSTLRTLCMQHGPLIT		
	i i		PHLNLPHGNALVRYSSKEEVVKAQKSLHISDLFLLTL		
7117	695	1261	LLISTPGGCHPPPSSIEFTYTGAWGKALPAPHMPCAPGALPQGA		
''	333	1 -20-	FVSQAARAIPLLQPSQAAQAEGLSQPARACGALCSLPWPLRNWG		
Ì			SPILRLPGGLRTPTNDRKTRTRSAMACWARAQWDTLGPLKLSHR		
1	Į	ł			
i			GKVCLRHPRPTGVRGGPGAAGRQGGMGTRRRGTFTSGARDPGGL		
2220		1023	RVKHRCQPTGHLP		
7118	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE		
			ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR		
1			LLLETHLPSKKKKVLLGVGDPKIGAAIQEBLGYNCQTGGVIAEI		
			LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD		
			NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT		
1	·	·	YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG		
1	1		MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS		
1		•	ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT		
1	·		RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF.		
į			SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKBAMVQAE		
1			EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE		
			EMSEKPKKKKKQKPQEVPQENGMBDPSISFSKPKKKKSFSKEEL		
			MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK		
			ECVERDUCCODDER & CVCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		
1]		FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED -		
7119	49	1863			
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE		
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR		
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI		
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD		
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT		
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLOPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG		
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS		
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLOPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT		
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLOPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF		
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLOPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE		
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLOPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE		
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL		
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEBL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED		
7119	1991	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALSSENSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKSPSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKBEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKSPSKEBL MSSDLEETAGSTSIPKRKKSTPKEETVNPPEEAGHRSGSKKKRK FSKBEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTVLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKSPSKEBL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKBEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTVLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEBL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKBEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEFQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERKFGPLGFNIPY		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEBL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKBEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEFQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTVLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEBL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKBEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEFQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEBL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSBKPKKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREBIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSBKPKKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLBLMA		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCIFHGNALERKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREBIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLBLMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKBEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILLGNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPBFINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLBLMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCIFHGNALERKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREBIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLBLMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKBEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILLGNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPBFINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLBLMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKBEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILLGNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREBIVEDVTQNILLKVPBFINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLBLMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLABSQPKELYTEM		
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPBPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLKALKGLVVMSSQLBLMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI		
7120	1991	64	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREBIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLBLMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYHGLFLEGARWDPEAFQLABSQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY		
7120	1991	64	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKBEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLBLMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYHGLFLEGARWDPEAFQLABSQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY		
7120	1991	64	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHBDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSBKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKSPSKEBL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKBEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFABEMKFSKKLSAISLGQGQGP RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGBINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREBIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLBLMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLABSQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV		

SEQ Predicted Predicted end Deginning	c Acid, E= =Glycine, ne, gine,
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence location corresponding to first amino acid sequence location corresponding to first amino acid residue of amino acid sequence location corresponding to first amino acid residue of amino acid sequence location Glutamic Acid, F=Phenylalanine, G-H=Histidine, I=Isoleucine, K=Lysin L=Leucine, M=Methionine, N=Asparace S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknow Codon, /=possible nucleotide deletation)	=Glycine, ne, gine,
location corresponding to first L=Leucine, M=Methionine, N=Asparace to first amino acid residue of amino acid sequence Codon, /=possible nucleotide delegation in the corresponding to first L=Leucine, M=Methionine, N=Asparace L=Leucine, M=Methionine, N=Asparace N=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknow Codon, /=possible nucleotide delegation	ne, gine,
corresponding to first L=Leucine, M=Methionine, N=Asparace to first amino acid residue of amino acid sequence L=Leucine, M=Methionine, N=Asparace L=Leucine, M=Methionine, N=Asparace N=Proline, Q=Glutamine, R=Arginine S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknow Codon, /=possible nucleotide delete N=possible nucleotide insertion)	gine,
to first amino acid residue of sequence to first amino acid residue of sequence p=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknow Codon, /=possible nucleotide deleteration)	
amino acid residue of S=Serine, T=Threonine, V=Valine, residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknot amino acid sequence Codon, /=possible nucleotide deleter sequence \=possible nucleotide insertion)	e.
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknot amino acid sequence Codon, /=possible nucleotide deleter sequence \=possible nucleotide insertion)	
amino acid sequence Codon, /=possible nucleotide delete sequence _=possible nucleotide insertion)	*
sequence \=possible nucleotide insertion)	
	tion,
ETRQE	
7122 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRI	LIPPFREASAK
LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRT	AALQEGLRRAV
SVPLTLAETVASLWPALQELARCGNLACRSDLQ	VAAKALEMGVF
GAYFNVLINLRDITDEAFKDQIHHRVSSLLQEAI	KTQAALVLDCL
ETRQE	
7123 1 1092 KPAVPEARSAGTSEAGRSGAEEVSCGSVSGDGA	AMRLTPRALCS
AAQAAWRENFPLCGRDVARWFPGHMAKGLKKMQ:	SSLKLVDCIIE
VHDARIPLSGRNPLFQETLGLKPHLLVLNKMDL	ADLTEQQKIMQ
HLEGEGLKNVIFTNCVKDENVKQIIPMVTELIG	RSHRYHRKENL
EYCIMVIGVPNVGKSSLINSLRRQHLRKGKATR	
MSKIQVSERPLMFLLDTPGVLAPRIESVETGLK	
VGBETMADYLLYTLNKHQRFGYVQHYGLGSACDI	
KLGKTQKVKVLTGTGNVNVIQPNYPAAARDFLQ	
LDLDVLRGHPRV	
7124 2 382 LPLTLLLAAPFAHLLLPPGHDOSPCWHPGPALS	PGTLGPLSWAM
ANSGLOLLGYFLALGGWYGI I ASTAL POWKOSS	
KVFVLESEWGGDSLGLPRDCGWSCLLHSAVRSE	
7125 166 1127 NCISEKRNYSFSMQKGKGRTSRIRRKLCGSSE	
FIBLRKWLKARKFQDSNLAPACFPGTGRGLMSQ'	
LPESCLLT\RDTVIRSYLGAYITKWKPPPSPLL	
AGHRSLLEA\YLEILPKAYTCPVCLEPEVVNLL	•
RAHVQEFFASSRDFFSSLQPLFAEAVDSIFSYS	-
RAVYL\SPGSGNAFLQSRTPVQLAPYLDLLNHS	
ETHSYEIRTTSRWRKHBEVFICYGPHDNORLFLI	
ACVYVSRGWNQLCS	BIOL AD AIMAL (I
7126 1 733 CRDMAAFIVPSPARRCSOKGSLGHLPTOPWLWAI	AMSPRGOERGT
SHSQAREPQRPGRWLLGSLQSSPGTLGQAGTASI	
QVATGRRAVQVPKGALGLALGETSPGASRGMSG	
PSPVLPSWLLEGPPPWLSIISDSGTQRPSPRRC	
WRGGRIASAEASST*TPGSGSRARSGRRSPGSRI	
PTDACA*SCVARPAGSRSSRPAAA	
7127 1311 277 GLPAMCST*KAGYYEETEGDCIPKDR*IEKRPF	KEI*RRTPRTF
AKQKQI*S*NSQKIGASEIDRGRKEADCSDAPA	
RSTQEARVSPRSNAKSANLRAVRAD*WEHFVLLI	
ICRST**K*WHQLC*PLSSL*TGLKRKLLL*VL	-
*FCQKIFATNFCNWQNLIQ*EE*KPVEYSVEN*I	•
CQSSLRDQTIVTWRM*RNYSMFRINMISSL*DGS	
PALIFTLTVPINSCCORPLPLFAHOSIKTLASSO	
LVKKRAFIHTPRSPGCSV*CKHVLVKDNKNNCV	
7128 2 5228 GRVDLWTILLGRSALRELSOIEAELNKHWRRLLI	
SSAEKVKANKDVASPLKELGLRISKFLGLDEEQ	
DYRGTRDSVKTVLQDERQSQALILKIADYYYEE	
LTYFQDERHPYRVEYADCVDKLEKELVSKYRQQI	
WETHGNLMTEROVSRWFVQCLREOSMLLEIIFL:	
· · · · · · · · · · · · · · · · · · ·	
LLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDR:	
GMDIESLHKCALDDRRELHQFAQDGLICQDMDCI	
APVILLAWALLRHTLNPEETSSVVRKIGGTAIQLI	
SLASGGNDCTTSTACMCVYGLLSFVLTSLELHTI	
CEVLADPSLPELFWGTEPTSGLGIILDSVCGMF	-
RALVSGKSTAKKVYSFLDKMSFYNELYKHKPHD	
RQTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYI	
TLFTCEIEMLLHVVSTADVIQHCQRVKPIIDLVI	HKVISTDLSIA
DCLLPITSRIYMLLQRLTTVISPPVDVIASCVNC	CLTVLAARNPA
KVWTDLRHTGFLPFVAHPVSSLSQMISAEGMNAC	GGYGNLLMNSE
QPQGEYGVT1AFLRL1TTLVKGQLGSTQSQGLVI	PCVMFVLKEML

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,	
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,	
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,	
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,	
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop	
	amino acid	sequence	Codon, /=possible nucleotide deletion,	
1	sequence	<u>-</u>	\=possible nucleotide insertion)	
	*-	·	PSYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHSSHTPS	
1	j.		LQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQPRSDGAEG	
			QGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGAH	
			GNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLG	
ł	·		NDAAAIRDAFLTRLQSK\IE\DMRIK\VMIL\EFLTVA\VETQP	
			GLIELFLNLEVKDG\SDGSKEFSLGMW\SCLHAV/VWELIDSQQ	
]]		QDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKFWENLT	
			SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSLDQP	
1			LKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLEYQM	
			LVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV	
			PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEG	
1			VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNV	
			CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQ	
1			RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTTLEV	
		•	SLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSICLPL	
•			LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQLLKT	
			LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADHTVG FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSRKML	
ĺ	· ·		QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAADTE	
]			ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLA	
ŀ			EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELDKKK	
		-	EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRYLRD	
· J			PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATGVLP	
Í			SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR	
7129	1	1054	FRRFRWRRRLH*AGPASSAGGSPGEASGTMSGELPPNINIKEPR	
	, .	•	WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRQGIV	
·			PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMNMTI	
	•		TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTVNEL	
		• •	GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAANCI	
			NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVSRIL	
	÷		MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCLVFA	
		• .	TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNKGL	
7130	2	780	HEVPSLQTSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLGRKG	
1	•		ISAKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQLLSLHRSS	
1	***		RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVVNRNLPLN	
		.·	AQIATQNYFSNFKETDGDEDDYVEIKSEEDESELELSHNRRRKS	
	•		DSKFVDADFSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYLTP	
7133			YNDSDKLNDYLWRGPSPNQQNIVQSLREKFQCLSSSSFA	
7131	805	573	AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVQFNHLEVV	
7132	1420		KLLQDYQDSYTLSETQAEAAAEALSKENLESMV	
1134	1420	1087	IDMLLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTVTA	
		İ	IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLFLI	
7133			RLIHKELSCPGSATGDQVPFKEQ	
,133	2	3648	QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLEKF	
			EEELLELHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGFVQ	
1	ĺ		RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRSRL RLPEMVGHPAFAVIFQLEYVFSSPAGVDGNAASVTSLSNLACMH	
			MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSASMS	
'			SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSRKP	
1 1	l		PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQHCL	
]		ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS	
			IAEQLQELPFTPLHAPIVVGTQTRSSAGOPSRASMVLLQSSGFP	
	į		EILDANKQPAEAVSATEPVTFNPQKEESDCLOSNEMVLQFLAFS	
	ļ		RVAQDCRGTSWPKTVYFTFQFYRFPPATTPRLQLVQLDEAGQPS	
		ł	SGALTHILVPVSRDGTFDAGSPGFOLRYMVGPGFLKPGERRCFA	
			RYLAVQTLQIDVWDGDSLLLIGSAAVQMKHLLRQGRPAVQASHE	
			ZZ T Zimannin/Quitti Ainnin	

0.00	T = 3	T		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,	
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,	
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,	
1 1 1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,	
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,	
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,	
	sequence	Dequence	\=possible nucleotide insertion)	
			LEVVATEYEQDNMVVSGDMLGFGRVKPIGVHSVVKGRLHLTLAN	
	1		VGHPCEQKVRGCSTLPPSRSRVISNDGASRFSGGSLLTTGSSRR	
			KHVVQAQKLADVDSELAAMLLTHARQGKGPQDVSRESDATRRK	
-	,		LERMRSVRLQEAGGDLGRRGTSVLAQQSVRTQHLRDLQVIAAYR	
j			ERTKAESIASLLSLAITTEHTLHATLGVAEFFEFVLKNPHNTQH	
			TVTVEIDNPELSVIVDSQEWRDFKGAAGLHTPVEEDMFHLRGSL	
J]		APQLYLRPHETAHVPFKFQSFSAGQLAMVQASPGLSNEKGMDAV	
			SPWKSSAVPTKHAKVLFRASGGKPIAVLCLTVELQPHVVDQVFR	
	1	}	FYHPELSFLKKAIRLPPWHTFPGAPVGMLGEDPPVHVRCSDPNV	
			ICETONVGPGEPRDIFLKVASGPSPEIKDFFVIIYSDRWLATPT	
	1		QTWQVYLHSLQRVDVSCVAGQLTRLSLVLRGTQTVRKVRAFTSH	
			PQELKTDPKGVFVLPPRGVQDLHVGVRPLRAGSRFVHLNLVDVD	
			CHQLVASWLVCLCCRQPLISKAFEIMLAAGEGKGVNKRITYTNP	
			YPSRRTFHLHSDHPELLRFREDSFQVGGGETYTIGLQFAPSQRV	
7134	2115	1111	GEBEILIYINDHEDKNEEAFCVKVIYQ GGEGFSYPPHVGLSLGTPLDPHYVLLEVHYDNPTYEEGLIDNSG	
, 151	2113	1111	LRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFOSEGHCTL	
			ECLEEALEAEKPSGIHVFAVLLHAHLAGRGIRLRHFRKGKEMKL	
	}		LAYDDDFDFNFQEFQYLKEEQTILPGDNLITECRYNTKDRAEMT	
			WGGLSTRSEMCLSYLLYYPRINLTRCASIPDIMEQLOFIGVKEI	
	,		YRPVTTWPF11KSPKQYKNLSFMDAMNKFKWTKKEGLSFNKLVL	
[1		SLPVNVRCSKTDNAEWSIQGMTALPPDIERPYKAEPLVCGTSSS	
			SSLHRDFSINLLVCLLLLSCTLSTKSL	
7135	2	2072	FVPRVTPRSLSLQGPKGESVGSITQPLPSSYLIFRAASESDGRC	
·			WLDALELALRCSSLLRLGTCKPGRDGEPGTSPDASPSSLCGLPA	
1 .				
1			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEBSDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAPHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAPHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKFYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSFGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPBLSDEEQDGDFVPGGESPC	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKFYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQRAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQBLHRHLSAMLSSTARAAQA	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKFYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPBLSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQBLHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK	
7136	2	418	SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKFYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK	
7136	2	418	SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKFYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM	
7136	2	418	SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKFYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET	
7136	2	418	SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK DFVPSFRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQBAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPFGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLOSPRSWFLLCVFLACQLFINHILK DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEABNLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLOSPRSWFLLCVFLACQLFINHILK DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEABNLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT	
7137	2	466	SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQRAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPFGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLOSPRSWFLLCVFLACQLFINHILK DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEABNLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP	
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP	
7137	2	466	SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG. ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEABNLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI	
7137	2	466	SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT	
7137	2	466	SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEABNLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP	
7137	2	466	SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHYSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ	
7137	2	466	SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEABNLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKBTGFHRGLGWVQFSSEEGLRNALQ	
7137	2	466 466 357	SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQBAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQBLHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEABNLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKBTGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF	
7137	2	466	SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEABNLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKBTGFHRGLGWVQFSSEEGLRNALQ	

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide		
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=		
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,		
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,		
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,		
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,		
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,		
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop		
	amino acid	sequence	Codon, /=possible nucleotide deletion,		
	sequence		\=possible nucleotide insertion)		
			QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLOSO		
			WTPKGQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNF		
			ADFMTNQCG		
7141	124	1073	LDSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL		
			VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD		
]			EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP		
1	1		VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK		
1			EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA		
1			AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP		
			GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM		
L	•		GATRSNLQPP		
7142	658	839	LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL		
			KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT		
		•	LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP		
			ECFEFIEEAKRKDGVVLVHCNA		
7143	3	773	SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ		
[GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG		
1			VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA		
l			SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR		
ĺ			KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG		
			HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI		
7144	1	988	FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR		
1			RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD		
		•	SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS		
]	·		DTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDR.		
	,		QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNQLGTII		
]			VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLLNRDGTQCLS		
[GSSDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDAFTHVYSGG		
			RDRKIYCTDLRNPDIRVLICE		

TRADOCS:1416260.1(%CSK01!.DOC)

WHAT IS CLAIMED IS:

- 1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.
- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

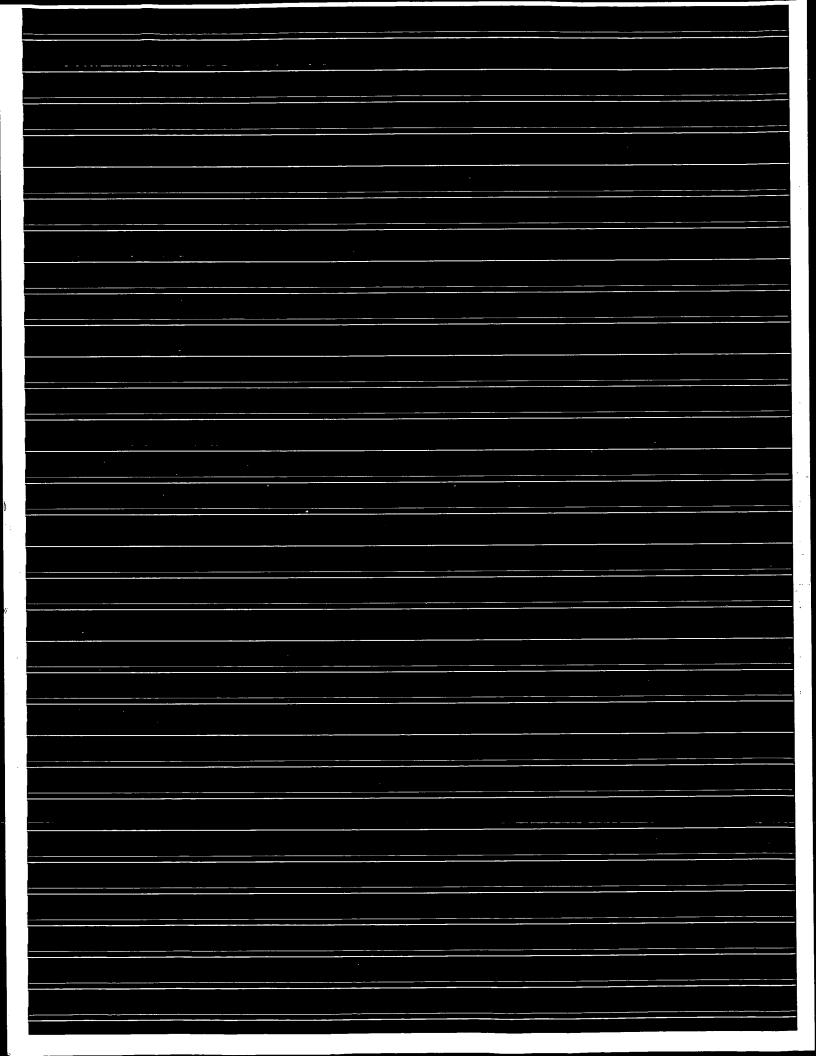
(a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.
- ·13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
 - 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
 - a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
 - b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
 - 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
 - a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
 - b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
 - 19. A method of producing the polypeptide of claim 10, comprising,
 - a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and
 - b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.

- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.



INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

IPC(7)	SIFICATION OF SUBJECT MATTER : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82	2, 15/85; C	07K 14/00	
US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350 According to International Patent Classification (IPC) or to both national classification and IPC				
	DS SEARCHED	itional class	incation and II C	
	cumentation searched (classification system followed last) 36/23.1; 435/320.1, 455, 468, 530/300, 350	by classific	ation symbols)	
Documentation	on searched other than minimum documentation to the	extent that	such documents are included in	n the fields searched
Electronic da MEDLINE, I	ta base consulted during the international search (nam EAST	e of data b	ase and, where practicable, sear	rch terms used)
	UMENTS CONSIDERED TO BE RELEVANT			
Category *	Citation of document, with indication, where a			Relevant to claim No.
A	WAJIMA et al. The cDNA cloning and transient ex hydroxysteroid dehydrogenase of chickens. Gene. 19			1-11, 13-16, and 19-26
A	US 5,175,095 A (MARTINEAU et al) 29 December columns 3-18.	r 1992 (29.	12.1992), see especially	1-11, 13-16, and 19-26
A	Database PubMed, ID No. 2393392, FREUDENST inhibitor of metalloproteinase: sequence and express Biophys. Res. Commun. August 1990. Vol.171. No.	ion in bovi	ne ovarian tissue. Biochem.	1-11, 13-16, and 19-26
A,P	Database PubMed, ID No. 10919256, HENNEBOL generation and characterization of an ovary-selective library. Endocrinology. August 2000. Vol.141. No.	D et al. O	vary-selective genes I: the ntary deoxyribonucleic acid	1-11, 13-16, and 19-26
A .	Database PubMed, ID No. 2760883, BEIL et al. Synthe baboon (Papio anubis). J. Reprod. Fertil. July 19 Abstract.			1-11, 13-16, and 19-26
A,P .	Database PubMed, ID No. 10830289, HINSHELWO upstream of the human CYP19 (aromatase) gene me transgenic mice. Endocrinology. June 2000. Vol.14	diates ovar	y-specific expression in	1-11, 13-16, and 19-26
				ļ
Further	documents are listed in the continuation of Box C.		See patent family annex.	:
• S _I	pecial categories of cited documents:	"T"	later document published after the inte	
	defining the general state of the art which is not considered to be lar relevance	4 V*	date and not in conflict with the applic principle or theory underlying the inve	ntion
• •	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive when the document is taken alone			
establish t	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) document of particular relevance; the claimed invention or considered to involve an inventive step when the document combined with one or more other such documents, such or		when the document is	
"O" document	referring to an oral disclosure, use, exhibition or other means		being obvious '3 a person skilled in the	
	published prior to the international filing date but later than the ate claimed	-&-	document member of the same patent	family
Date of the ac	ctual completion of the international search		nailing of the international search	ch report
	illing address of the ISA/US missioner of Patents and Trademarks PCT	Authorize Azh Michael	woofficer area Woodward	Allen for
	hingson, D.C. 20231 . (703)305-3230	Telephon	e No. (703) 308-0196	/)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)				
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:				
Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:				
2. Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:				
3. Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).				
Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)				
This International Searching Authority found multiple inventions in this international application, as follows: This includes 4 invention Groups and 3572 sequence species				
1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims. 2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite				
payment of any additional fee. 3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:				
4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:				
Remark on Protest The additional search fees were accompanied by the applicant's protest.				
No protest accompanied the payment of additional search fees.				

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

THIS PAGE BLANK (USPTO)